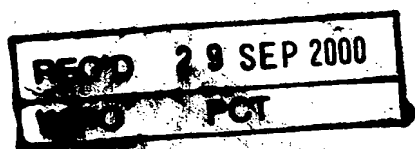




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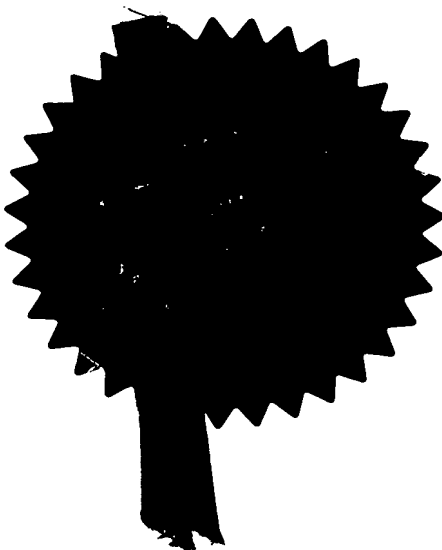
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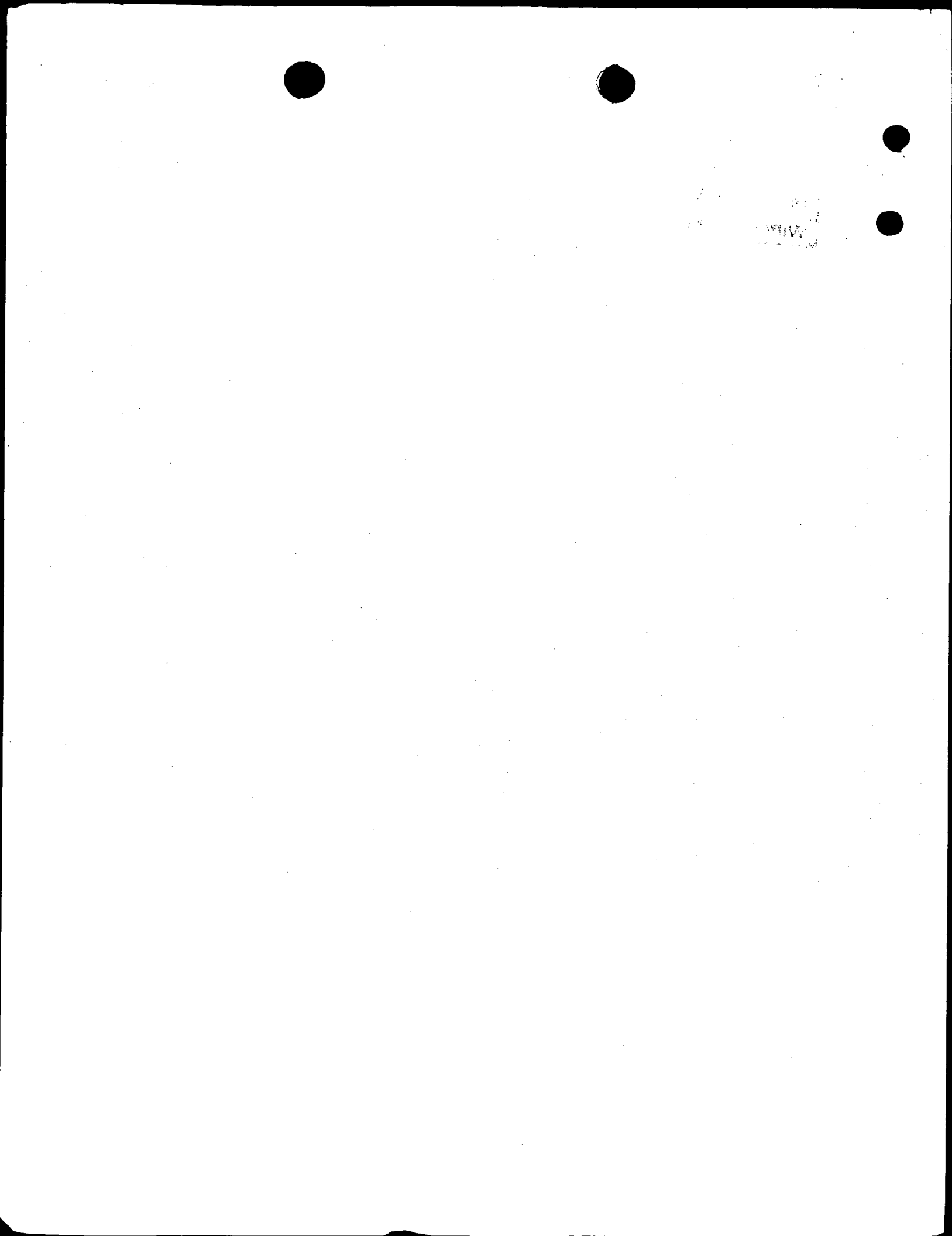
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SECTION 30(1)(A) APPLICATION FILED 21/8/2000

Patents ADP number (if you know it)

7288202001

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4. Title of the invention

"ESSENTIAL GENES AND ASSAYS RELATING THERETO"

5. Name of your agent (if you have one)

CRUIKSHANK & FAIRWEATHER

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ESSENTIAL GENES AND ASSAYS RELATING THERETO

The present invention relates to screening assays particularly for pesticides based on the use of essential genes/proteins, as well as the novel genes/proteins themselves. It also relates to screening assays for compounds with therapeutic use in cancer therapy.

Crop destruction by pests such as insects results in a considerable economic loss and serious reduction in productivity. Chemical pesticides are typically used in order to control the pests and reduce crop loss. However pesticide development has generally been less than controlled or focussed, such that the biochemical or genetical functions of the pesticide have not been a major concern, but rather simply whether or not the pesticide was effective ie. killed the pests.

However, increasing environmental concerns and development of resistance to existing pesticides has led to a more rational approach to pesticide development being voiced.

It is amongst the objects of the present invention to provide a more rational approach to pesticide development by providing pesticide screening assays based on the identification of genes/proteins which are considered to be essential to the pest.

Each of the genes identified are shown to be essential for cell or organism survival and/or reproduction based on the evidence of the effect of a complete loss of gene function caused by a mutation. Since the action of the protein encoded by such a gene is essential for cell and/or organism survival or reproduction, it follows that chemical interference with the action or production of the protein will mimic the effect of mutation and result in the death of cells and the organism (or failure to reproduce). Thus chemical interference with the action of each essential gene and protein represents a way to kill cells and organisms, and specifically insects.

The present inventors have used genetic techniques in order to study a model pest, namely *Drosophila*. As a result of these studies, the present inventors have identified a considerable number of essential genes/proteins, which may be used in functional and/or ligand binding assays for screening for pesticides.

Thus, in a first aspect the present invention provides a screening assay for identifying compounds which have a physiological effect on an organism, the assay comprising the steps of:

- a) reacting a test compound with a protein encoded by an essential gene from the organism; and
- b) detecting any physiological effect the compound has on the protein.

A physiological effect is one which alters the function and/or activity of the protein. Typically the assay is designed to be used to screen for compounds which are harmful or pesticidal. However, the assay may be used to screen for other effects, such as beneficial or therapeutic effects.

An essential gene is one for which it has been determined that the expression of a functional protein is necessary in order to avoid a lethal or semi-lethal phenotype. A lethal phenotype is defined as a phenotype characterised by organism death due to cellular or system failure at some developmental stage, or by the failure of adults that do occur to leave any viable offspring. A semi-lethal phenotype is characterised by low fecundity (the tendency to produce few offspring compared to wildtype), and frequently by short lifespan.

Studies carried out by the present inventors have identified over 900 distinct fly lines, in the model organism, *Drosophila*, which display a lethal or semi-lethal phenotype. Fly lines which display such a lethal or semi-lethal phenotype have been generated using the technique of P-element transposon-tagged insertion (1) Torok, T.G. Tick, M. Alvarado and I. Kiss, 1993 P-lacW Insertional

Mutagenesis on the second chromosome of *Drosophila melanogaster*: Isolation of lethals with different overgrowth phenotypes. Genetics 135: 71 - 80; (2) Dèak, P., M.M. Omar, R.D.C. Saunders, M. Pal, O. Komonyi, J. Szidonya, P. Maroy, Y. Zhang, M. Ashburner, P. Benos, C. Savakis, I. Siden-Kiamos, C. Louis, V.N. Bolshakov, F.C. Kafatos, E. Madueno, J. Modolell and D.M. Glover, 1998 P element insertion alleles of essential gens on the third chromosome of *Drosophila melanogaster*: Correlation of physical and cytogenetics maps in chromosomal region 86E-87F. Genetics 14: 1697 - 1722). Using the technique of transposon rescue, it has been possible to determine the nucleotide sequence surrounding the site of transposon insertion. The partial sequences of regions surrounding the P-element insertion site from distinct fly lines are identified herein as SEQ ID NOS. 1 - 902. It is immediately evident to one skilled in the art how to use this information to clone a larger portion of nucleic acid containing the complete gene and thereafter express the encoded protein. Such techniques are disclosed for example in Sambrook et al (1989). It will be appreciated that the P-element may be inserted within a particular gene, or in regulatory sequences associated with a gene, such that P-element insertion affects expression of the gene, resulting in the lack of the expressed protein or expression of a dysfunctional form.

In a further aspect the present invention provides a polynucleotide fragment comprising nucleotides capable of encoding or partially encoding an essential gene for use in assays of the present invention. More particular the present invention provides means for obtaining essential proteins for use in assays of the present invention.

"Polynucleotide fragment" as used herein refers to a chain of nucleotides such as deoxyribose nucleic acid (DNA) and transcription products thereof, such as RNA. Naturally, the skilled addressee will appreciate the whole naturally occurring PoEV genome is not included in the

definition of polynucleotide fragment.

The polynucleotide fragment can be isolated in the sense that it is substantially free of biological material with which the whole genome is normally associated *in vivo*. The isolated polynucleotide fragment may be cloned to provide a recombinant molecule comprising the polynucleotide fragment. Thus, "polynucleotide fragment" includes double and single stranded DNA, RNA and polynucleotide sequences derived therefrom, for example, subsequences of said fragment and which are of any desirable length. Where a nucleic acid is single stranded then both a given strand and a sequence complementary thereto is within the scope of the present invention.

In general, the term "expression product" refers to both transcription and translation products of said polynucleotide fragments. When the expression product is a "polypeptide" (i.e. a chain or sequence of amino acids displaying a biological activity substantially similar to the biological activity of an essential protein, it does not refer to a specific length of the product as such. Thus, the skilled addressee will appreciate that "polypeptide" encompasses *inter alia* peptides, polypeptides and proteins. The polypeptide if required, can be modified *in vivo* and *in vitro*, for example by glycosylation, amidation, carboxylation, phosphorylation and/or post-translational cleavage.

The present invention further provides an isolated polynucleotide fragment capable of specifically hybridising to a related polynucleotide sequence from another species. In this manner, the present invention provides probes and/or primers for use in *ex vivo* and/or *in situ* detection and expression studies. Typical detection studies include polymerase chain reaction (PCR) studies, hybridisation studies, or sequencing studies. In principle any specific polynucleotide sequence from the identified sequences may be used in detection and/or expression studies.

"Capable of specifically hybridising" is taken to mean that said polynucleotide fragment preferably hybridises to a related or similar polynucleotide sequence in preference to unrelated or dissimilar polynucleotide sequences.

The invention includes polynucleotide sequence(s) which are capable of specifically hybridising to an essential polynucleotide sequence or to a part thereof without necessarily being completely complementary to said related polynucleotide sequence or fragment thereof. For example, there may be at least 50% preferably at least 75%, most preferably at least 90% or at least 95% complementarity. Of course, in some cases the sequences may be exactly complementary (100% complementary) or nearly so (e.g. there may be less than 10, preferably less than 5 mismatches). Thus, the present invention also provides anti-sense or complementary nucleotide sequence(s) which is/are capable of specifically hybridising to the disclosed DNA sequence. If a specific polynucleotide is to be used as a primer in PCR and/or sequencing studies, the polynucleotide must be capable of hybridising to related nucleic acid and capable of initiating chain extension from 3' end of the polynucleotide, but not able to correctly initiate chain extension from unrelated sequences.

If a polynucleotide sequence of the present invention is to be used in hybridisation studies to obtain a related sequence from another organism the polynucleotide sequence should preferably remain hybridised to a sample polynucleotide under stringent conditions. If desired, either the test or sample polynucleotide may be immobilised. Generally the test polynucleotide sequence is at least 10 or at least 50 bases in length. It may be labelled by suitable techniques known in the art. Preferably the test polynucleotide sequence is at least 200 bases in length and may even be several kilobases in length. Thus, either a denatured sample or test sequence can be first bound to a support. Hybridization can be effected at a temperature of between 50 and 70°C in double

strength SSC (2xNaCl 17.5g/l and sodium citrate (SC) at 8.8g/l) buffered saline containing 0.1% sodium dodecyl sulphate (SDS). This can be followed by rinsing of the support at the same temperature but with a buffer having a reduced SSC concentration. Depending upon the degree of stringency required, and thus the degree of similarity of the sequences, such reduced concentration buffers are typically single strength SSC containing 0.1%SDS, half strength SSC containing 0.1%SDS and one tenth strength SSC containing 0.1%SDS. Sequences having the greatest degree of similarity are those the hybridisation of which is least affected by washing in buffers of reduced concentration. It is most preferred that the sample and inventive sequences are so similar that the hybridisation between them is substantially unaffected by washing or incubation in standard sodium citrate (0.1 x SSC) buffer containing 0.1%SDS.

Oligonucleotides may be designed to specifically hybridise to essential nucleic acid. They may be synthesised, by known techniques and used as primers in PCR or sequencing reactions or as probes in hybridisations designed to detect the presence of related material in a sample. The oligonucleotides may be labelled by suitable labels known in the art, such as, radioactive labels, chemiluminescent labels or fluorescent labels and the like. Thus, the present invention also provides oligonucleotide probes and primers for use in detecting essential genes.

The term "oligonucleotide" is not meant to indicate any particular length of sequence and encompasses nucleotides of preferably at least 10b (e.g. 10b to 1kb) in length, more preferably 12b-500b in length and most preferably 15b to 100b.

The oligonucleotides may be determined from the sequences shown in SEQ ID Nos. 1-902 and may be manufactured according to known techniques. They may have substantial sequence identity (e.g. at least 50%, at least 75%, at least 90% or at least 95% sequence identity) with

one of the strands shown therein or an RNA equivalent, or with a part of such a strand. Preferably such a part is at least 10, at least 30, at least 50 or at least 200 bases long. It may be an ORF or a part thereof.

Oligonucleotides which are generally greater than 30 bases in length should preferably remain hybridised to a sample polynucleotide under one or more of the stringent conditions mentioned above. Oligonucleotides which are generally less than 30 bases in length should also preferably remain hybridised to a sample polynucleotide but under different conditions of high stringency. Typically the melting temperature of an oligonucleotide less than 30 bases may be calculated according to the formula of; 2°C for every A or T, plus 4°C for every G or C, minus 5°C . Hybridization may take place at or around the calculated melting temperature for any particular oligonucleotide, in 6 x SSC and 1% SDS. Non specifically hybridised oligonucleotides may then be removed by stringent washing, for example in 3 x SSC and 0.1% SDS at the same temperature. Only substantially similar matched sequences remain hybridised i.e. said oligonucleotide and corresponding PoEV nucleic acid.

When oligonucleotides of generally less than 30 bases in length are used in sequencing and/or PCR studies, the melting temperature may be calculated in the same manner as described above. The oligonucleotide may then be allowed to anneal or hybridise at a temperature around the oligonucleotides calculated melting temperature. In the case of PCR studies the annealing temperature should be around the lower of the calculated melting temperatures for the two priming oligonucleotides. It is to be appreciated that the conditions and melting temperature calculations are provided by way of example only and are not intended to be limiting. It is possible through the experience of the experimenter to vary the conditions of hybridisation and thus anneal/hybridise oligonucleotides at temperatures above their calculated melting temperature. Indeed this

can be desirable in preventing so-called non-specific hybridisation from occurring.

It is possible when conducting PCR studies to predict an expected size or sizes of PCR product(s) obtainable using an appropriate combination of two or more PoEV oligonucleotides, based on where they would hybridise to the sequences SEQ ID Nos. 1-902. If, on conducting such a PCR on a sample of PoEV DNA, a fragment of the predicted size is obtained, then this is predictive that the DNA is PoEV.

The partial sequences of the essential genes, identified as SEQ ID NOS. 1 - 902, have been analysed in order to ascertain if there is any homology to previously identified sequences contained in nucleotide sequence databases such as the GENBANK and EMBL databases. Database searching has ascertained that a number of the nucleotide sequences have been previously identified. However, the lack of the gene/protein associated with the sequence may not have been suggested to result in a lethal/semi-lethal phenotype. Moreover, a number of the sequences appear to show no significant database matches and others match only sequences for which no putative function has been ascribed.

Table 1 discloses details of the sequences identified by the present invention which display a match with sequences already deposited in a nucleic acid database.

As described above, genes described herein generally fall into two classes:

- A. Genes encoding proteins with recognizable similarity to proteins of known functional class e.g. protein kinases, neurotransmitter receptors; and
- B. Genes encoding proteins of unknown function.

Assays for proteins of known function are known in the art. A list of typical assays for some of the major classes of protein that are estimated to represent likely insecticide targets is exemplified herein. Where a functional assay is available, it is to be preferred to a ligand binding assay.

Assays for proteins of unknown function rely on assessment of ligand binding only.

The typical purpose of the assays described herein is to select for pesticides/insecticides, though in some cases lead compounds may have therapeutic activity, such as in inducing cell death which may be applicable in cancer therapy. A relative specificity of action based on species groups or species may be achieved based on differences in protein sequence and structure, differences in protein expression, variations in development role and/or variations in degree of redundancy with related proteins.

The information disclosed herein teaches that the loss of the function of each of the proteins encoded by the genes comprising the partial sequences identified by SEQ 1D Nos. 1-902, causes death of insects at some point during development, or causes reproductive failure. An insecticidal chemical compound will therefore be a compound that strongly modulates, either agonistically or antagonistically, the activity of such a protein. Thus, where the purpose of the assay is selection of insecticides, chemicals will be sought that interfere with the normal function of the protein.

For proteins of known function with available functional assays, application of these assays will rapidly select a set of chemicals having the desired effect on the protein in the appropriate assay system.

In a second step, each member of the set of chemicals may then be tested directly for killing activity on insects. *Drosophila* itself is a convenient assay insect. In a typical fly killing assay, young flies are kept without fluid for a time, then transferred to vials containing filter paper dosed with a solution of the chemical to be tested. A range of chemical concentrations is used. After a defined treatment, flies are returned to normal conditions and observed. Rate of killing and percentage lethality are the parameters assessed.

In a third step, compounds with very effective killing activity on *Drosophila* are then tested on pest species or accepted model pest related insects. For example, aphid species may be maintained on isolated lettuce plants: the time of death and the numbers of aphids falling dead onto paper traps beneath the plants after spraying with defined doses of the candidate chemical is assessed. As another example, lepidopteran pest larvae may be maintained on artificial media or plant leaves, which are treated with defined doses of chemicals, and survival is assessed.

For proteins of unknown function, the ligand binding assays outlined herein will also define a group of candidate chemicals. However, this group is likely to be large, since binding may occur to a number of different sites on the exposed surface of the protein, and binding alone does not predict the effect of ligand binding on the activity of the protein. Stringent selection among the candidate chemicals for those with the greatest affinity will define a set of chemicals small enough to be tested for insect killing. The use of *Drosophila* as a test organism enables large numbers of compounds to be assessed. Therefore the same procedure may be used as for proteins for which functional assays are available.

An alternative or additional procedure is to use a cellular killing assay as an intermediate step. For example, a gene of unknown function can be examined for location and timing of gene expression in tissues throughout development. The primary sites of tissue death may be determined by apoptosis assays or direct observation. In many cases, particular cell types e.g. nerve cells, can be defined as subject to death when the protein is not expressed. Appropriate cell types can be isolated from the appropriate tissue and developmental stage of *Drosophila* or a larger insect. Effects of candidate chemicals from the binding assay screen on survival of these cells in culture may then be ascertained, using commercially available live/dead cell assessment

methods.

A further alternative or additional procedure is to express the protein target in a cell which has been manipulated genetically to contain a sensor for calcium ions, cyclic AMP or other components of cell signaling pathways. This may be achieved, for example, by generating transgenic *Drosophila* containing the gene encoding the protein with its expression driven by a promoter that is utilized in the cell type of choice. Alternatively, permanent cell lines of any suitable origin may be transfected, and lines expressing the protein permanently selected. In many cases, expression of an unknown protein will cause a shift in the level of cell signaling components, which will be detected by the sensor and can be read, for example, as a fluorescent or luminescent signal. The difference between the protein-expressing cells and control cells forms the basis of the assay. Effects of chemicals on the difference between protein expressing and control lines are assessed.

Proteins for all the assays described can be produced by cloning the gene into plasmid vectors that allow high expression in a system of choice e.g. insect cell culture, yeast, animal cells, *Escherichia coli*. To enable effective purification of the protein, a vector may be used that incorporates an epitope tag onto the protein on synthesis. A number of such vectors and purification systems are commercially available.

The polynucleotide fragment can be molecularly cloned into a prokaryotic or eukaryotic expression vector using standard techniques and administered to a host. The expression vector is taken up by cells and the polynucleotide fragment of interest expressed, producing protein.

The cloning and expression of a recombinant "essential" polynucleotide fragment also facilitates in producing anti-"essential" antibodies and fragments thereof (particularly monoclonal antibodies).

It will be understood that for the particular polypeptides embraced herein, natural variations can exist between individuals or between members of the family. These variations may be demonstrated by (an) amino acid difference(s) in the overall sequence or by deletions, substitutions, insertions, inversions or additions of (an) amino acid(s) in said sequence. All such derivatives showing active polymerase and/or envelope polypeptide physiological and/or immunological activity are included within the scope of the invention. For example, for the purpose of the present invention conservative replacements may be made between amino acids within the following groups:

- (I) Alanine, serine, threonine;
- (II) Glutamic acid and aspartic acid;
- (III) Arginine and leucine;
- (IV) Asparagine and glutamine;
- (V) Isoleucine, leucine and valine;
- (VI) Phenylalanine, tyrosine and tryptophan

Moreover, recombinant DNA technology may be used to prepare nucleic acid sequences encoding the various derivatives outlined above.

As is well known in the art, the degeneracy of the genetic code permits substitution of bases in a codon resulting in a different codon which is still capable of coding for the same amino acid, e.g. the codon for amino acid glutamic acid is both GAT and GAA. Consequently, it is clear that for the expression of polypeptides from nucleotide sequences shown in SEQ. ID Nos. 1-902 or fragments thereof, use can be made of a derivative nucleic acid sequence with such an alternative codon composition different from the nucleic acid sequence shown in said Figure 1.

The polynucleotide fragment of the present invention are preferably linked to regulatory control sequences. Such control sequences may comprise promoters, operators, inducers, enhancers, ribosome binding sites, terminators etc. Suitable control sequences for a given host may be selected by those of ordinary skill in the art.

A polynucleotide fragment according to the present invention can be ligated to various expression controlling sequences, resulting in a so called recombinant nucleic acid molecule. Thus, the present invention also includes an expression vector containing an expressible nucleic acid molecule. The recombinant nucleic acid molecule can then be used for the transformation of a suitable host. Such hybrid molecules are preferably derived from, for example, plasmids or from nucleic acid sequences present in bacteriophages or viruses and are termed vector molecules.

Specific vectors which can be used to clone nucleic acid sequences according to the invention are known in the art (e.g. Rodriguez, R.L. and Denhardt, D.T., Edit., Vectors: a survey of molecular cloning vectors and their uses, Butterworths, 1988).

The methods to be used for the construction of a recombinant nucleic acid molecule according to the invention are known to those of ordinary skill in the art and are inter alia set forth in Sambrook, et al. (Molecular Cloning: a laboratory manual Cold Spring Harbour Laboratory, 1989).

The present invention also relates to a transformed cell containing the polynucleotide fragment in an expressible form. "Transformation", as used herein, refer to the introduction of a heterologous polynucleotide fragment into a host cell. The method used may be any known in the art, for example, direct uptake, transfection transduction or electroporation (Current Protocols in Molecular Biology, 1995. John Wiley and Sons Inc.). The heterologous polynucleotide fragment may be maintained through autonomous replication or alternatively, may be

integrated into the host genome. The recombinant nucleic acid molecules preferably are provided with appropriate control sequences compatible with the designated host which can regulate the expression of the inserted polynucleotide fragment, e.g. tetracycline responsive promoter, thymidine kinase promoter, SV-40 promoter and the like.

Suitable hosts for the expression of recombinant nucleic acid molecules may be prokaryotic or eukaryotic in origin. Hosts suitable for the expression of recombinant nucleic acid molecules may be selected from bacteria, yeast, insect cells and mammalian cells.

1. Binding assays for proteins of unknown function

Ligands for any protein may be discovered by direct binding assays. In order to select true lead chemicals for insecticide or therapeutic development, these must be followed by insect killing assays or other functional assays as indicated in pages 8 and 9 above.

In binding assays one partner molecule is immobilized, and the other is labeled in some fashion (e.g. using a fluorescent tag, or by the incorporation of a radioactive isotope) and added free in solution. After incubation to allow molecular interaction, and a wash step, the amount of bound ligand is measured using an appropriate detection system. This may be used in a qualitative mode at first. Ligands showing significant binding may then be studied further by ensuring that the protein is in excess, and carrying out experiments with a dilution series of the ligand at a set of known concentrations.

In the assay taught herein, the protein encoded by the essential insect gene is identified, and the chemical ligand is unknown. Therefore the protein may be purified using an affinity system and immobilized. The chemical ligands will be labeled, incubated with the immobilized protein, washed, and the amount of retained label assessed.

Proteins may conveniently be immobilized using an epitope or other affinity tags provided by the expression vector (see above), on a support material to which the appropriate antibody or binding agent for the tag is attached. The support material may be nitrocellulose membrane, Sephadex or other type of protein purification column support, or specialized beads such as those commercially available from Dynal or Promega. Alternatively, the protein may for example be biotinylated to a low level, and the same support materials derivatised with streptavidin (which has a very high affinity for biotin) used. Further, proteins may be modified chemically in a variety of ways, and covalently attached to support materials.

Nucleic acid or peptide ligands may conveniently be radioactively labeled by standard procedures. Organic chemical ligands may also be provided in radioactively labeled form. However, a more convenient labeling system for large scale screening by binding assays is the use of chemicals that are tagged with oligonucleotide sequence labels, or by other means. This allows many chemicals to be tested together initially, since each can be identified by the use of a PCR based detection system.

Monoclonal antibodies raised against a particular protein may be used to select chemicals that bind to particular regions of the protein - the epitope recognised by the antibody. In such an assay, chemicals are assessed for displacement or reduction in binding of the antibody. Remaining bound antibody is detected by a standard fluorescently labeled second antibody.

2. Binding assays for proteins with known ligands

For proteins belonging to families for which chemical or peptide ligands can be predicted, binding assays may be employed in a ligand-competition mode. This measures chemical interaction with the site on the protein at which the natural ligand binds, and is thus going to give a

higher rate of significant hits. This type of assay is also more quantitative.

Examples of typical known ligands which would be labeled (typically radioactively) and used in displacement assays are: pharmacological agonists and antagonists, activators and inhibitors, neurotransmitters, growth factors and cytokines, cAMP, cGMP, enzyme cofactors such as NAD and FAD, regulatory polypeptides (e.g. calmodulin) and other subunits of multicomponent proteins.

A typical assay relies on the generation of purified protein as discussed above. In general, binding assays rely on labeled ligand, usually radiolabeled, to enable competition for the binding site to be detected. A set concentration (enough to saturate the binding site) of labeled ligand is incubated with a purified sample containing the purified protein. In a parallel tube, the test chemical is also added. Bound ligand/protein complexes are washed (to remove free ligand), precipitated e.g. by TCA, collected with a cell harvester (for example) and the level of radioactivity measured. Displacement can be observed as a reduction in the amount of radioactivity detected in the assay. Enhancement of binding can also be observed in this type of assay, where radioactivity levels are increased - this indicates activity of the test chemical near to but not competing with the site of ligand interaction.

Examples of some possible functional assays

1. Kinases

Kinases are enzymes that transfer the terminal phosphate group of ATP to their substrate molecule. These enzymes have been shown to be involved in many cell processes including signal transduction, apoptosis and regulation of the cell cycle. Protein kinases are the largest known protein family and have been characterised in mammals, plants, fungi and microorganisms.

An assay of kinase activity generally requires two distinct steps: (1) transfer of the (labeled) terminal phosphoryl group of the nucleoside triphosphate donor to the substrate and (2) separation of the phosphorylated product from unutilized nucleotide. Step 1 is generally carried out in solution, with both the enzyme and the substrate in the liquid phase. Step 2 is usually accomplished by trichloroacetic acid (TCA) precipitation, by sodium dodecyl sulphate (SDS) gel electrophoresis, or by binding the labeled product to a solid support such as phosphocellulose paper or nitrocellulose membrane. These steps are then followed by detection of the amount of labeled phosphoryl that has been transferred to the substrate.

Step 1 can also be carried out with either the enzyme or the substrate immobilized on a solid support. For example, complex protein mixtures can be fractionated by SDS gel electrophoresis, blotted onto membrane, and then tested as potential substrates by incubating the membrane with a non-specific blocking agent followed by the desired protein sample plus labeled ATP.

Another variation on this type of assay involves detection of the phosphorylated form of a protein using a monoclonal antibody directed to the phosphorylated form. The amount of phosphorylation may then be assayed in an enzyme-linked immunosorbent assay (ELISA).

Typical assay of kinase activity

The kinase activity of a particular sample or protein can be assayed using histone H-1 as a substrate to which the kinase transfers phosphate. For example in a reaction volume of 100 μ l containing 30 mM HEPES (pH 7.5), 5 μ M MgCl₂, 40 μ g of histone, 100 μ M CaCl₂, 10 μ M [γ -³²P] ATP and 1.25 mg/ml phosphatidylserine. Assays are started by the addition of 2.5m-units (arbitrary units, dilution series) of sample, incubated at 30°C for 10 minutes and terminated either by spotting on to P81 paper (Whatman) or by the

addition of Laemmli buffer. Spotting onto Whatman paper is followed by extensive washing in 75 mM orthophosphoric acid. The papers are then washed in ethanol, dried and incorporated radioactivity determined either by autoradiography, scintillation spectroscopy or phosphoimaging. After the addition of Laemmli sample buffer the sample is resolved on a 10% SDS-PAGE gel; the gel is dried and then autoradiographed. The amount of incorporated nucleotide is then determined using either autoradiography or phosphoimaging. It may be essential to add certain co-factors that activate a particular kinase e.g. Calcium-dependant kinases would require calcium within the assay.

Such an assay is described for example in Wilkinson SE, Parker P and Nixon JS (1993) *Biochem. J.*, 294, 335-337.

2. Phosphatases

Protein phosphorylation provides one means of regulating cellular processes. Protein dephosphorylation by protein phosphatases plays an equally important role. Phosphatases are involved in the removal of the phosphoryl group from proteins that have been phosphorylated by kinases.

Typical assay for phosphatase activity

Assays for phosphatase activity can be carried out in the same way as a kinase assay. This would involve the pre-phosphorylation of histone by a kinase in the presence of radioactive ATP, followed by desphorylation by the test protein. The sample is then spotted onto P81 paper and the amount of radioactive ATP still incorporated is measured as previously described.

3. Adenylyl cyclases - cAMP formation from ATP

Measurement of intracellular cAMP.

Cyclic adenosine 3',5' monophosphate (cAMP) can be measured in tissue slices, dissociated tissue, cultured cells and membrane preparations.

Two procedures are currently used for measurement of cAMP: (1) radioimmunoassay and (2) the cAMP binding protein method

Radioimmunoassay uses antibody raised to acetylated cAMP and involves competition between cAMP in the sample and ^{125}I -labelled cAMP (Steiner, A.L., Wehmann, R.E., Parker, C.W. and Kipnis, D.M. (1972). *Adv. Cyc. Nucleotide Res.*, 2, 51.). Following an overnight incubation, unbound cAMP is removed using charcoal. cAMP levels are quantified by comparison with a cAMP standard curve and expressed relative to protein content of sample. This method is sensitive in the femtomolar range if the sample cAMP and the standard curve cAMP are acetylated before assay. Kits are available commercially (Amersham).

The cAMP binding protein method is based on competition between ^3H -labelled cAMP and sample cAMP for binding sites on the regulatory subunit of cAMP-dependent protein kinase (Gilman, A.G. (1970). *Proc. Natl. Acad. Sci. USA*, 67, 305.). The procedure is analogous to radioimmunoassay but is more rapid because competition equilibrium is achieved in a 2 hour incubation. cAMP-dependent protein kinase preparation (Sigma) and binding protein assay kits (Amersham) are available commercially.

Measurement of adenylyl cyclase activity.

Adenylyl cyclase catalyses the formation of cAMP from ATP in the presence of Mg^{2+} . The main methods are: (1) the measurement of ^{32}P -labelled cAMP formed from ^{32}P -labelled ATP and (2) the measurement of cAMP formed in a non-labelled reaction using either the radioimmunoassay or the binding protein assay.

Assay for adenylyl cyclase using ^{32}P -labelled ATP: Radioactively labelled cAMP produced from ^{32}P -ATP in an *in vitro* reaction is separated from unreacted substrate and radioactive contaminants by sequential chromatography steps on Dowex and alumina columns and measured by liquid scintillation counting (Salomon, Y., Londos, C., and Rodell, M. (1974). *Anal.Biochem.*, 58, 541.). Crude or partially purified adenylyl cyclase samples may contain contaminating activities that interfere with the assay. Problems with nucleoside triphosphatase are minimised using a high substrate concentration in the adenylyl cyclase reaction and by including phosphoenol pyruvate and pyruvate kinase as an ATP regenerating system. Degradation of ^{32}P -labelled cAMP can be prevented by including a high concentration of unlabelled cAMP in the reaction. The enzymatic reaction is terminated by addition of unlabelled ATP and by boiling for 2 minutes. Addition of $[^3\text{H}]\text{cAMP}$ as a recovery label allows correction for differences in the performance of the individual chromatography columns. To isolate cAMP from the adenylyl cyclase reactions the samples are first layered on a column of Dowex AG 50 WX 4 resin (200-400 mesh, H^+ form) equilibrated in water. The cAMP has a greater affinity for the resin than ATP so the bulk of the $[^{32}\text{P}]\text{ATP}$ can be washed off the column with water before eluting the cAMP directly onto an alumina column equilibrated with 0.1 M imidazole HCl, pH 7.5. The remaining $[^{32}\text{P}]\text{ATP}$ binds to the alumina and the labelled cAMP is eluted using imidazole buffer. Samples are counted in ^{32}P and ^3H channels using a scintillation counter. Measurement of total $[^{32}\text{P}]\text{ATP}$ and $[^3\text{H}]\text{cAMP}$ allows calculation of pmols of cAMP present in the sample. Adenylyl cyclase enzymatic activities are expressed as pmol cAMP formed per min per mg protein in the sample. The Dowex and alumina columns must be calibrated before use to determine elution profiles of ATP and cAMP but they may be regenerated after each assay and used repeatedly. The assay is sensitive, relatively simple and may be completed

in one day. Apparatus for the double chromatography should be constructed from perspex to reduce risk from exposure to radioactivity.

Non-labelled adenylate cyclase reactions. Reactions contain ATP, Mg^{2+} , an ATP regenerating system and an inhibitor of cAMP phosphodiesterase such as 3-isobutyl-1-methylxanthine (IBMX). Reactions are terminated by boiling and cAMP formed is measured by radioimmunoassay or cAMP protein binding assay.

4. Guanylyl cyclases - cGMP formation from GTP

Measurement of guanylate cyclase activity.

Guanylate cyclase catalyses the hydrolysis of guanosine triphosphate (GTP) to cyclic guanosine 3',5' monophosphate (cGMP) in a reaction analogous to that of adenylate cyclase. Methodology used in the assay of guanylate cyclase activity is essentially the same as that for adenylate cyclase. Manganese is required as a cofactor for guanylate cyclase activity. Reactions are terminated by addition of HCl and boiling for 3 minutes.

Assay for guanylate cyclase using [^{32}P] GTP: This method depends on the separation of labelled-cGMP from unreacted substrate [^{32}P] GTP by sequential chromatography (Karczewski, P. and Krause, E.G. (1978). *Acta Biol. Med. Ger.*, 37, 961.). Dowex 50 cation exchange columns and alumina columns are prepared and calibrated in exactly the same way as for the separation of cAMP except that the Dowex columns should be longer. cGTP is eluted from the alumina column with 0.2M ammonium formate buffer.

Non-labelled guanylate cyclase reactions. Reactions contain GTP, Mn^{2+} , a GTP regenerating system and IBMX. Reactions are terminated by boiling and cGMP formed is measured by radioimmunoassay using antibody against acetylated cGMP. Kits are available commercially (Amersham).

5. Phosphodiesterases - cAMP/cGMP hydrolysis

Assay of cyclic nucleotide phosphodiesterase activity.

Cyclic nucleotide phosphodiesterase catalyses the hydrolysis of the 3',5'-phosphodiester bond of the cyclic nucleotides, cAMP and cGMP.

The radioactive assay uses ^3H -labelled cAMP or cGMP and involves quantification of the reaction product (5'-nucleotide monophosphate) (Thompson,, W.J. and Appleman, M.M. (1971). *Biochemistry*, 10, 311.). The labelled NMP formed in the first reaction is converted to 5'-nucleotide in a second reaction by a 5'-nucleotidase present in snake venom. The labelled 5'-nucleotide is isolated by Dowex-1-chloride anion exchange chromatography and quantified by liquid scintillation counting.

6. ATPases - hydrolysis of ATP to ADP

Enzyme immunoassay for cAMP. The Biotrack™ assay (Amersham Pharmacia Biotech) is an enzyme immunoassay in which the sample cAMP and peroxidase-linked cAMP compete for binding to antibody raised against acylated cAMP.

Assay for adenosine 5'-triphosphatase

Adenosine 5'-triphosphatases (ATPases) catalyse the hydrolysis of ATP to ADP and inorganic phosphate in the presence of Mg^{2+} , Na^+ and K^+ . The colorimetric assay quantifies the inorganic phosphate released from ATP by measuring the $A_{660\text{nm}}$ following treatment of the enzyme reaction with TCA and Taussky-Shorr Colour Reagent (Bonting, S.L., Simon, K.A., and Hawkins, N.M. (1961) *Arch. Biochem. Biophys.*, 95, 416-423. Tausky, HH and Shorr, E. (1953) *J. Biol. Chem.*, 202, 675-685.). Similar methods are used to assay guanosine 5'-triphosphatases (GTPases).

7. GTPases - hydrolysis of GTP to GDP

Assays essentially the same as for ATPases (see Sections 6 and 17). Commercial kits available.

8. Proteases

General Assay for Proteolytic activity Proteases

This assay is based on the proteolytic digestion of casein and the spectrophotometric detection of released aromatic amino-acids. Briefly, casein is incubated with the suspected protease and then acid precipitated. The solution is then filtered and the absorbance of the acid soluble phase is measured at 280-290nm. See for example W. Rick in "Methoden der Enzymatischen Analyse", (H.U. Bergmeyer ed.) 3rd edition, 1046 and 1056. Verlag Chemie, Weinheim.

Example of a specific protease assay - Assay for the serine protease Chymotrypsin.

Endpoint titration with the fluorescent molecule 4-methylumbelliferyl p-(N,N,N-triethylammonium) cinnamate. This compound is sensitive to 10^{-11} moles of enzyme with a 2 min reaction time, see for example G.W. Jameson, D.V. Roberts, R.W. Adams, W.S.A Kyle and D.T. Elmore. (1973) Biochem. J., 131, 107.

9. Assays for secretion and import of proteins

These assays fall into three groups

- A) Reconstitution in cell-free extracts
- B) Reconstitution in semi-intact perforated cells
- C) Assays for Endocytosis

A) Reconstitution in cell free extracts

The general principle of this type of assay is based on the detection of membrane fusion events and/or the delivery of protein contents using purified membrane compartments. The detection methods include immunodetection, fluorescence and release of chromogenic substances.

Example:- The detection of endocytic vesicle fusion in vitro using an assay based on the avidin-biotin association reaction.

The assay involves the use of two different populations of vesicles, each containing a different molecular probe conjugated to a marker protein. Upon fusion the probes bind to one another to generate a detectible signal, in this case the binding of avidin to biotin. Complexes are detected by an ELISA protocol (detecting the biotinylated protein e.g. transferrin) and fluorescent detection of avidin conjugated β -galactosidase, see for example William A. Braell in "Methods in Enzymology" 219, 12-21 Academic Press inc. 1992.

B) Reconstitution using Semi-intact/perforated cells

Semi-intact/perforated cells are those which have lost a part of their plasma membrane by physical perforation. These assays can be done in Yeast or mammalian cells. Though lacking many soluble cytoplasmic factors, these cells retain their internal membrane and organellar structure and can efficiently reconstitute vesicular transport between compartments. They are also accessible to exogenously added factors such as antibodies and inhibitors.

Example:- Transport of a Protein between the Endoplasmic Reticulum and Golgi compartments.

This assay is based on the expression and transport of the Vesicular stomatitis virus (VSV) G protein. This viral glycoprotein has two Asparagine linked oligosaccharide chains which undergo extensive modifications as the protein transverse the ER and Golgi compartments. Oligosaccharide processing intermediates confer different electrophoretic mobilities on the VSV polypeptide, these intermediates can therefore be detected by SDS PAGE, see for example C.J.M. Beckers, D.S. Keller and W.E. Balch. Cell. 50, 523 (1987)

C) Assays for Endocytosis

Assays for the endocytic pathway include those for detection of the binding of proteins to cell surface receptors, formation of clathryn coated endocytic vesicles, transport to the endosome, uncoating of the vesicles, delivery of the vesicle contents and recycling to the plasma membrane.

Example:- Detection of Functional Clathryn Coated Vesicles.

This assay involves the preparation of two vesicle fractions

- i) The "donor" population containing ^{125}I -labelled transferrin.
- ii) The "acceptor" vesicles, these being the clathryn coated vesicles under test. The acceptor vesicles contain internalised Anti-transferrin antibody.

The donor and acceptor populations are mixed in a solution containing cytosol and an ATP cocktail. Upon vesicle fusion a radiolabelled immunocomplex is formed. The vesicles are then solubilised and the mix passed through a *Staphylococcus aureus* column to isolate the immunocomplexes, which are then eluted from the column and the radioactivity measured, see for example P.G. Woodman and G. Warren in "Methods in Enzymology", 219, 251 (1992)

9. Ribo/deoxyribo-nucleases - endo/exo-nuclease activity Deoxyribonuclease

An endonuclease with preference for DNA. Pancreatic DNase I yields di- and oligo-nucleotide 5' phosphates, pancreatic DNase II yields 3' phosphates. In chromatin, the sensitivity of DNA to digestion by DNase I depends on its state of organization, transcriptionally active genes being much more sensitive than inactive genes.

Ribonuclease

Widely distributed type of enzyme that cleaves RNA. May act as endonucleases or exonucleases depending upon the type of enzyme. Generally recognise target by tertiary structure rather than sequence. Ribonuclease E is an RNase involved in the formation of 5S ribosomal RNA from pre-rRNA. F is stimulated by interferons and cleaves viral and host RNAs and thus inhibits protein synthesis. H specifically cleaves an RNA base-paired to a complementary DNA strand. P is an endonuclease that generate t-RNAs from their precursor transcripts. T is an endonuclease that removes the terminal AMP from the 3' CCA end of a non-aminoacylated tRNA. RNase T1 cleaves RNA specifically at guanosine residues. RNase III cleaves double-stranded regions of RNA molecules.

Endonuclease

One of a large group of enzymes that cleave nucleic acids at positions within the chain. Some act on both RNA and DNA (eg. S1 nuclease, EC.3.1.30.1, that is specific for single stranded molecules). Ribonucleases such as pancreatic, T1 etc. are specific for RNA, Deoxyribonucleases for DNA. Bacterial restriction endonucleases are crucial in recombinant DNA technology for their ability to cleave double-stranded DNA at highly specific sites.

Nuclease

An enzyme capable of cleaving the phosphodiester bonds between nucleotide subunits of nucleic acids.

Restriction Endonuclease

Class of bacterial enzymes that cut DNA at specific sites. In bacteria their function is to destroy foreign DNA, such as that of bacteriophages (host DNA is specifically modified at these sites). Type I restriction endonucleases occur as a complex with the methylase and a

polypeptide that binds to the recognition site on DNA. They are often not very specific and cut at a remote site. Type II restriction endonucleases are the classic experimental tools. They have very specific recognition and cutting sites. The recognition sites are short, 4-8 nucleotides, and are usually palindromic sequences. Because both strands have the same sequence running in opposite directions the enzymes make double-stranded breaks, which, if the site of cleavage is off-centre, generates fragments with short single-stranded tails; these can hybridise to the tails of other fragments and are called sticky ends. They are generally named according to the bacterium from which they were isolated (first letter of genus name and the first two letters of the specific name). The bacterial strain is identified next and multiple enzymes are given Roman numerals. For example the two enzymes isolated from the R strain of E. coli are designated Eco RI and Eco RII. The more commonly used restriction endonucleases are shown in Table R1.

Ref: Definitions taken from the Dictionary of Cell Biology (Second Edition), Academic Press.

General Assay

All of the above nucleases cleave DNA and/or RNA, therefore a general assay would be to incubate unknown/test protein/chemical with a known quantity and type of DNA or RNA for a given time, and separate the products using gel electrophoresis along with a known set of standards. Any nuclease activity will be readily visible on the gel. Once nuclease activity has been detected, direct comparisons can be made with the DNA cleavage patterns generated by known nucleases in order to identify the type of nuclease involved.

10. DNA metabolism - ligase, topoisomerase, etc
DNA glycosidase

Class of enzymes involved in DNA repair. They recognise altered bases in DNA and catalyse their removal by cleaving the glycosidic bond between the base and the deoxyribose sugar. At least 20 such enzymes occur in cells.

DNA ligase

Enzyme involved in DNA replication. The DNA ligase of *E.coli* seals nicks in one strand of double-stranded DNA, a reaction required for linking precursor fragments during discontinuous synthesis on the lagging strand. Nicks are breaks in the phosphodiester linkage that leave a free 3'-OH and 5'-phosphate. The ligase from phage T4 has the additional property of joining two DNA molecules having completely base-paired ends. DNA ligases are crucial in joining DNA molecules and preparing radioactive probes (by nick translation) in recombinant DNA technology.

DNA methylation

Process by which methyl groups are added to certain nucleotides in genomic DNA. This affects gene expression, as methylated DNA is not easily transcribed. The degree of methylation is passed on to daughter strands at mitosis by maintenance DNA methylases. Accordingly, DNA methylation is thought to play an important developmental role in sequentially restricting the transcribable genes available to distinct cell lineages. In bacteria, methylation plays an important role in the restriction systems, as restriction enzymes cannot cut sequences with certain specific methylations.

DNA/RNA synthesis

DNA polymerase and RNA polymerase are enzymes involved in template-directed synthesis of DNA from deoxyribonucleotide triphosphates and RNA from ribonucleotide triphosphates.

Repair nuclease

Class of enzymes involved in DNA repair. It includes endonucleases that recognise a site of damage or an incorrect base pairing and cut it out, and exonucleases that remove neighbouring nucleotides on one strand. These are then replaced by a DNA polymerase.

Topoisomerase

An enzyme capable of altering the degree of supercoiling of double-stranded DNA molecules. Various topoisomerases can increase or relax supercoiling, convert single-stranded rings to intertwined double-stranded rings, tie and untie knots in single stranded and duplex rings, catenate and decatenate duplex rings. Topoisomerase II of *E.coli* = gyrase.

General Assay

All of the above act to modify the structure of DNA. For each enzyme involved in DNA metabolism, a corresponding assay is available commercially.

11. Transcription factorsTranscription Factor Assays

Transcription factor activity lies in the centre of a signalling cascade that begins at the cell surface by the activation of a receptor. Intracellular signal transduction events activate or repress specific transcription factors, which in turn regulate the expression of specific genes.

The activity of a transcription factor can be assessed by linking the appropriate regulatory sequence to a reporter gene encoding among other reporters β -galactosidase, CAT, luciferase and GFP in an engineered plasmid vector. This vector is used to transfect a cell line and the activity of the transcription factor of interest analysed by measuring the amount of reporter activity (Brannon, M. et al (1997) Gen. Dev. 11, 2359.).

Of the many different strategies available for using genetic reporters, luciferase offers the most ideal situation because the reporter measurements are nearly instantaneous, exceptionally sensitive and there is little or no endogenous activity in the host cells to interfere with quantitation. Firefly luciferase (Ow, D et al (1986) Science 234, 856.) is by far the most commonly used of bioluminescent reporters. The enzyme catalyses a two-step oxidation reaction to yield light at 550-570nm that can be detected by the use of a luminometer. The assay can be adapted for use with single or multiple samples depending on the type of luminometer available, i.e. tube or plate.

The above is an *in vivo* transcription factor assay requiring the transfection of an appropriate cell line with the reporter vector. However, an *in vitro* method for transcription/DNA binding factor analysis also exists.

The gel shift or electrophoretic mobility shift assay provides a simple and rapid method for detecting sequence-specific binding proteins, such as transcription factors (Ausubel, F.M. et al. (1989) In: Current Protocols in Molecular Biology, Vol. 2, John Wiley and Sons, New York.). The assay is based upon the observation that complexes of protein and DNA migrate through a non-denaturing polyacrylamide gel more slowly than free DNA fragments or double stranded oligonucleotides. The gel shift assay is performed by incubating a purified protein or a complex mixture of proteins such as a nuclear extract preparation with a ^{32}P labelled DNA fragment containing the putative binding site. The reaction products are then analysed on a

nondenaturing polyacrylamide gel. The specificity of the DNA-binding protein for the putative binding site is established by competition experiments using DNA fragments or oligonucleotides containing a binding site for the protein of interest.

12 Apoptosis

Apoptosis is the physiological process by which unwanted or useless cells are eliminated during development and other normal biological processes, e.g. tissue homeostasis, embryogenesis, induction and maintenance of immune tolerance, development of the nervous system and endocrine-dependent tissue atrophy.

The process of apoptosis involves a cascade of cytoplasmic and nuclear events that result in a series of morphological changes and eventually cause the demise of the cell. Apoptosis can be initiated by a variety of different stimuli that lead to a convergence of biochemical signalling pathways into a common collection of executioner molecules.

In the early stages of apoptosis, changes occur at the cell surface and plasma membrane. One of these plasma membrane alterations is the translocation of phosphatidylserine (PS) from the inner side of the plasma membrane to the outer layer, where PS becomes exposed at the external surface of the cell. Mitochondrial physiology is disrupted in cells undergoing apoptosis. Permeability is altered and specific protease activators are released. Specifically, the discontinuity of the outer mitochondrial membrane results in the redistribution of cytochrome C to the cytosol followed by subsequent depolarisation of the inner mitochondrial membrane. Cytochrome C release further promotes apoptosis by the activation of the caspases, cysteine proteases. Active caspases participate in a cascade of cleavage events, which disable key homeostatic and repair enzymes and bring about a systematic structural disassembly of dying cells. The biological substrates of

caspases include poly(ADP ribose) polymerase (PARP), DNA-dependent protein kinase (DNA-PK), lamins, topoisomerases, Gas2, protein kinase C (PKC), sterol regulatory element binding proteins (SREBP), U1-70kDa protein and Huntingtin protein.

The biochemical hallmark of apoptosis is the fragmentation of genomic DNA, an irreversible event that commits the cell to die and occurs before changes in plasma membrane permeability.

In concert with increased understanding of the physiological events that occur during apoptosis, a number of assay methods have been developed for its detection. These assay methods can measure one of the following apoptotic parameters:

1. Fragmentation of DNA in populations of cells or in individual cells, in which apoptotic DNA breaks into different length pieces.
2. Alterations in membrane asymmetry. PS translocates from the cytoplasmic to the extracellular side of the cell membrane.
3. Activation of apoptotic caspases.
4. Release of cytochrome C into the cytoplasm by mitochondria.

Each provides the researcher with a different level of information as each of these events occurs at a different stage in apoptosis.

The early proteolytic events of apoptosis can be monitored using an adaptation of the absorbance-based assay originally devised by Thornberry, N.A. (1994) Interleukin-1 beta converting enzyme. Meth.Enzymol. 244, 615. The colorimetric substrate (Ac-DEVD-pNA) is labelled with the chromophore p-nitroaniline(pNA). pNA is released from the substrate upon cleavage by DEVDase. Free pNA produces a yellow colour that is monitored by a photometer at 405nm. The amount of yellow colour that is produced upon cleavage is proportional to the amount of DEVDase activity present in the sample. The potent, irreversible, pan-caspase

inhibitor Z-VAD-FMK can be used as a negative control and it is suggested that apoptosis be induced by the addition of Fas or TNF agonist antibodies.

The protocol can be used to test multiple samples by performing the assay in a total volume of 100ml using cells cultured in 96 well plates. The absorbance produced by each sample is read using a plate reader.

13 Calcium

Calcium dynamics

In a multicellular organism, cell communication is essential to regulate the different activities of specialised tissues. In all animal cells, there are conserved intracellular second messenger pathways. For many of these, calcium is an important second messenger. In nerve cells, muscle and other cells, modulation of intracellular calcium activity from typical resting levels of 100 nM regulates many short and long-term processes. Measurement of calcium can thus be of great utility in following the responses of transgene products to applied pharmacological agents including insecticides.

Calcium dynamics may be detected directly or indirectly by a range of methods; including but not restricted to: a) transgenic apoaeguorin, a calcium-sensitive luminescent protein; b) other methods that monitor intracellular calcium concentration; c) other methods that monitor the operation of intracellular calcium signalling pathways; d) methods that monitor the operation of other types of signalling pathway; e) methods that monitor neuronal electrical potentials.

For example, transgenic apoaeguorin has been used to monitor calcium dynamics in the intact *Drosophila* renal system and the intact *Drosophila* brain (Rosay et al (1997) J. Cell. Sci. 110, 1683-1692; O'Donnell et al. (1998) Am. J. Physiol. 43(4), R1039-R1049.). It has also been used to provide a bioluminescent assay for agonist activity against G protein coupled receptors (Stables et al. (1997) Anal.

Biochem. 252, 115-126). Transgenic apoaeguorin can thus be used to assess the effect of an exogenous gene on intracellular calcium dynamics, the method comprising detecting a pattern of calcium dynamics in cells, tissues or organisms expressing the exogenous gene, and comparing said pattern with a pattern of calcium dynamics in cells, tissues or organisms without said exogenous gene.

Additionally, fluorescent probes (such as fura-2, indo-1, quin-2) show a spectral response upon binding calcium and it is then possible to detect changes in intracellular free calcium concentrations using fluorescence microscopy, flow cytometry and fluorescence spectroscopy. Most of these fluorescent indicators are variations of the nonfluorescent calcium chelators EGTA and BAPTA (Cobbold and Rink (1987) Biochem. J., 248, 313.).

New fluorescent indicators for calcium called "cameleons" may also be used and are genetically encoded without cofactors and are targetable to specific intracellular locations. These so-called "cameleons" consist of tandem fusions of a blue- or cyan-emitting mutant of the green fluorescent protein (GFP), calmodulin, the calmodulin-binding peptide M13, and an enhanced green- or yellow-emitting GFP. Binding of calcium makes calmodulin wrap around the M13 domain, increasing (Miyawaki et al., (1997) Nature, 388, 882-887.) or decreasing (Romoser et al., (1997) JBC, 272, 13270-13274.) the fluorescence resonance energy transfer between flanking GFPs.

Additionally, potentiometric optical probes may be used. Potentiometric optical probes measure membrane potential in organelles and in cells. In conjunction with imaging techniques, these probes can be employed to map variations in membrane potential along neurons and among cell populations with high spatial resolution and sampling frequency (Rohr and Salzberg (1994) Biophys. J., 67, 1301.).

Additionally, GFP-based reporter genes that monitor intracellular cAMP dynamics may be used, and to monitor intracellular pH changes (Miesenbock et al. (1998) Nature

394, 192-5).

14 cAMP

Effects on dynamics of intracellular cAMP as reported by appropriate dyes or reporter constructs (eg. aequorin). See section 13.

15 Voltage

Analysis of transmembrane potential permits study of the elements which mediate electrical behaviour of cells. This form of study may be undertaken in a number of ways, including: voltage (patch) - clamping and the use of voltage sensitive dyes.

Patch clamping

In brief, this involves sealing a blunt micropipette tip to a cell membrane. This is termed a gigaseal. The gigaseal electrically isolates the whole cell or a patch of the membrane allowing detection of picoampere, ionic currents while accurately controlling the voltage. This form of analysis may be utilised in the study of cultured cells, tissue slices or recombinant ion channels expressed post DNA transfection in heterologous cells. Whole cell recording measures the activity of the full complement of active channels in a cell; typically specific populations of channels are isolated using channel-blocking agents. It is also possible to isolate single ion channels, providing information on the unitary conductance and kinetic behaviour of individual channels, and allow the factors which alter these properties to be studied in exquisite detail (Crawley et al., 1997 Neurophysiology Current protocols in neuroscience Volume 1 [John Wiley and Sons, Inc.]). Patch Clamp techniques are widely used and cited throughout scientific literature (Siegel M.S and Isacoff E.Y (1997) *Neuron* 19, 735 - 741; Sensi S., Canzoniero L.M, Yu S.P, Ying H.S, Koh J.Y, Kerchner G.A, Choi D.W. (1997) *J. Neuroscience* 17, 9554 - 9564; Piller S.C, Jans P., Gage

P.W., Jans D.A (1998) Proc. Natl. Acad. Sci. USA, 95, 4595 - 4600; Maric D., Maric I., Wen X., Fritschy J.M, Sieghart W., Barker J.L, Serafini R., (1999) J. Neuroscience 19, 4921 - 4937). An example of how this kind of analysis may be used is outlined below.

Whole cell patch clamp recording to study the effects of a viral protein on whole cell currents of cultured hippocampal neurons.

Whole cell currents represent the integrated channel activity over the whole cell. Cultured cells on coverslips were perfused with bath solution (140 mM NaCl, 5 mM KCl, 3 mM CaCl₂, 2 mM MgCl₂, 10 mM glucose, 10 mM TES [pH7.3]) at room temperature (23 to 28C). Pipettes made from borosilicate glass were fire polished and filled with pipette solution normally containing 150 mM NaCl, 0.5 mM CaCl₂, 2 mM MgCl₂, 5 mM EGTA and 10 mM TES [pH7.3]. Reversal potentials were determined experimentally by altering the holding potential until currents reversed direction and the potential for zero current was recorded. Cells were routinely clamped at - 60 mV. Whole cell currents were recorded both before and after the addition of purified viral protein by using an Axopatch 200A. Viral protein @ 0.6 nM in bath solution was applied directly onto patched cells through gravity fed drug delivery tubing. whole-cell currents were filtered at 5 or 10 kHz, digitized at 44 kHz, and stored on videotape. For data analysis currents were replayed through the same system and digitized using an A to D converter interfaced with an IBM-compatible computer. Inward currents are depicted as downward deflections from the zero current level.

Electrical potential may also be measured using voltage sensitive dyes. e.g. Oxonol VI / Bis-oxonol (Dall'Asta V., Gahi R., Orlandini G., Rossi P.A, Rotoli B.M, Sala R., Bussolati O., Gazzola G.C, (1997) Experimental Cell Research 231, 260 - 268; Salvador J.M, Inesi G, Rigaud J.L,

Mata A.M, (1998) J. Biol. Chem. 273, 18230 - 18234).

In the study by Salvador et al., 1998, transmembrane electrical potential was measured by analysis of the differential absorption (625 - 603 nm) of 2 μ M oxonol using dual wavelength spectrophotometry. The medium comprised Pipes buffer, pH7.1; 0.42 μ g/ml calmodulin; 5mM MgCl₂ and 2 μ M Oxonol VI. The callibration was performed by several additions 130 mM KCl to the medium in the presence of 1 μ M of the K⁺ ionophore valinomycin and in the absence of ATP. Absorption changes were standardized using the Nernst equation. Within a range 0 - 40 mV Absorption by oxonol demonstrates a linear increase with increasing membrane potential. This proportionality permits straightforward assay of changes in membrane potential.

Dall'Asta et al., 1997 visualize changes in membrane potential using Bis-oxonol. Bis-oxonol is a fluorescent dye which distributes across biological membranes according to the membrane potential and binds to hydrophobic components: since the quantum yield of the dye increases with binding, the fluorescence of the cells incubated in a medium containing the dye increases with depolarization and decreases with hyperpolarization.

16. Receptors/ion channels

Ion Channels/Receptors

Neuronal signaling depends on rapid changes in the electrical potential difference across nerve cell membranes. These rapid changes in potential are made possible by ion channels, a class of integral membrane proteins that traverse the cell membrane. These channels have three important properties: (1) they conductions, (2) they recognise and select among specific ions, and (3) they open and close in response to specific electrical, mechanical, or chemical signals. [Principles of Neural Science, (Kandel and Schwartz), Chapter 5 Ion Channels]. Ion channels are large integral membrane glycoproteins, which have a central aqueous pore that spans the entire

width of the membrane. Many ion channels are made up of two or more subunits, which may be identical or distinct. Three major signals gate ion channels: voltage (voltage-gated channels), chemical transmitters (transmitter-gated channels), and pressure or stretch (mechanically-gated channels). Gating involves a conformational change of the channel in response to the above stimuli.

Several major classes of ion channels have now been identified. Primary sequence information has been used to suggest the structure of different channel proteins. Efforts to determine secondary structure rely on X-ray crystallography. However, additional information can be obtained by comparing the primary amino acid sequence of related channels from different species and identifying regions of sequence homology, suggesting the importance of such regions in channel structure and function. Further insight into structure-function relationships can be obtained from sequence homologies among different, but related, channels. Such homologous regions are likely to underlie a common biophysical function shared by the different channels, i.e. Voltage-gated versus transmitter-gated channels.

The flux of ions through ion channels is passive, requiring no expenditure of metabolic energy. The direction and eventual equilibrium for this flux is determined not by the channel itself, but rather by the electrochemical driving force across the membrane. Ion channels select the type of ions that they allow to cross the membrane through physio-chemical interaction between the ion and various amino acid residues that line the walls of the channel pore (on the basis of ionic charge), allowing either cations or anions to permeate. Some cation-selective channel types are relatively non-selective, passing Na^+ , K^+ , Ca^{2+} , and Mg^{2+} . However, most cation-selective channels are more selective; each one is permeable primarily to a single type of ion, either Na^+ , K^+ , or Ca^{2+} . All known types of anion-selective channel are

permeable to Cl^- . Note that the Ca^{2+} influx controlled by channels can alter many metabolic processes within cells, leading to activation of various enzymes and proteins. Ca^{2+} influx also acts as a trigger for the release of neurotransmitter.

The activity of channels can be modified by cellular metabolic reactions, including protein phosphorylation, by various channel blockers, toxins, poisons, and drugs. Channels are important targets in various diseases, eg myasthenia gravis and cystic fibrosis.

Molecular analysis: Starting with an unknown chemical for which no information is available, and depending on the size of the starting molecule, peptide sequence can be obtained either directly or by using the chemical bound to a column to purify the target molecule in the cell (e.g., benzodiazepine affinity chromatography purification columns were used to isolate and identify the first cDNA clones encoding GABA receptor subunits in 1987 - Schofield P.R., Darlison M.G., Fujita N., Burt D.R., Stephenson F.A., Rodriguez H., Rhee L.M., Ramachandran J., Reale V., Glencorse T.A., Seeburg P. And Barnard E.A (1987) *Nature* **328**, 221 - 227). From peptide sequence, best-guess oligonucleotides can be synthesized and used to screen species-specific cDNA libraries. Any cDNA clones identified can then be sub-cloned, sequenced and the primary sequence analysed for known sequence homologies with BLAST database searches. The full-length sequence, cDNA and corresponding expressed protein, can then be subjected to standard biochemical and molecular characterisation procedures.

Functional analysis: single-channel recording can measure the activity of a single protein molecule (electrophysiology). The patch clamp technique has made it possible to measure directly the activity of single ion channel molecules by recording the unit current flow through single open channels. Expression of cRNAs in the *Xenopus* oocyte system, cDNA in transfected cell lines or

whole tissue slice cultures can be used.

Example of cRNA expression in *Xenopus* oocyte: pure mRNA, produced by *in vitro* transcription from cDNA, is microinjected into *Xenopus* oocytes and pulses of known compounds (eg GABA, glutamate, etc) can be superfused over the oocyte while recording membrane currents under voltage-clamp conditions. Current response to applied compound can be measured.

Two main gene families:

- | | |
|--|---|
| 1. Voltage gated channels: | Na ⁺ , K ⁺ and Ca ²⁺ |
| 2. Ligand-gated ion-channel receptors: | cation: nACh, |
| either Integral (pore forming, | 5HT, glutamate, |
| Ion gating) or Second messenger | anion: GABA |
| systems (associated) | Glycine |

Methods

1. cloning: sequence analysis primary and secondary
2. structure: crystallography, *in situ*, immunocyto, immunohisto, immunoEM
3. function: electrophysiology: slice culture/patch clamp transfection/patch clamp

Voltage-Gated Channels

In nerve cells at rest (membrane potential: -65mV), the steady Na⁺ influx through non-gated channels is balanced by steady K⁺ efflux, so that the membrane potential is constant. This steady state balance changes when the cell is sufficiently depolarised to trigger an action potential. A transient depolarising potential, such as excitatory synaptic potential, causes some voltage-gated Na⁺ channels to open, and the resultant increase in membrane Na⁺ permeability allows Na⁺ influx to outstrip the K⁺ efflux. Thus, a net influx of positive charge flows through the membrane, and positive charges accumulate inside the cell, causing further depolarisation. The increase in

depolarisation causes more voltage-gated Na^+ channels to open, resulting in a greater influx of positive charge, which accelerates the depolarisation further.

This regenerative, positive feedback cycle develops explosively, driving the membrane potential toward the Na^+ equilibrium potential of +55mV. Because K^+ efflux continues through the K^+ channels, the membrane potential never actually reaches the equilibrium potential of sodium. A slight diffusion of Cl^- into the cell also counteracts the depolarising tendency of the Na^+ influx.

As depolarisation continues, it slowly turns off, or inactivates, the voltage-gated Na^+ channels. That is, the Na^+ channels have two types of gating mechanisms: activation, which rapidly opens the channel in response to depolarisation, and inactivation, which slowly closes the channel if depolarisation is maintained. The second repolarising process results from the delayed opening of voltage-gated K^+ channels. The delayed increase in K^+ efflux combines with a decreased Na^+ influx to produce a net efflux of positive charge from the cell, which continues until the cell has repolarised to its resting membrane potential.

Intracellular recording: this technique uses two glass capillary electrodes full of an ionic conductor solution (usually 3M KCl). To measure the resting membrane potential, an intracellular electrode is inserted into the nerve cell (grown in culture or via slice culture) - the pipette acts as a salt bridge, providing electrical connection between the cytoplasm and a metal electrode that is connected to the electronic apparatus. The second extracellular electrode can be used to confirm resting potential and/or stimulate the cell. Both electrodes are connected to a voltage amplifier, which in turn is connected to an oscilloscope that displays the amplitude of the membrane potential (-65mV, at rest).

Ligand-Gated Channels - Integral Channel

(e.g., nACh, 5HT₃, glutamate, GABA_A, Glycine)

A transmembrane ion channel whose permeability is increased by the binding of a specific ligand, typically a neurotransmitter at a chemical synapse. The permeability change is often drastic; such channels let through effectively no ions when shut, but allow passage at up to 10^7 ions s^{-1} when a ligand is bound. These receptors have been found to share considerable sequence homology, implying that there may be a family of structurally related ligand-gated ion channels.

Ion channel receptors are composed of 4 or 5 subunits, which may be the same or different, each of which contains 4 or 5 membrane-spanning α -helical regions. These α -helices are thought to align to form the pore of the channel, through which ions can flow. The characteristics of each channel is determined by the type of subunits that are present in each receptor subtype. Annals of the New York Academy of Sciences (1999) Volume 868) Current flow depends on the number of open channels, the concentration of the transmitter, channel conductance and membrane potential.

Receptor specific assays will have to be created for each receptor/ion channel under investigation. The best/easiest way to do this is to create permanent cell lines expressing a particular combination of receptor subunits in order to form particular receptor subtypes. There are many examples of these in the literature, and of the differences in receptor characteristics when different combinations of receptor subtypes are expressed. Initial assays established by the inventors will focus on the most clinically relevant subtype(s) of each receptor. With these permanent cell lines, functional assays can be used to investigate the effects of any chemical on the receptor characteristics e.g., electrophysiology (patch-clamp single-channel recording), binding assays (see section 1), etc.

Ligand-Gated G-protein linked Receptors

(e.g., mACh, 5HT, GABA_A, Glutamate, Dopamine, etc)

Many cell surface receptors are coupled to G-proteins (GTP-binding protein). G-protein-coupled receptors are thought to have seven membrane spanning domains, and have been divided into 2 subclasses: those in which the binding site is in the extracellular domain e.g. receptors for glycoprotein hormones, such as thyroid stimulating hormone (TSH) and follicle stimulating hormone (FSH), and those in which the ligand-binding site is likely to be in the plane of the 7 transmembrane domains e.g. rhodopsin and receptors for small neurotransmitters (nACh, 5HT, glutamate-NMDA, GABA, Glycine) and hormones. All transduce their signal by conformational change activation of an associated G-protein (see section 17).

There are two main classes of G proteins, the heterotrimeric G proteins that associate with receptors of the seven transmembrane domain superfamily and are involved in signal transduction, and the small cytoplasmic G proteins. The small G proteins are a diverse group of monomeric GTPases that include ras, rab, rac and rho and that play an important part in regulating many intracellular processes including cytoskeletal organisation and secretion. Their GTPase activity is regulated by activators (GAPs) and inhibitors (GIPs) that determine the duration of the active state. (see section 17), see for example Principles of Neural Science, (Kandel and Schwartz), Third Edition 1991.

17. G-proteins (GTP binding proteins)

GTP binding proteins are a superfamily of related proteins which bind to guanosine nucleotides (Kaziro Y., Itoh H., Kozasa T., Nakafuku M. and Satoh T. Ann. Rev. Biochem. (1991). They are found in an inactive form which is bound to GDP and an active form which is bound to GTP. Other proteins such as ligand bound receptors promote the exchange of GDP with GTP, activating

the protein. G proteins are inactivated by hydrolysis of the GTP to GDP. This reaction is catalysed by the G protein itself but the rate of GTP hydrolysis can be influenced by interaction with other proteins. Activated G proteins regulates the activities of a large number of target proteins including adenylate cyclase, phospholipase C and ion-channels.

Heterotrimeric G proteins.

Heterotrimeric G proteins are a large family of GTPases which consist of an α , a β and a γ subunit. They are involved in signal transduction from receptor proteins in the plasma membrane to second messenger systems within the cell receptors that activate. Activation of a receptor (e.g. by ligand binding) activates the G protein by promoting the exchange of bound GDP with GTP. The presence of GTP in the active site causes the dissociation of the α subunit from the $\alpha\beta\gamma$ complex. The free α subunits is most active. Different α subunit subtypes interact with a wide variety of different target proteins including adenylate cyclase, phospholipase C and ion-channels. The free $\beta\gamma$ complex also has also been show to have some regulatory activity.

Small(p21) GTPases

These proteins consist of a single subunit similar to the α subunit of heterotrimeric G proteins. These include the RAS family of proteins the abnormal activity of which can contribute to tumour formation.

Other GTP binding proteins

Other members of the Guanosine nucleotide binding protein superfamily include GTP binding translation elongation factors and members of the Dynamin family of proteins.

Use of Recombinant G proteins

Expression of recombinant G proteins allows the biochemical properties of proteins identified by DNA sequencing to be studied and allows the isolation of large amounts of the proteins for structural and biochemical studies. It also allows the production of mutant proteins produced by site directed modification of cDNA sequences.

Active recombinant G proteins have been expressed in large amounts in bacterial and insect-cell/baculovirus systems. Expression of G proteins in cell free translation systems is a convenient way of producing small amounts of protein for biochemical studies. The addition of ^{35}S methionine to the *in-vitro* translation reaction results in the production of specifically labelled protein.

It is also possible to express the proteins in cultured cells and look for whole cell effects such as increased cell proliferation, increased DNA synthesis or changes in the activity of various enzymes.

The use of cell lines lacking G protein subunits.

Several cell lines have been isolated, or made using gene-disruption techniques, which lack particular G protein subunits. The most widely used of these is the *cyc⁻* variant of the S49 mouse lymphoma cell line lack the G_{α} subunit. It is possible to add back recombinant or purified G proteins to investigate their function. Purified or *in-vitro* translated protein can be added back to membrane preparations from the cell lines or the cells can be transfected with plasmid constructs which express the protein.

GTP binding assays

The nonhydrolyzable GTP analogue $^{35}\text{S}\gamma\text{GTP}$ will bind to most GTP binding proteins in the absence of any activator molecule. Purified or *in-vitro* translated G protein can be incubated with $^{35}\text{S}\gamma\text{GTP}$ and the reaction products passed through a nitrocelulose filter. Protein bound $^{35}\text{S}\gamma\text{GTP}$ will

be retained on the filter and the activity measured (Carty D.J. and Iyengar R. (1994). Methods in Enzymology. 237: 38-45.).

GTP γ S activation

Conformational changes in G proteins and changes in subunit interaction can be studied by incubating the G protein with GTP γ S which binds to, and irreversibly activates, the protein. Conformational changes in subunits and changes in subunit interaction alter the sites available for degradation by trypsin. The tryptic fragments of radio-labelled protein can be run on a SDS PAGE gel and visualised by autoradiography. Subunit interaction can also be studied by looking at sedimentation rates during ultra centrifugation and by using chemical crosslinking agents (Audigier Y. (1994). Methods in Enzymology. 237: 239-254.

Activation of other proteins as a result of G protein activation

G proteins in cell extracts can be activated by incubation with GTP γ S and the activities of possible downstream target proteins such as adenylate cyclase and phospholipaseC measured.

Receptor stimulated GTP binding and GTP hydrolysis.

Receptor stimulated binding of the radio-labelled non-hydrolyzable GTP analog $^{35}\text{S}\gamma\text{GTP}$ can be used to show if the addition of a receptor ligand leads to the activation of a G protein (Wieland T and Jakobs K.H (1994) Methods in Enzymology 237, 3 - 13). It is possible to study the activation of endogenous G proteins or to use a membrane preparation lacking particular G proteins and add back a purified or recombinant G protein.

$^{35}\text{S}\gamma\text{GTP}$ is added to a reaction mix containing a membrane preparation of the cells being studied. After incubation at 37°C for an appropriate length of time the

reaction is stopped. The reaction mix is then passed through a filter which binds protein of membrane. The amount of radioactivity incorporated into the protein/membrane fraction is then measured. The amount of radioactivity incorporated in the presence and absence of candidate receptor ligand molecules can then be compared.

As an alternative to measuring the binding of $^{35}\text{S}\gamma\text{GTP}$ it is possible to measure GTPase activity. Activation of a G protein by a ligand bound receptor results in an increase in GTP hydrolysis activity. This is more often a result of increasing the rate of exchange of GDP with GTP rather than an increasing the rate of hydrolysis of bound GTP. $\gamma^{32}\text{P}$ GTP is added to a reaction mix containing a membrane preparation of cells and the amount of ^{32}P released from the labelled GTP is measured.

The present invention will now be further described by way of non-limiting example.

Example 1

The construct of the P{lacW} element used below is a defective P-element. A defective P-element is one which cannot transpose itself without the provision of a transposase enzyme from another source. Thus, once inserted into a site in the genome, a defective P-element will remain in position and will not distribute copies of itself. The reporter gene in P{lacW} is an *E. Col* β -gal lacZ gene under the control of a weak promoter. This weak promoter, however, responds to enhancer elements in the neighbourhood of the insertion site to give a pattern of lacZ expression that is related, to a variable extent, to the pattern of expression of the gene targeted. This provides temporal and/or tissue expression patterns which may be useful in deciding whether a gene/protein could be a potentially valuable target for insecticide or therapeutic development.

In addition to the reporter gene, P{lacW} carries a mini-white eye colour gene to identify flies that contain insertions. P{lacW} also contains a bacterial origin of replication and the β -lactamase gene coding for ampicillin resistance at its 3' end. This feature permits easy cloning of DNA flanking the insertion site of P{lacW} and further clone relevant genes (Bire, E., H. Vaessin, S. Shepherd, K. Lee, K. McCall, S. Barbel, L. Ackermam, R. Carretto, T. Uemura, E. Grell, L.Y. Jan and Y.N. Jan, 1989 Searching for pattern and mutation in the *Drosophila* genome with a P-lacZ vector. *Genes and Development* 3: 1273 - 1287).

The mutant flies, in which P{lacW} was inserted on the second chromosome are on the *y w*; P{lacZ,w⁺}CyO genotype (Torok, T.G. Tick, M. Alvarado and I. Kiss, 1993 P-lacW Insertional Mutagenesis on the second chromosome of *Drosophila melanogaster*: Isolation of lethals with different overgrowth phenotypes. *Genetics* 135: 71 - 80). The mutant flies, in which P{lacW} was inserted on the third chromosome are of the *y w*; P{lacZ,w⁺}TM3, *sb ser* genotype (Dèak, P., M.M. Omar, R.D.C. Saunders, M. Pal, O. Komonyi, J. Szidonya, P. Maroy, Y. Zhang, M. Ashburner, P. Benos, C. Savakis, I. Siden-Kiamos, C. Louis, V.N. Bolshakov, F.C. Kafatos, E. Madueno, J. Modolell and D.M. Glover, 1998 P element insertion alleles of essential genes on the third chromosome of *Drosophila melanogaster*: Correlation of physical and cytogenetics maps in chromosomal region 86E-87F. *Genetics* 14: 1697 - 1722).

The genetic background of the *w/w*;P(lacW) mutants was equilibrated with that of the wild-type (Canton-S) strain by repeatedly backcrossing heterozygous *w/w*;P(lacW)/+ females (which carried the *w*⁺ eye-color marker) to *w*(CS) males for more than five generations. The *w*(CS) strain was derived by backcrossing *w*¹¹¹⁸ flies to wild-type (Canton-S) flies for 10 generations; the *w*(isoCJ1) strain was derived from *w*(CS) and carries isogenic X, 2nd and 3rd chromosomes.

Example 2 - Plasmid Rescue and cDNA Cloning

Genomic sequences flanking the P-element were cloned by plasmid rescue using standard techniques (*Drosophila*: A practical Approach, the 2nd ed. 1998). Briefly, genomic DNA was digested with *EcoRI*, followed by ligation to form a rescue plasmid, which was propagated in *E. coli*. The rescue fragment then was ^{32}P -radiolabeled by random priming and used to screen plaques from a *Drosophila* genomic bacteriophage lambda library. The lambda genomic fragment was subcloned into the plasmid vector pBluescript, radiolabeled and used to probe a *Drosophila* adult head cDNA library and a Northern blot of adult whole fly polyA⁺ RNA, etc.

Southern blotting was carried out essentially as described by Sambrook et al. (1989). Hybridization was carried out at 64°C in 6xSSC, 5xDenhardt's reagent, 0.5% SDS, 100µg/ml denatured, fragmented salmon sperm DNA. Filters were washed in 1xSSC and 0.1%SDS for 15 min, and then in 0.1XSSC and 0.1%SDS for 30 min.

Example 3 - DNA Sequencing

Prior to DNA sequencing, rescued plasmids were quantified by restriction digestion with *EcoRI* to linearise followed by electrophoresis on a 1% agarose gel, comparisons being made to a Bacteriophage lambda 1kb marker ladder. For DNA sequencing 500ng-2µg of rescued plasmid was used in each sequencing reaction. Sequencing was carried out using a BigDye dideoxy terminator kit (Perkin-Elmer) with the following sequencing primers:-

- 1) 3' primer 5'-CGCACTTATTGCAAGCATACG-3' sequences into the rescued chromosomal DNA immediately 3' to the point of insertion (5' end of the chromosomal DNA insert)
- 2) 5' primer 5'-GCCACCTGACGTCTAAGAAACC-3' sequences the rescued chromosomal DNA from a point in the P-element vector 5' to the *EcoRI* site, in a reverse orientation to Primer 1 (ie the 3' end of the chromosomal DNA)

NB. Sequence obtained from Primer 2 is only included in those sequences where the combined sequence runs yielded the complete insert of a particular clone.

The reactions were run on 5% polyacrylamide sequencing gels in 373A STRETCH PE Biosystems automated sequencer. Greater than 900 separate lethal/semi-lethal fly lines were identified by sequencing. The sequence obtained from these fly lines is represented in SEQ 10 Nos. 1-902.

DNA sequence analysis/storage was performed using GeneJockey II (Biosoft, Cambridge, UK). BLAST queries and Flybase queries were carried out on secure mirror servers within the Neuropa computing network.

Table 1 shows in summary the fly lines which display similarity to previously identified sequences deposited in nucleotide databases. Over 400 fly displayed no apparent sequence similarity with previous sequences.

Table 2 shows in summary details of the sequences of the fly lines which display a similarity to previously submitted mammalian sequences.

Example 4 - X-Gal Staining of Tissues

The procedure for X-gal staining of embryo is essentially as described by O'Kane (1998). Embryos are collected from yeasted apple/grape juice agar plates into a container with a nylon mesh screen at the bottom, dechorionated by dipping into 50% bleach for 4 minutes and washed thoroughly with water. Embryos are placed into an Eppendorf tube containing a mixture of 0.35ml fix solution (1% glutaraldehyde in PBS) and 0.7ml n-heptane and fixed for 15 minutes at room temperature on a rotating mixer. After removing heptane and fix solution from tube, embryos are washed three times for 10 min. in PBS and 0.1% Triton X-100, and resuspended in staining buffer with 0.2% X-gal for 1-2 hours at 37°C. After staining, staining solution are removed and about 400µl of mixture solution (Glycerol : staining buffer = 2:1) are replaced. Embryos can then be mounted on a slide in a coverslip chamber.

For whole-mounts, larval, pupal and adult brains were dissected in PBS, and fixed in 4% paraformaldehyde for 20 min. They were then washed three times for 20 min in PBS, and stained with staining buffer and 2% X-gal for 1-2 h at 37°C (Ashburner, *Drosophila. A Laboratory Manual*, Plainview N.Y.: CSH Lab. Press 1989). They were then washed for 20 min in PBS, cleared overnight at 4°C with PBS/12.5% hydrogen peroxide, washed for 10 min with PBS, dehydrated through graded ethanol, and mounted in glycerol gelatin (Sigma).

To obtain sections, flies were mounted in "fly collars" (modified from Heisenberg and Böhl 1979), soaked in OCT embedding medium (Miles, USA) for 10 min and then embedded in the OCT medium. 12 μ m serial sections of head or body were cut in a cryostat (Anglia Scientific) at -18°C. The sections were stained and mounted as described by Yang et al. (1995). Thereafter sections were examined and photographed on a Nomarski optical microscope.

Example 5 - In situ Hybridisation to Polytene Chromosome

In situ hybridisation to polytene chromosomes localises a DNA sequence (such as a gene, or an inserted P-element) on the physical DNA map of *Drosophila*, and may be related to the genetic map. For those insertion mutations which affect genes of known function, localisation of the P-element to the site where the gene mutated is known to reside is evidence that lethality does in fact result from insertion of the P-element in this gene.

Tagging the genes with a PlacW transposon allowed its immediate localization in situ to a precise cytological region using P element DNA as a probe. The procedure for in situ hybridization to third larval instar polytene chromosomes was essentially as described by Pardue (1986). pBluescript were labelled with Bio-16-dUTP by nick-translation. Hybridization was detected using DAB/H₂O₂. After hybridization, the slides were stained with Giemsa and mounted using DPX.

TABLE 1

SEQ ID NO.	ID Number	Class	Chr	Feature	AccNo	Name of match
1	NPS1	GNL	2	4-133	X54648	Frizzled gene
2	NPS2	GNL	2	68-345	D17389	Ryanodine receptor
3	NPS3	GNL	2	1-354	M23412	Muscarinic acetylcholine receptor. Genomic AC006938 intron.
4	NPS4	GNL	2	9-277	U91980	Tpr homologue
5	NPS5	GNL	2	1-587	X61209	Type II topoisomerase
6	NPS6	GNL	2	270-408	U22439	Neuron surface antigen 2
7	NPS7	GNL	2	30-461INV	Y13272	Indora
8	NPS8	GNL	2	1-267	L03209	GDP dissociation inhibitor homologue
9	NPS9	GNL	2	345-583INV	L17340	germline transcription factor gene
10	NPS10	GNL	2	1-480	AB003784	Histone H3
11	NPS11	GNL	2	179-360	AA699128	EST matching 5' of V-ATPase C subunit
12	NPS13	GNL	2	226-409	U94702	MtPolB
13	NPS14	GNL	2	110-191	L13305	AND 396-472, integrin beta subunit (beta neu)
14	NPS15	GNL	2	1-432	X57484	tra-2 gene
15	NPS16	GNL	2	61-276	X15805	EF2 Translation factor
16	NPS18	GNL	2	1-532	X15008	49bp upstream of TU-36B gene, cytochrome b related protein.
17	NPS19	GNL	2	250-536	M29602	G0 protein alpha subunit homolog class II
18	NPS20	GNL	2	81-476	L13255	Lachesin
19	NPS21	GNL	2	119-457inv	U63556	larval serum protein 1 beta subunit
20	NPS22	GNL	2	121-417	AF027300	418-481intron, 481-577exon. Positive transcription elongation factor b
21	NPS23	GNL	2	1-577	X84681	organellar-type Ca-ATPase gene.
22	NPS26	GNL	2	1-534	X71866	GTP-binding protein.
23	NPS27	GNL	2	1-523	M23094	Intron of G protein alpha subunit gene
24	NPS28	GNL	2	19-215	AF041048	AA246996 est match. EST matches CD39-like NTPase gene
25	NPS30	GNL	2	387-473inv	AF071417	phosphatidylinositol 4-phosphate 5-kinase, skt11
26	NPS31	GNL	2	1-319	S55886	rbp9
27	NPS32	GNL	2	1-493	L34276	manganese superoxide dismutase (mnSOD)
28	NPS33	GNL	2	233-377inv	D84313	rab2
29	NPS34	GNL	2	1-63inv	AF003826	myosin V
30	NPS35	GNL	2	325-528	U09369	ribonucleoside-diphosphate reductase large subunit gene
31	NPS36	GNL	3	234-271	U95821	transmembrane GTPase (fzo)
32	NPS38	GNL	3	322-450	U00669	mitochondrial single-stranded DNA-binding protein
33	NPS39	GNL	3	14-385	X52846	RM62
34	NPS40	GNL	3	1-422inv	AF069297	pterin-4a-carbinolamine dehydratase gene
35	NPS41	GNL	3	329-346	Y09065	330-414 intron, 415-511 exon. cytochrome c oxidase subunit Va preprotein
36	NPS42	GNL	3	1-283	M22428	Ubiquitin

37	NPS43	GNL	3	1-213	M28870	heterogeneous nuclear ribonucleoprotein isoforms, exon 1A.
38	NPS44	GNL	3	1-380	M17719	Intron of Rhodopsin 4 and M17730
39	NPS45	GNL	3	1-449	U27561	TipE
40	NPS46	GNL	3	463-528	X99665	mitochondrial ATPase coupling factor 6. Match on EST AI405330
41	NPS47	GNL	3	1-246	K01294	heat shock locus 87C1: proximal gene, 3' end.
42	NPS48	GNL	3	221-318	U73160	AA440389 EST matching Dros fas gene
43	NPS49	GNL	3	15-95	M32141	AI297861 1st EST in 8 contig matches 49-kilodalton phosphoprotein gene
44	NPS50	GNL	3	231-293	M21159	Tcp-1
45	NPS51	GNL	3	1-349	V00213	Hsp70
46	NPS52	GNL	3	1-241	U59923	glutamyl-prolyl-tRNA synthetase gene,
47	NPS53	GNL	3	225-237	D16257	238-333 intron, 334-499 exon ribosomal protein S4
48	NPS54	GNL	3	1-462	X73216	Rib1
49	NPS55	GNL	3	1-164inv	U62005	Rel/NF-kappa B homolog (Relish)
50	NPS56	GNL	3	1-207inv	X07311	HSP2
51	NPS57	GNL	3	15-438	X54061	205K microtubule-associated protein (MAP)
52	NPS58	GNL	3	1-80inv	J01102	HSP68
53	NPS59	GNL	3	1-450	Y10015	anon-66Da gene
54	NPS60	GNL	3	56-187	M63792	RAD6
55	NPS61	GNL	3	391-465	U28966	Septin 2
56	NPS62	GNL	3	1-514	M98351	fructose 1,6 biphosphate aldolase gene,
57	NPS63	GNL	3	46-251inv	U01035	Bottleneck gene
58	NPS64	GNL	3	49-450	U38238	HLH106
59	NPS65	GNL	3	328-581	AB004232	DAD gene
60	NPS66	GNL	3	1-436	U22176	15bp upstream of Brother gene on AC005557
61	NPS67	GNL	3	46-176	M90755	Transcriptional repressor protein Aef-1
62	NPS68	GNL	3	224-298	Y07908	Match to EST AI292767. This then matches serine/threonine protein kinase.
63	NPS69	GNL	3	1-531	M32311	Fascin 1
64	NPS70	GNL	3	1-421inv	X03889	HSP23
65	NPS71	GNL	3	548-882inv	Y12861	bifunctional ATP sulfurylase/APS kinase.
66	NPS72	GNL	3	83-135	U12010	putative serine/threonine protein kinase (nemo)
67	NPS73	GNL	3	1-357	U20554	UDP-glucose:glycoprotein glucosyltransferase mRNA
68	NPS74	GNL	3	1-20bp	U87925	Cbl gene confirmed by match to EST AA441040
69	NPS75	GNL	3	468-539	U23485	Guanylate cyclase. Match found via EST AA392994
70	NPS76	GNL	3	1-547	Y11349	UbcD4
71	NPS77	GNL	3	1-163	U09374	SNAP
72	NPS78	GNL	3	1-104inv	U62388	chromatin assembly factor 1 p55 subunit
73	NPS79	GNL	3	374-518inv	AB007692	Elongin B

74	NPS80	GNL	3	1-231	L06861	232-401 intron, 402-590 exon matching TAF110
75	NPS81	EST	2	1-314inv	AI259618	From genomic data.40bp upstream Prob. cytochrome B5. AC005641
76	NPS82	EST	2	509-591	AA202837	hypothetical yeast/arabidopsis/prot and mouse EST
77	NPS83	EST	2	166-393	AI293734	
78	NPS84	EST	2	261-377inv	AA202757	Match to Human EST
79	NPS86	EST	2	1-247	AA696498	
80	NPS87	EST	2	100-646	AA950073	
81	NPS89	EST	2	1-50inv	AA695104	
82	NPS91	EST	2	1-427	AA942153	
83	NPS92	EST	2	42-334	AA540352	
84	NPS93	EST	2	115-162	AI238523	
85	NPS97	EST	2	1-69inv	AI260872	EST matches mouse signalling factor U29156
86	NPS98	EST	2	5-77bp	AA801728	
87	NPS99	GNL	2	228-675	AF053083	Drosophila SMT3 gene
88	NPS100	EST	2	1-210inv	AA439866	
89	NPS105	EST	2	31-590	AA820803	Poss related to human aldolase
90	NPS106	EST	2	30-478	AA803545	AA697132 match to frog/human MSS1
91	NPS108	EST	2	76-178	AA438591	
92	NPS109	EST	2	1-169	AA979551	also AA567400
93	NPS111	EST	2	138-414	AA439261	Match to Rat EST
94	NPS113	EST	2	7-354	AI107509	
95	NPS114	EST	2	1-48bp	AA540348	
96	NPS115	EST	2	1-311inv	AA735555	
97	NPS118	EST	2	1-582	AI064020	match to AC005646. 26bp 5' to EST match area. AI542218/AI25740 765bp. Def SEC61 homologue
98	NPS119	EST	2	7-170	AA263700	also AA978721
99	NPS120	EST	2	364-583	AA941785	also AA695548
100	NPS121	EST	2	1-260 and 562-645	AA802928	also AA817115
101	NPS122	EST	2	1-395	AA539001	
102	NPS123	EST	2	1-35inv	AA735863	Poss. related to human death assoc prot 3 X83544
103	NPS125	EST	2	68-195 and 475-621	AA941860	
104	NPS127	EST	2	1-210inv	AA246460	
105	NPS128	EST	2	66-593	AA141928	
106	NPS131	EST	2	1-332	AA979014	
107	NPS134	EST	2	52-475	AA817254	
108	NPS137	EST	2	1-37bp	AA536262	1209bp EST contig.AA948897. AA539274, AA392320. Poss glycogen synthase

109	NPS139	GNL	2	35-86 and 475-581	AF113612	Drosophila Aspartate ligase
110	NPS140	EST	2	368-636	AA390587	
111	NPS141	EST	2	55-110inv	AA979454	sim to human REC1L protein. Acc. X57303
112	NPS142	EST	2	31-460	AA941359	
113	NPS143	EST	2	65-299	AA201303	also AA541066
114	NPS144	EST	2	538-581inv	AA698119	Matc to Human glycerol-3-phosphate dehydrogenase
115	NPS145	EST	2	111-549	AA696174	
116	NPS146	EST	2	107-243	AI064230	Also AA263288. Match to Mouse proteasome subunit
117	NPS147	EST	2	1-212 and 276-382	AI106957	1756bp EST contig. Also AA391125, AA567307, AA735971
118	NPS149	EST	2	1-107inv	AI114218	Also AA820473. (AF034644) putative cytochrome bc-1 complex core protein [Haematobia irritans irritans]
119	NPS150	EST	2	19-102 and 115-485	AA978449	Also AA940834. 103-114 gap of unknown length
120	NPS152	EST	2	182-362	AA802905	
121	NPS154	EST	2	235-279 and 376-452	AI259166	Also AI296787. Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex precursor (human)P10515
122	NPS155	EST	2	1-238inv	AA951193	
123	NPS156	EST	2	326-482	AA696743	Also AA803977
124	NPS157	EST	2	11-512	AA990758	Also AA246427. 975bp contig
125	NPS158	EST	2	1-406	AA697797	
126	NPS159	EST	2	1-29inv	AA802206	1341contig. AA202662, AA801949, AA942041
127	NPS160	EST	2	344-592	AA978904	
128	NPS161	EST	2	101-223 and 292-551	AA202366	
129	NPS162	EST	2	103-468	AA950164	
130	NPS163	EST	2	23-98 and 102-602	AA952159	99-101 gap of unknown length. Match to mouse EST
131	NPS166	EST	2	102-512	AA392519	also AA695318 and AA441243. 758bp contig.
132	NPS168	EST	2	304-541	AI515517	also AI404462. Poss Ras related protein
133	NPS169	EST	2	191-387	AA698481	
134	NPS170	EST	2	451-606inv	AA803082	2166bp EST contig. Poss. Alt splice. AA941565, AA820668, AA978815 and AA697381
135	NPS1067	EST	2	1-570	AI405762	Seq.sim to hypothetical prots from arabidopsis and C. elegans
136	NPS173	EST	2	1-38inv	AA391495	1135bp contig. AA439145 and AA949325. Match to mouse EST
137	NPS174	EST	2	353-476	AA942305	
138	NPS178	EST	2	72-391	AA951839	also AA979603
139	NPS179	EST	2	1-112	AI386817	also AI404737
140	NPS180	EST	2	435-475	AA438658	
141	NPS181	EST	2	31-212	AI106794	also AI107315

142	NPS1068	EST	2	1-228	AI403747	
143	NPS188	EST	2	1-272	AA802791	also AA390699
144	NPS189	EST	2	1-190	AA949990	also AA246423
145	NPS190	EST	2	1-202	AA201161	also AA438658
146	NPS191	EST	2	202-472	AA978927	poss. PCF11p homolog (Homo sapiens)
147	NPS192	EST	2	84-318	AA541084	also AA538937
148	NPS195	EST	2	390-509	AA951890	RIR2_mouse ribonucleoside- diphosphate reductase m2 chain
149	NPS198	EST	2	1-140	AA439230	
150	NPS199	EST	2	3-522	AA948907	also AA942191
151	NPS200	EST	2	25-76inv	AA802379	also AA246624
152	NPS1069	EST	2	9-100 AND 179-411	AI404485	
153	NPS1070	EST	2	60-449	AI108647	
154	NPS1071	EST	2	1-49inv	AA951902	other ESTs inc AA949796
155	NPS204	GNL	2	1-489	AF143860	Drosophila RanGap gene
156	NPS205	EST	2	1-278	AA940865	Xenopus/ human chromosomal assembly protein(U1367)
157	NPS206	EST	2	117-263	AA803314	also AA941391. Human B-cell receptor associated protein.
158	NPS207	EST	2	209-405	AA201448	856bp contig.AA438721 and AA247046
159	NPS209	EST	2	37-243	AA696343	also AA696180. Match to human/ C. elegans calponin
160	NPS210	EST	2	261-580inv	AA540783	
161	NPS211	EST	2	26-267 and 336-459	AA695850	also AA698310. FK84_RABIT P59 PROTEIN
162	NPS212	EST	2	1-224	AA441346	also AA390646 and AA696470. 1677 contig
163	NPS213	EST	2	1-514	AI064375	
164	NPS216	EST	2	181-299	AA540197	also AA695503 and AA941503.732bp contig
165	NPS217	EST	2	167-212inv	AA979442	also AA392418
166	NPS218	EST	2	89-159	AA536378	also AA949458
167	NPS219	EST	2	1-570	AI515537	Genomic AC004345. Also AI062109. 50bp upstream of EST.
168	NPS220	EST	2	1-184	AA390646	1705bp contig with AA440523 and AA696470
169	NPS225	EST	2	1-104 and 310-467	AI064169	also AA816652
170	NPS226	EST	2	1-288	AA439345	802contig with AA949877 and AA439626
171	NPS227	EST	2	1-350	AA979503	181bp upstream of EST Genomic AC005452
172	NPS228	EST	2	1-93 and 170-446	AI293141	
173	NPS229	EST	2	12-244	AI107445	also AA390813
174	NPS233	EST	2	12-478	AA390942	
175	NPS235	EST	2	11-103 and 296-389	AA802688	Poss 10k HSP

176	NPS236	EST	2	1-414	AA392415	
177	NPS239	EST	2	1-22bp	AA695619	
178	NPS240	EST	2	399-542	AA142132	
179	NPS241	EST	2	366-520	AA536537	
180	NPS242	EST	2	26-303	AA264253	Poss. SNF7 homologue
181	NPS243	EST	2	186-593	AA441247	also AA820771
182	NPS244	EST	2	318-431	AA202196	1942bp contig with AI108811, AA950029, AA202725, AA440491, and AA697007. Match to mouse EST
183	NPS245	EST	2	83-319inv	AI064123	also AA263284. Match to human androgen induced prostate proliferative shutoff assoc. protein.
184	NPS247	EST	2	1-89bp	AA441173	
185	NPS250	EST	2	65-414inv	AA440852	also AA541034
186	NPS251	EST	2	2-131	AI062640	
187	NPS252	EST	2	1-77inv	AA695507	Poss. match to Rat cytochrome C
188	NPS254	EST	2	89-251	AA736186	also AA801973. Poss. match to horse Thioredoxin
189	NPS255	EST	2	1-417	AA697603	also AA801716
190	NPS256	EST	2	1-528	AA950741	
191	NPS257	EST	2	1-53bp	AI063204	887bp contig with AA697347 and AA201878
192	NPS258	EST	2	1-44bp	AA441029	
193	NPS259	EST	2	1-157	AI114266	1141bp contig with AA949325, AA735675 and AA391495. Poss. match to human GMP
194	NPS260	EST	2	1-562	AA951648	1340bp contig with AA539581, AA802940 and AA263326
195	NPS261	EST	2	26-137 and 360-422	AA391135	Match to SEC61, different area to NPS118
196	NPS262	EST	2	1-124	AA696531	C.elegans pro7, Z66519/ mouse EST
197	NPS265	EST	2	442-549	AI124332	
198	NPS266	EST	2	52-382	AA949873	
199	NPS1073	EST	2	1-167	AI133902	see also AC006562 poss phosphate transporter
200	NPS269	EST	2	1-550	AI403609	Genomic AC005129, 420bp upstream of EST
201	NPS271	EST	2	299-375	AA391470	
202	NPS272	GNL	2	37-77bp	AF085601	Drosophila inorganic pyrophosphatase NURF-38
203	NPS273	EST	2	1-76inv	AA696584	
204	NPS275	EST	2	1-319	AA439099	1132bp contig with AA949325 and AA940848 poss. GMP synthase (human)
205	NPS276	EST	2	21-377	AA695424	
206	NPS277	EST	2	152-590inv	AA440949	
207	NPS278	EST	2	132-312	AI062455	also AA440915
208	NPS279	EST	2	68-311	AA816432	
209	NPS281	EST	2	1-258	AA979191	Match to human CGI-28
210	NPS283	EST	2	2-318	AA391495	

211	NPS285	EST	2	1-89bp	AA441636	AA820540 and AA817484. Alt splice
212	NPS1075	EST	2	59-488	AI295363	
213	NPS288	EST	2	51-170	AI114059	also AA941565
214	NPS289	EST	2	3-355 and 443-479	AA801691	also AA441008
215	NPS290	EST	2	378-471	AA950084	also AA978669
216	NPS291	EST	2	20-236 and 292-439	AI062945	
217	NPS293	EST	2	1-312	AA440345	2293bp EST contig. Poss. human cleavage and polyadenylation specificity factor, 160 kd subunit. AA201536, AA539993, AA942332, AA979174, AA202096
218	NPS294	EST	2	10-501	AA696930	
219	NPS295	EST	2	8-437inv	AA440135	
220	NPS296	EST	2	75-157	AI063979	also AA802032
221	NPS297	EST	2	1-144	AA699194	
222	NPS298	EST	3	507-547	AA441233	also AA392152
223	NPS299	EST	3	1-79inv	AA438352	33% over 113 AA Plant oxygenase
224	NPS300	EST	3	480-534	AI455428	
225	NPS301	EST	3	11-190inv	AA246916	Rat Mitochondrial import receptor
226	NPS302	EST	3	233-348	AA392258	
227	NPS304	EST	3	1-41inv	AI296848	Prob. 40-kDa V-ATPase subunit (mam)
228	NPS305	EST	3	255-354	AI388389	
229	NPS306	EST	3	335-448inv	AA441471	also AA540182. 52% over 107 AA like Bov/Hum/Mouse RHO GDP-dissoc. inhibitor 1
230	NPS307	EST	3	22-242	AA439855	also AA567284.
231	NPS308	EST	3	1-141 and 397-446inv	AA941606	
232	NPS310	EST	3	209-435	AA392324	
233	NPS311	EST	3	1-393inv	AA264796	
234	NPS312	EST	3	1-152	AA540030	Poss rat calcium binding prot.
235	NPS313	EST	3	85-596	AI109898	
236	NPS314	EST	3	365-473	AI259723	
237	NPS316	EST	3	1-141	AI294469	
238	NPS317	EST	3	145-325	AA140945	
239	NPS318	EST	3	1-331	AI259816	Related to Epsin (Hum)
240	NPS322	EST	3	209-433	AA141103	
241	NPS323	EST	3	1-98inv	AA246767	also AA141059
242	NPS324	EST	3	1180239inv	AA441468	also AA142226. 42% over 128 AA like C. elegans prot. Z66496
243	NPS327	EST	3	1-82inv	AA247070	1366bp contig with AA567381, AA568013, AA540724. C. elegans prot/human EST
244	NPS328	EST	3	433-469	AA802401	Prob. Alg2, glycosyltransferase hom./ Mouse MER 5

245	NPS330	EST	3	1-96inv	AI135263	Alt splice	
246	NPS331	EST	3	243-489	AA695904		
247	NPS334	EST	3	1-317	AA246386	also AA541060	
248	NPS335	EST	3	311-427	AA264961	57% over 82AA like mouse/ human Thioredoxin	
249	NPS337	EST	3	136-293inv	AA202880	Poss Ca 2 + ATPase	
250	NPS338	EST	3	74-276 and 344-438	AA263803		
251	NPS339	EST	3	3-166inv	AA202200	also AA202128	
252	NPS340	EST	3	1-48 inv	AA439530		
253	NPS341	EST	3	28-207	AI109459	Poss GPI-anchored protein(human)	
254	NPS342	EST	3	471-506inv	AI109779		
255	NPS343	EST	3	147-247	AA141054		
256	NPS1061	EST	3	65-118inv	AA141365		
257	NPS345	EST	3	144-549	AI063643		
258	NPS346	EST	3	1-148	AI107445	also AA390813	
259	NPS347	EST	3	1-75bp	AI297362		
260	NPS348	EST	3	96-230inv	AA392916		
261	NPS349	EST	3	1-47 and 145-317inv	AA201223	2631bp contig.	
262	NPS351	EST	3	537-687	AI454966	AA538867/AA439491/AA390780/AA390983/AA201661/AA391700/AA202007. Human 88	
263	NPS352	EST	3	10-441	AA202767	715bpcontig with AA201231 and AA392823. 31% over 129AA like Rat Nup84 and Human 88	
264	NPS353	EST	3	3-40inv	AA201212	KDa nucleopore complex	
265	NPS354	EST	3	1-33inv	AI404994	And AI260898. Alt splice	
266	NPS356	EST	3	1-292	AA539914	1042bp contig with AA201959	
267	NPS357	EST	3	36-454	AA440953		
268	NPS359	EST	3	145-253	AA264591		
269	NPS360	EST	3	47-380	AA539491		
270	NPS361	EST	3	202-381inv	AI403737		
271	NPS362	EST	3	270-443inv	AA567141		
272	NPS363	EST	3	1-478	AI134670		
273	NPS364	EST	3	413-535inv	AA263763		
274	NPS365	EST	3	1-99bp	AA568011		
275	NPS367	EST	3	64-449	AI107456		
276	NPS370	GNL	3	212-414	AF074957	Drosophila Karyopherin alpha	
277	NPS371	EST	3	1-146	AI295205	and AA141054. Alt splice	
278	NPS372	EST	3	8-382	AA567704		

279	NPS373	EST	3	74-224 and 297-344	AA539252	
280	NPS374	EST	3	1-347inv	AI260759	
281	NPS375	EST	3	1-77inv	AI260646	
282	NPS377	EST	3	160-306	AA202424	and AA264609.
283	NPS379	EST	3	300-379	AA802555	
284	NPS380	EST	3	322-573	AA802438	1030bp contig with AI063681
285	NPS381	EST	3	34-470inv	AA438500	
286	NPS382	EST	3	14-153 and 216- 348, 419-445	AI456286	
287	NPS383	EST	3	41-56 and 223-353	AI062265	1475 contig. AA694862 and AI064128. UNC51 ser/thr kinase (C.elegans)
288	NPS384	EST	3	1-429inv	AA247020	
289	NPS385	EST	3	1-143	AA264635	
290	NPS387	EST	3	58-491	AA201749	877bp contig with AA803278/ human hypothetical gene
291	NPS388	EST	3	1-162	AA392551	
292	NPS389	EST	3	1-379	AA438539	EST contig 1200bp, ORF at 5' end. Matches Human ERF 1. AA201773, AA263752 and
293	NPS390	EST	3	297-447	AA141715	
294	NPS392	EST	3	80-161	AA695862	
295	NPS393	EST	3	2-132	AA201517	
296	NPS394	EST	3	176-239	AA202297	Vertebrate vacuolar ATPase
297	NPS395	EST	3	1-33bpinv	AA567483	
298	NPS396	EST	3	1-209 and 271-468	AA817479	
299	NPS397	EST	3	17-139	AA441327	ATG orf hits Rat (and other) sodium dependant dicarboxylate transporter AB001321 58% over 74 AA
300	NPS398	EST	3	1-391	AA698011	
301	NPS399	EST	3	67-207	AA951986	nucleolar protein p40 [Homo sapiens]
302	NPS400	EST	3	1-186	AI295731	2018contig with AI258429, AA696170, AI109519, AA391348. MouseAPG-1, hsp/osmotic shock gene
303	NPS402	EST	3	1-82bp	AA201430	
304	NPS403	GNL	3	15-54bp	AF132912	Drosophila ARP gene. Match to EST matching ARP
305	NPS404	EST	3	1-140	AA541045	May be distantly related to cystatin
306	NPS406	EST	3	392-501	AA390337	
307	NPS407	EST	3	1-202 and 273- 440inv	AA141555	Matches mouse/human ESTs
308	NPS408	EST	3	158-252	AA263730	A little like yeast hypothetical protein YOL124c
309	NPS409	EST	3	324-370 and 448-545	AI259832	and AA990765. Human Ubiquitin conjugating enzyme 12

310	NPS410	EST	3	75-483	AI514268	20bp 5' to EST on AC006562. Part of ORF similar to molybdenum cofactor biosynthesis protein
311	NPS411	EST	3	1-435	AI293256	AI[Homo sapiens]
312	NPS412	EST	3	1-71 and 148-435	AA201987	Poss Asparaginase
313	NPS413	EST	3	12-408	AA540020	
314	NPS415	EST	3	1-38bp	AA201670	
315	NPS416	EST	3	15-404	AA201957	Mouse ESTs
316	NPS417	EST	3	1-353	AA695344	
317	NPS418	EST	3	1-450	AA441018	
318	NPS419	EST	3	301-334inv	AA202301	
319	NPS420	EST	3	245-393	AA735819	
320	NPS421	EST	3	1-147	AA440886	also AA695395. matches UMP kinase from C.elegans and bacteria
321	NPS422	EST	3	76-217	AA803640	859bp with AA803683 and AA803676. Human Ribosomal L28 protein
322	NPS424	EST	3	472-786 and 842-1073	AI257267	chick glycine cleavage system h protein
323	NPS425	EST	3	1-75bp	AA539327	
324	NPS426	EST	3	419-468	AI530922	
325	NPS427	EST	3	92-265	AI402854	
326	NPS428	EST	3	1-222 and 291-354	AA441362	40% like human/mouse proteasome subunit HsN3
327	NPS429	EST	3	1-219	AA202487	A little like hypothetical yeast protein YEY6
328	NPS430	EST	3	328-455	AA263590	39% over 61AA like human hRNP F
329	NPS431	EST	3	50-113	AA201496	57% over 50 AA like human oxoglutarate dehydrogenase
330	NPS432	EST	3	281-510	AA391430	
331	NPS434	EST	3	1-50 inv	AI292722	also AI534704
332	NPS435	EST	3	1-65inv	AA439393	
333	NPS436	EST	3	299-512inv	AA820797	also AA438876
334	NPS437	EST	3	1-52inv	AA697891	Homologue of Bovine gamma COP
335	NPS438	EST	3	1-31inv	AA696845	
336	NPS439	EST	3	1-384	AI259031	
337	NPS440	EST	3	1-82bp	AA803464	may match human hypothetical protein KIAA0258
338	NPS441	EST	3	169-489	AA539974	
339	NPS442	EST	3	1-46 and 432-524	AA941993	
340	NPS443	EST	3	43-431	AA803074	
341	NPS444	EST	3	1-197 and 268-534	AA695870	Dog/rat/ Yeast signal peptidase 18kd subunit
342	NPS445	EST	3	775-911	AA433251	
343	NPS446	EST	3	718-1007	AI297203	1122bp contig with AA438815 and AI455195
344	NPS448	EST	3	1-106inv	AA694869	1632bp with AA735812, AA568063 and AA695306. mammalian transketolase

345	NPS449	EST	3	1-99inv	AA392932	
346	NPS451	EST	3	1-260 and 310-510	AA391707	
347	NPS452	EST	3	45-141 AND 445-582	AI294564	Match to mouse EST
348	NPS453	GNL	3	345-460	AF152928	Drosophila karyophyllin alpha 3.
349	NPS454	EST	3	1-177	AA540743	1129bp with AI064582, AI519458 and AA568024
350	NPS456	EST	3	1-325	AA539054	Match to rat EST
351	NPS457	EST	3	1-73bp	AI062939	
352	NPS458	EST	3	927-1070	AI109224	
353	NPS459	EST	3	43-146	AA696728	Poss. isopentyl pyrophosphate isomerase
354	NPS460	EST	3	59-533	AI518328	
355	NPS461	EST	3	43-432	AA263622	
356	NPS463	EST	3	1-164	AA539661	Matches Human Proton ATPase like protein
357	NPS464	EST	3	1-152 and 214-579	AI388964	
358	NPS465	EST	3	365-462	AA438987	also AA264877. FXR1 mental retardation gene, Human
359	NPS466	EST	3	6-257	AA392117	
360	NPS468	EST	3	45-120 and 545-591	AA821194	987bp with AA736168. human 40s ribosomal protein s29
361	NPS469	EST	3	12-469	AA539752	
362	NPS473	EST	3	1-382 and 456-484	AA803203	
363	NPS476	EST	3	105-154	AA802887	also AA820871. Hypothetical C. elegans prot B0336.11
364	NPS477	EST	3	22-177	AA817394	V. similar to Dead box family of DNA helicases (initiation factors)
365	NPS479	EST	3	1-77inv	AI064638	
366	NPS480	EST	3	1-37bp	AA736157	also AA140746. Match tomouseEST
367	NPS482	EST	3	7-369	AA820427	
368	NPS483	EST	3	1-533	AA391736	1692bp with AA202259 and AA820861.
369	NPS484	EST	3	158-470	AA567184	
370	NPS486	EST	3	1-122	AA735277	1176bp with AA697907
371	NPS487	GNL	3	514-616	AF129080_1	Drosophila COP9 complex homolog subunit 1-2 DCH1-2
372	NPS489	EST	3	140-189	AA202581	Match to human EST
373	NPS490	EST	3	41-377	AA390775	
374	NPS491	EST	3	169-488	AA539898	
375	NPS492	EST	3	1-127	AA390453	
376	NPS493	EST	3	1-321inv	AA568061	1356bp with AA264532 and AA441674
377	NPS495	EST	3	102-311	AA141908	794bp with AA802528
378	NPS496	EST	3	1-100inv	AA539224	
379	NPS497	EST	3	431-622inv	AA246367	Hum ribosome S6 PK

380	NPS499	EST	3	46-319	AA817295	
381	NPS501	EST	3	35-383	AA439743	
382	NPS503	EST	3	1-264	AA441568	
383	NPS504	EST	3	337-408 and 479-568	AA247082	
384	NPS505	EST	3	1-321inv	AA201685	868bp contig with AA540405
385	NPS506	EST	3	83-218	AA540693	1450bp with AA441321, AA440080 and AA392794. Match to mouse EST
386	NPS507	EST	3	452-1044	AI295950	
387	NPS508	EST	3	2-339	AA439667	
388	NPS509	EST	3	12-394	AA539198	
389	NPS510	EST	3	83-227 and 498-518	AA696927	Match to human citrin
390	NPS512	EST	3	360-501	AA438961	Human KIAA0160 gene
391	NPS513	EST	3	53-260inv	AA735138	
392	NPS514	EST	3	1-237inv	AI064414	
393	NPS515	EST	3	1-67inv	AA540712	809bp with AA440879 and AA440431.human cyclin G assoc. Kinase.
394	NPS516	GNL	3	596-682inv	AF132145	Drosophila damage-specific DNA binding protein DDBa p127 subunit
395	NPS517	EST	3	1-513	AF007159	
396	NPS518	EST	3	13-235inv	AI511691	
397	NPS519	EST	3	1-61inv	AA264883	also AA392712. Alt splice.
398	NPS520	EST	3	30-451	AA438399	821bp contig with AA439438
399	NPS521	EST	3	600-627	AA440272	1324bp contig with AA438941
400	NPS526	EST	3	65-483	AA264865	
401	NPS527	EST	3	1-246	AA263693	
402	NPS528	EST	3	137-160 and 379-475	AA698620	
403	NPS529	EST	3	1-51inv	AA391350	
404	NPS530	EST	3	100-499	AA392183	DNA J homologue
405	NPS531	EST	3	149-348 and 412-457	AA696390	mouse/human yeast/ub fusion protein 1
406	NPS532	EST	3	1-267inv	AA802961	816bp with AA817584
407	NPS533	EST	3	1-259inv	AA699045	Poss. Slug cDNA25
408	NPS534	EST	3	1-99bp	AA952055	1205bp with AA202358, AA202625 and AA951416. Siah binding protein 1(human)
409	NPS535	EST	3	1-610inv	AA142266	
410	NPS536	EST	3	52-534	AA696974	Matches Human CGI-37 protein
411	NPS537	EST	3	503-626 and 734-1069	AI532170	1565bp with AI544333 and AI062662. Definite transcription factor, MTF-1

412	NPS538	EST	3	442-569	AA567128	Match to mouse EST
413	NPS540	EST	3	1-79bp	AA950480	
414	NPS541	EST	3	2-360	AA950161	1217bp with AA950864 and AA950181
415	NPS542	EST	3	30-194 and 291-366	AA539625	882bp with AA202440 and AA390927
416	NPS543	EST	3	1-255	AA951297	
417	NPS544	EST	3	20-95 and 479-654	AA948996	781bp with AA541068 and AA950730
418	NPS545	EST	3	1-378	AA941568	
419	NPS546	EST	3	228-522	AA801928	
420	NPS547	EST	3	14-98	AA951147	695bp with AA695598 and AA540269
421	NPS548	EST	3	1-279	AA697191	1002bp with AA392404 and AA438791
422	NPS549	EST	3	650-689	AI518422	
423	NPS1065	EST	3	27-689	AI535025	
424	NPS551	EST	3	8-563	AA950826	
425	NPS553	EST	3	48-150	AA949934	Mam. Casein kinase
426	NPS555	EST	3	411-582	AI109292	
427	NPS556	EST	3	1-279inv	AA202259	1693bp with AA391736 and AA820861
428	NPS557	EST	3	131-647	AA142065	poss. succinate semialdehyde dehydrogenase
429	NPS558	EST	3	76-559	AA536402	
784	NPS921	GENO.	2	1-537INV	AC006073	In intron of gene coding for 246AA protein at 1663-44895. No database matches
785	NPS922	GENO.	2	1-720	AC004299	In space before Drosophila Homologue of Human C-TAK 1 ser/thr kinase
786	NPS924	GENO.	2	1-599	AC004115	In space before gene coding for 372AA protein. 16297-18074. No database matches.
787	NPS925	GENO.	2	1-581	AC004716	In intron of gene coding for 355AA protien. 51777-83843bp. No database matches
788	NPS926	GENO.	2	1-628	AC005889	No good predicted exons in this area.
789	NPS927	GENO.	2	1-536	L49408	space before gene coding for 401AA protein. 75943-77148bp. Sequence similarity to Mammalian glia maturation factor.
790	NPS928	GENO.	2	1-86inv	AC004296	In space before gene coding for 878AA protein. 39765-47183bp. Sequence similarity to Mouse G-protein
791	NPS929	GENO.	2	1-573inv	AC004306	No good predicted exons in this area.
792	NPS1077	GENO.	2	1-648	AC006472	In intron of gene coding for 1876AA protein at 62506-79351. Seq similarity hypothetical proteins from human and yeast
793	NPS931	GENO.	2	1-463inv	AC006092	In space before gene represented by ESTs AA990657 and AI294791.
794	NPS932	GENO.	2	1-519	AC006073	No good predicted exons in this area.
795	NPS933	GENO.	2	1-704inv	AC007176	In gene coding for 566AA protein. 85106-110350bp(complement). Possible transcription factor
796	NPS935	GENO.	2	1-307inv	AC004423	In space before gene coding for a 702AA prootein at 47585-59400bp. Sequence similarity to Xenopus DNA repair protein XPGC

797	NPS336	GENO.	2	1-412inv	AC005448	Part of gene coding for 422AA protein at 34104-35373(complement). Strong sequence similarity to Drosophila Septin 2
798	NPS937	GENO.	2	1-478	AC004313	Possibly in 3'UTR of gene coding for 355AA protein at 39720-40727. Weak sequence similarity to potassium channel gene
799	NPS938	GENO.	2	1-489	AC004641	In intron of gene coding for 402AA protein at 101233-153110bp. Strong sequence similarity to Xenopus FLAP endonuclease.
800	NPS1078	GENO.	2	1-558inv	AC004306	No good predicted exons in this area.
801	NPS940	GENO.	2	1-623	AC001646	In intron of gene coding for 724AA protein at 9930-72686 (complement). Strong sequence similarity to Mouse serine C-palmitoyltransferase
802	NPS941	GENO.	2	1-544	AC005334	ESTs matching at 74650 (AA803646, AI518976, AI108114) Sequence similarity to U5 snRNP
803	NPS942	GENO.	2	1-201	AC004154	In intron of gene coding for a 292AA protein at 12210-30840bp. Sequence similarity to human geranylgeranyltransferase
804	NPS943	GENO.	2	1-524	AC004766	In intron of gene coding for a 1442AA protein at 40620-93241(complement). Sequence similarity to hypothetical C.elegans gene ZK1128.2.
805	NPS944	GENO.	2	1-621	AC004361	No good predicted exons in this area.
806	NPS945	GENO.	2	1-569inv	AC007185	No good predicted exons in this area.
807	NPS946	GENO.	2	1-462	L49408	In space before gene coding for 401AA protein at 75943-77148bp. Sequence similarity to Mammalian glia maturation factor.
808	NPS947	GENO.	2	1-233inv	AC005750	In intron of gene coding for an 1813AA protein at 51190-77775 (complement). Sequence similarity to Rat CPG2 protein
809	NPS948	GENO.	2	1-525	AC005269	No good predicted exons in this area.
810	NPS949	GENO.	2	1-531	AC005554	In intron of gene coding for 2355AA gene at 16134-35638. Sequence similarity to Rat Fatty acid synthase.
811	NPS951	GENO.	2	1-443inv	AC004758	No good predicted exons in this area.
812	NPS952	GENO.	2	1-498inv	AC005894	In intron gene coding for 196AA protein at 57158-63906bp. Weak sequence similarity to rat metalloprotease.
813	NPS954	GENO.	2	1-320	AC004564	In intron of gene coding for a 156AA protein at 20899-39698bp. Sequence similarity to Arabidopsis Immunophilin
814	NPS956	GENO.	2	1-429	AC005716	In intron of gene coding for 732 AA protein at 63422-80946bp. Sequence similarity to Rat follistatin
815	NPS958	GENO.	2	1-71bp	AC007180	In intron of gene coding for 217AA protein at 81722-84603 (complement). No database matches
816	NPS1079	GENO.	2	1-75bp	AC004758	In intron of gene coding for a 945AA protein at 87648-113518. Strong sequence similarity to Human retinoblastoma binding protein 2
817	NPS962	GNL.	2	1-116inv	AC001661	In intron of gene coding for a 286AA protein at 49143-60866bp (complement). Is Dros Wing blister gene
818	NPS963	GENO.	2	1-512inv	AC004758	In intron of gene coding for a 945AA protein at 87648-113518. Strong sequence similarity to Human retinoblastoma binding protein 2

819 NPS964 GENO. 2 1-54bp In space before gene coding for 433AA proetin at 21602-22903. No database matches.

820 NPS666 GENO. 2 1-557inv In intron of gene coding for 424AA protein at 70149-97938. No database matches.

821 NPS968 GENO. 2 1-202 No good predicted exons in this area.

822 NPS970 GENO. 2 1-534inv In intron of gene coding for 309AA protein at 64276-77888bp. No database matches

823 NPS971 GENO. 2 1-438 No good predicted exons in this area.

824 NPS972 GENO. 2 1-524INV No good predicted exons in this area.

825 NPS973 GENO. 2 1-492 space before gene coding for 310AA protein at 39927-45298bp. Sequence similarity to mammalian Uridine phosphorylase.

826 NPS974 GENO. 2 1-535 No good predicted exons in this area.

827 NPS975 GENO. 2 1-47bp In intron of gene coding for 826AA protein at 3650 -13339bp (complement) ESTs AA949050 and AA817663 come from this gene. Sequence similarity to Helix-loop-helix genes

828 NPS976 GENO. 2 1-551 In intron of gene coding for 2355AA gene at 16134-35638. Sequence similarity to Rat Fatty acid synthase.

829 NPS977 GNL 2 1-100, 146-499 *Drosophila Drongo* gene

830 NPS978 GENO. 2 1-580 Part of gene coding for 2355AA gene at 16134-35638. Sequence similarity to Rat Fatty acid synthase.

831 NPS979 GENO. 2 1-256inv Space before gene coding for 834AA protein at 33470-40630. Sequence similarity to bromodomain containing proteins.

832 NPS980 GENO. 2 1-406 In intron of gene coding for a 822AA protein at 9312-46969. No database matches.

833 NPS982 GENO. 2 1-460 No good predicted exons in this area.

834 NPS983 GENO. 2 1-99bp In intron of gene coding for a 289AA protein at 43804-61450bp. No database matches

835 NPS985 GENO. 2 1-178inv In intron of gene coding for 300AA protein at 30647-46841. Weak sequence similarity to Mouse surfeit gene

836 NPS986 GENO. 2 1-602 No good predicted exons in this area.

837 NPS987 GENO. 2 1-562 No good predicted exons in this area.

838 NPS988 GENO. 2 1-521 In intron of gene coding for 1277AA protein at 40819-69834 (complement). Sequence similarity to human nuclear transport receptor.

839 NPS989 GENO. 2 1-619 No good predicted exons in this area.

840 NPS991 GENO. 2 1-535inv In intron of gene coding for a 802AA protein at 28001-49228bp. No database matches.

841 NPS992 GENO. 2 1-342 No good predicted exons in this area.

842 NPS993 GENO. 2 1-512 In space before gene coding for a 399AA protein at 66560-68732bp. Sequence similarity to mitochondrial carrier protein genes.

843 NPS994 GENO. 2 1-515inv No good predicted exons in this area.

844 NPS995 GENO. 2 1-499bp No good predicted exons in this area.

845 NPS997 GENO. 2 1-565inv No good predicted exons in this area.

846 NPS998 GENO. 2 1-568 3bp overlap with gene coding for 1365AA protein at 67351-74867bp. ESTs AI106939 and AI296430 come from this gene

847	NPS999	GENO.	2	1-503	AC005558	In intron of gene coding for 1277AA protein at 40819-69834bp (complement). Sequence similarity to human nuclear transport receptor.
848	NPS1000	GENO.	2	1-620	AC004351	In gene coding for 676AA protein at 34511-37955bp. Sequence similarity to mouse LUN gene.
849	NPS1001	GENO.	2	1-519inv	AC004766	In intron of gene coding for 1467AA protein at 867-18363bp. Sequence similarity to Drosophila Lipase 3.
850	NPS1002	GENO.	2	1-80inv	AC005247	In gene coding for 805AA protein at 160506-163420bp. Sequence similarity to Mammalian Valyl tRNA synthetase.
851	NPS1003	GENO.	2	1-370inv	AC005129	In intron of gene coding for a 1208AA protein at 56208-83122bp (complement). No database matches.
852	NPS1004	GENO.	2	1-748inv	AC005894	No good predicted exons in this area.
853	NPS1005	GENO.	2	1-535inv	AC005447	Part of gene coding for 239AA protein at 507-13551bp (complement). Sequence similarity to C. elegans gene acc. no. AF002196
854	NPS1006	GENO.	2	1-581inv	AC005643	In intron of gene coding for 242AA protein at 33006-40459bp (complement, incomplete sequence). No database matches.
855	NPS1007	GENO.	2	1-342	AC005554	Part of gene coding for 2355AA gene at 16134-35638. Sequence similarity to Rat Fatty acid synthase.
856	NPS1009	GENO.	2	1-77inv	AC004532	In intron of gene coding for 1145AA protein at 5993-19843. Sequence similarity to C.elegans AF067608.
857	NPS1010	GENO.	2	1-496inv	AC007186	Space before gene coding for 351AA protein at 110375-111625bp. Sequence similarity to Human YL gene.
858	NPS1011	GENO.	2	1-582	AC007176	In intron of gene coding for 566AA protein at 84105-109350 (complement). Sequence similarity to zinc finger transcription factors.
859	NPS1012	GENO.	2	1-483	AC004423	In intron of gene coding for 604AA protein at 3052-8810bp. Sequence similarity to C.elegans AL021481 gene.
860	NPS1013	GENO.	2	1-560	AC005811	No good predicted exons in this area.
861	NPS1016	GENO.	2	1-596	AC005653	In intron of gene coding for 528AA at 40963-70180bp. Sequence similarity to C.elegans
862	NPS1017	GENO.	2	1-539	AC004516	Part of gene coding for 1730AA protein at 50171-62324bp. Sequence similarity to C.elegans UNC89
863	NPS1019	GENO.	2	1-505inv	AC005285	In intron of gene coding for 1142AA protein at 116605-128877bp. Sequence similarity to Guanine nucleotide exchange genes.
864	NPS1021	GENO.	2	1-504inv	AC007137	No good predicted exons in this area.
865	NPS1022	GENO.	2	1-191inv	AC005643	No good predicted exons in this area.
866	NPS1023	GENO.	2	1-468	AC004642	In intron of gene coding for 1296AA protein at 1037-28442(complement). Sequence similarity to putative lysophosphatidic acid acyltransferase [Mus musculus]
867	NPS1024	GENO.	2	1-578inv	AC005749	In intron of gene coding for 1481AA protein at 159-11694bp. Sequence similarity to KIAA0596 protein [Homo sapiens]
868	NPS1025	GENO.	2	1-598	AC007185	No good predicted exons in this area.

869	NPS1027	GENO.	2	1-634	AC004340	In space before gene coding for 864AA protein at 20219-29453 (complement). Good sequence similarity to Human sec24 homologue
870	NPS1028	GENO.	2	1-415	AC005456	Space before gene coding for 450AA protein at 45629-48055bp (complement). Sequence similarity to Human GMP synthase.
871	NPS1029	GENO.	2	1-198	AC004375	No good predicted exons in this area.
872	NPS1030	GENO.	2	1-316	AC005472	Space before gene coding for 626AA protein at 20859-27089bp. Sequence similarity to human NAT1/death assoc. prot
873	NPS1031	GENO.	2	1-495inv	AC004154	Space before gene coding for 292AA protein at 12210-30840bp. Sequence similarity to human rab geranylgeranyl transferase
874	NPS1032	GENO.	2	1-116	AC004328	In intron of gene coding for 1063AA protein at 63470-78557 (complement). Has been predicted from Dros genomic ALO35311 and has similarity to mouse BOP1
875	NPS1033	GENO.	2	1-581inv	AC005112	In intron of gene coding for 407AA protein at 3680-49217 (complement). No database matches
876	NPS1034	GENO.	2	1-506inv	AC004367	Space before gene coding for 387AA protein at 3496-35348bp. No database matches
877	NPS1036	GENO.	2	1-411	AC005472	1st exon of gene coding for 626AA protein at 20859-27089bp. Sequence similarity to human NAT1/death assoc. prot
878	NPS1080	GENO.	2	1-492	AC007121	gene coding for 365AA protein at 22511-56594 (complement). No database matches
879	NPS1038	GENO.	3	1-291	L49405	In intron of gene coding for 665AA protein at 632-41487 (complement). Sequence similarity to human hypothetical SBB103 protein
880	NPS1039	GENO.	3	1-454	AC004658	In intron of gene coding for 394AA protein (complement). No database matches
881	NPS1062	GENO.	3	1-376	AC007757	Also matches Dros. EST A951801. Poss. Transcription factor.
882	NPS1044	GENO.	3	1-597	AC006091	In intron of gene coding for 564AA protein at 74249-97818bp. Sequence similarity to YH3_Yeast hypothetical protein.
883	NPS1045	GENO.	3	1-498	AC005720	No good predicted exons in this area.
884	NPS1046	GENO.	3	1-375	AC005814	Space before gene coding for 562AA protein at 60626-68675. Sequence similarity to Rat NAB1.
885	NPS1049	GENO.	3	1-486	AC004713	In intron of gene coding for 575AA protein at 10435-29297. Weak sequence similarity to CD36 genes.
886	NPS1050	GENO.	3	1-544	AC005813	No good predicted exons in this area.
887	NPS1051	GENO.	3	1-549	AC006936	No good predicted exons in this area.
888	NPS1052	GENO.	3	1-306inv	AC005425	No good predicted exons in this area.
889	NPS1053	GENO.	3	1-579inv	AC005720	In intron of gene coding for 394AA protein at 61401-93968. No database matches
890	NPS1056	GENO.	3	1-191inv	AC004266	In intron of gene coding for 931AA at 52045-70222bp (complement). Sequencw similarity to C. elegans Zinc finger protein. Drosophila EST A1259457 comes from this gene
891	NPS1059	GENO.	3	1-264	AC006936	No good predicted exons in this area.
892	NPS1063	GNL	3	488-536	A1062190	EST comes from Dros ferrochelatase
893	NPS1064	OG	3		AF104256	Sequence similarity to Human transcriptional co-activator CRSP150
894	NPS1076	EST	2	101-597	A1388606	1249bp contig with A1258281 and A1258326
895	NPS1081	GENO.	2	1-491	L49408	No good predicted exons in this area.

896	NPS1082	GENO.	2	1-475inv	AC005714	space before 390AA orf at 162294-163466. Hom to hum. death assoc prot 3
897	NPS1083	GENO.	2	1-461	AC004375	No good predicted exons in this area.
898	NPS1084	OG	2	12-419	AF000177	translational sequence similarity to human CaSm protein

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caaatacttg gcaatttttt aaccaggtaa gcagaaagtg ctgaatcata atcgtagaat 300
tggtgtgacc gtagaaccta agagccctgt ctaattaatc ctttaatatg atggatatag 360
caatttttcg gtggcgtcgc ttgcaaatta aaaatggcga taccgcgtat agacatttag 420
ctaatttttg gccttttaaa accatagttt tttgattttt tagcgcggag cgccgtatgt 480
aggcctgaat ttgtttacta taaagtgaac cccctcgaag aacctaata ggaaataata 540
aatagccggt gactaccggc aacgccatt aacacgcaca cttac 585

<210> 6

<211> 408

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (270)..(408)

<223> Area matching *Drosophila* Neuron surface antigen 2
gene, Acc. No. U22439.

<400> 6

gcttagatga tgattcagtg gagaagctcg gcgtcggatt gtcgtctact ccgaacttga 60
gaagcggcgg agcttggggg ttgaccccat ttgtttatac ggccctctcg agccggcgtc 120
gttggtcaatt atcggtttaa cccatgtcga ccgcgggggc cagtggcaat taattaattc 180
aatcgcttca attgactgcg tategtgtt aggaacggct ttaatcgctg taattcaata 240
aacatttcct gctctctctt cccatcgcag ccaaaatcgg aatcttctat gtggccttct 300
acggagtcct agccgccctc gttgccatct gcatgtgggc cttcttccaa actctcgatc 360
ctcgcatccc caagtggacc ctggaccggt ccctgatagg tacaaatc 408

<210> 7

<211> 540

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (30)..(461)

<223> Area matching *Drosophila* Indora gene, Acc. No.
Y13272.

<400> 7

cgacgggacc accttatgtt attatatgag ctgaaccata cttttttcga taaccgaatt 60
atcccaaact tatcgggtgc agcttataag agttgcacac cgtccgata cttagctcac 120
catactnnnt ttacattggt atgaccacgc tgactgcaag ccactaccg attattcatc 180
gagactttat cgccaactgc ttcagtcgcc tctacaaaac cccccgtac actcagacta 240
gggtactcat agacacccta ggctgagacc gactgaaggc accttactgc cgaatgtcct 300
tggcatgata ggttcccaca actcgtcctt ggaggtcttc cggcgcgtaa tacgcgttgc 360
cgatcttctt ccgaagtcgc gattttatga acgtcgggcc aaacttggcg ttataaccag 420
tttgaaagca gcttggttg aaattccggc gataaacttc ttggccttcg acaaacgata 480
ccatacgaga acngatatta tatctcttct cgntctcgnt gggcttactt ctcactcgac 540

<210> 8

<211> 267

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(267)

<223> Area matching *Drosophila* GDP dissociation
inhibitor homologue gene, Acc. No. L03209

<400> 8

gtctgtacga caagttcgga ttggacaaga acacgcagga cttcaccggc cacgccctgg 60
cccttttccg cgacgatgag tatctgaacg agccggccgt gaacaccatc cggcggatta 120
agctctactc cgattcgtg gcgcgttacg gcaagtcgcc ctacctttat cccatgtacg 180

gcctgggtga gctgccccag ggattcgac gtctgtcggc catctacggc ggcacctaca 240
tgcttgacaa gcccatcgac gagattg 267

<210> 9

<211> 583

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (345)..(583)

<223> Area matching *Drosophila* Germline transcription
factor gene, Acc. No. L17340

<400> 9

cgatactctt tggcgctacc acgagatagc agggctgccg aaacatcgat tgctgcatta 60
tcgattgtgc ttcgcaacat catcgatttg tttcaggcca aaaacgttat tatgttataa 120
tatatttata ataattaatt aagtataaat taaagactta aattaatttt taaattgtaa 180
acgtattttt cacaaatgta aatgtacgat agtacaaatt agtttaaatt atagagcatg 240
gagtgaccat cactgatcgc gttaccaaca atttttttta aataaatttg agcttgacat 300
attcgcgctc ttgatcetta tacagttaaa gcaaacaatt gatcaattaa aaaatcatca 360
tctcaattct ttcgtagtat tattcataca gacaattatt gtattaccaa tttttccctt 420
tttagtttac acctacgcca ctacgtgtta taataaaagg tttgcaattc agcacatatt 480
ttattggtaa tatatatattt cagcagtata aacagtgccg gccatgccgg ccattcatga 540
agaatttaac caaaactact tacaaatggg aaatttgatg gca 583

<210> 10

<211> 480

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(480)

<223> Area matching *Drosophila* Histone H3 gene, Acc. No.

AB003784

<400> 10

gtttattgtg ttttcaaacg tgaagtagtg aacgtgaact ttagtgaaac ccaaatacga 60
gatggctcgt accaagcaaa ctgctcgcaa atcgactggg ggaaaggcgc cacgcaaaca 120
actggctact aaggccgctc gcaagagtgc tccagccacc ggaggtgtga agaagccaca 180
ccgctatcgc cctggaaccg tggccttgcg tgaaattcgt cgctaccaa agagcaccga 240
gcttctaata cgcaagctgc ctttccagcg tctgggtgct gaaatcgctc aggacttta 300
gacggacttg cgattccaga gctcggcggt tatggctctg caggaagcta gcgaagccta 360
cctggttggt ctcttcgaag ataccaactt gtgtgccatt catgccaagc gtgtcaccat 420
aatgccccaa gacatccagt tagcgcgacg cattcttagg ccacgtgct taagctgaca 480

<210> 11

<211> 542

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (179)..(360)

<223> Area matching *Drosophila* EST AA699128, this EST
matches the 5' of *drosophila* V-ATP ase gene
AF006655 gene.

<400> 11

ggccatggcg cctttttcct ttcctgcctt ccgtgccctt cgtgcggctt cgtcatcaca 60
accggacgga ttcgtgttcg gctgacgaac cggatcgag atacttcggc cgttggtttt 120
ttcgacttcc atggcatctg gtcgttaggc cagccgttca ttcggcaacg aacccccgac 180
atagaagcac gtcagcatgt ggcacaaccg gagaaagtag gaaaaacaaa cggagtagag 240
gaaaagccca acaaaaaaaaa aaaacgaacg acggccaggg aaaaatgcc aaaaacctgg 300
tggaaaaagt tcctaaccat tctattgaga cgcaaggagt gcttaggatc aagtgttttg 360
tgtaagcaac gaggcctgta ccagtgtcac catgtgcata tataccatcg aaacatagac 420
aaactggcct ggactgttgc gccagagatt tgggtggtgtg aatgggtcat tcggggaaat 480
gggtcctttg ctgaaaaaaaa ggccttttca ggcttcgaca tttttacgta atggacgatt 540
ac

542

<210> 12

<211> 409

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (226)..(409)

<223> Area matching *Drosophila* mitochondrial PolB gene

Acc. No. U94702

<400> 12

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gattgttggt ctcgtttcgg atttatagct agatttttaa caataagggc tggatatatt 60
aaattgaaca aatgtgatgg agacatgtta attaaactag atcacaataa caagaaaatt 120
gcttttaaatt aagatagaat aaacacataa atcaacattt ttgcaaggac aatacttttc 180
agataacatt tagctgattg ttccgaaact cagttccacc tctgattttg tgctggtgag 240
aatgtttgct ctgttcagca gcccgttttt actgcaaaat tgcaacaaaa tcgaatgaaa 300
aggccctaaa ttggacttca agcagctaac gcatccaccc aaggtgccac agacacccag 360
tggactccga agtttccgac accagcgcct tcgaaatcca gatcgacac 409
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<210> 13

<211> 507

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (110)..(191)

<223> Area matching *Drosophila* Integrin beta subunit
gene, Acc. No. L13305.

<220>

<221> intron

<222> (192)..(395)

<223> Probable Intron in *Drosophila integrin* gene

<220>

<221> misc_feature

<222> (396)..(472)

<223> Area matching *Drosophila integrin* gene

<400> 13

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gtagtgggga agaattggaa ggggtgacaca catgaaaaag tgttggtagc cacatgataa 60
atcaaatttg ataagataag aaaagctaaa taaaacaatt atccannnga ccaacttaag 120
gtatgcccgc tggggtgtga cttggacagc ctgatcactg gtttcgtagt cctttagggg 180
cttatactga aggctctagg accggctggg tctcgatat atccgtttca ctgcagttgt 240
agttaagtag ttgccggcga gagagacaac gatatccac ctggtattcc tgatatgcaa 300
ccaaatagga aaatgattga cttcgcaagg atgacagcag cagtaggaac aggaaccgtt 360
tatgttttct tgccatctcc ctcgtactca ccttggtccg tgcaccaagc cgcattccag 420
atgagcggat aaacatcttt cgcagctgct gcgtgcctgc actgatcatc tgcgtaaaag 480
aatggcgat aacaaatccg ttatgtc                                     507
```

<210> 14

<211> 432

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(432)

<223> Area matching *Drosophila* Tra-2 gene. Acc. No.

X57484

<400> 14

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atcgggagcc actcagtagc gggcgtctcc attgcagcgc cagatataaa cacaagcgat 60
cggcgtcatc atcgtcagcg gggacaactt catccggaca caaggaccgc aggtaaatgt 120
gtacacacat atgtgagacg accctaaacg atacctcttt tgacatgaag catcgagtag 180
ttttgactgg cagtttgga aaaaggttca actgtcatag ggccctttca tttggatttg 240
ccccctcagc cgattcagct ggtgctcttg ccaagaaagt taaaaccaa aatcattcaa 300
```


gccgatttca tttcattgga agaaaccaac caaccaacca accaaccaac gaacatcact 360
atgtaagaac ccaccgaagc aatcattttc attctacgtc cactaccaa gaatttggcc 420
gaaagaggtc ga 432

<210> 15

<211> 439

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (61)..(276)

<223> Area matching *Drosophila* EF2 gene. Acc. No.

X15805

<400> 15

gtatagatcg agtggaaact cgttataata tgtacataac gatgccttat ttattttaca 60
ggtcaacttc accgtcgacg agatccgtgg cctcatggnn nacatccgca acatgtctgt 120
gattgccccg tagaccacgg caagtccact ctgaccgatt cccttgtgtc gaaggctggg 180
tattggcagg agccaaggct ggtgagactc gtttactga caccgcaag gacgagcagg 240
agcgctgcat taccatcaag tcgacgtaag accagtcatg ttccagcacc cacggctttt 300
ttaataagct ttcttttttg cgtggctttc ctgttatttg aggtggagga aaaggatctt 360
ggtgttgatt taccaccggg ttagcgcgag aaggagtgc aagggtttcc tgatcacttt 420
gatcgattgc ccggttcac 439

<210> 16

<211> 532

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(532)

<223> Area matching *Drosophila* genomic sequence

AC005121. *Drosophila* TU-36B gene matches this

sequence 49bp 3' to NPS0018.

<400> 16

atcgagcgag tgcgatacga aaacaaaagc cgagcgccgc tccaataaaa gttcagttgg 60
cgctacgtaa acaaactttg cggttagtct gcatctgggg tgtccagaac gaccggttct 120
ttcgttaggg actaagatga acttggggaat caaacggcta gttatcagca acgattaagc 180
actagcgttc aaggtacttc tgggggttaa ataaactcca tttatcagtg tacatcgatt 240
aacaacagc gcacaaaatg acgccaatg ttaaggacga tggtgactgg agagtatccg 300
gaatatccag aaattaccg agctatcgcc agcatcgacc gattaccagt gaaagggttg 360
catcgaatat acccataaat ttcaaattaa ttaaataaaa ctacatattt acattttctc 420
ttgctcagct ggctggaggg gaaaaatgta gatgacgaag ccgaaggctt ttggcgaatt 480
aacgatcgct ctacgactta agcgactttg ccggctcgctc cgggtgggctc at 532

<210> 17

<211> 536

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (250)..(536)

<223> Area matching *Drosophila* GO protein alpha subunit
homolog class II gene, Acc. No. M29602

<400> 17

atcggtgcaa taaaaacagc gagtcgcaa aaagaagcgc aaagcgaacg gaaccaataa 60
gaacagccaa acgcaaagag agcctcctgc acacacacgc acacagcagg ctgaagcaga 120
cccacacaca cgcatacact agtgcggtgt gtatacgact ggaaaactag gcggtggtaa 180
atgtgaagct gaaaaaagct gaaaaaaagg aaaaggaaaa ctctgggggg ggtgggtggc 240
ggcccagtg ggggggggtg tggcagtggt cagcgcgtga gagtgccgta gtgcgtgccg 300
tgtgagtgag tgagtgtgtg cgcgcgtgtg agtgaaacag cgacaaaacta aatgaaaatt 360
tatacatccg aaatgggttaa cagtttgcac aaaaacggca ttactttttg catatgttaa 420
tgtgcttagg caaacgctcg aaaaagaaaa cttcacacc caccggcttt tttttcacca 480
accggcgct ttttttagcg ctacgcccac gcttaataca taccctgca taaaaa 536

<210> 18

<211> 476

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (81)..(476)

<223> Area matching *Drosophila Lachesin* gene, Acc. No.

L13255

<400> 18

ggcacattca aggtgcccac ctccaggcaa gttgcgctct tgatggcgca cttttcaaag 60
ccagagattc attcgtttcg cgactttcga actgtgaagt tgtctctccg gcgcgttatc 120
tccgtcttgg ccaaaactcg tgactgatcg agagaagaag tctgaaacca gctctgagcg 180
agaagacaag tgtggagact gcagttcagc atccgcgttt gctgtgctca agaaagaaac 240
ggcaatagtt gtcttcggtt tcttggaaga cgtcttcgcc gcgctctcac cctatttgga 300
gaagatttgg agatcttgga gcgcagctct tgagaaacac tacatatatt aaatcgcgcg 360
cttgcaagggt ggtggtgcta aaagtcaatt ttaaagatgt ggcggccgag tatctcgaat 420
tggcgtgtgg agcacctgct ctggccattt tttgtgcaca aacgctagca cagcga 476

<210> 19

<211> 457

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (119)..(457)

<223> Area matching *Drosophila larval serum protein 1*

beta subunit gene (inverted), Acc. No. U63556

<400> 19

ctcgtgcgtg taatttttgg tagccgggaa tggcgttcgc gccgtcccga catctgcaat 60
aaattttaaa agtatcatta ttttcatata tgtagcctgc cttgcaacta cattgataga 120

atcaaatgac ccccgaaagt gtattactac cgatgaggaa cgaacgcctt ttcaaattgt 180
 gggatcccct ttagatatat ggaaaacagt gccactttta cttgggttttc gaaagtttat 240
 tagacttttt gcacacctta ctagctaggt atcagacact ctaaaaacat ccgcgctcat 300
 tcagtagatc gttccgtgga tcgttttccg gatttcgcaa tcgaagccgc acacacaacg 360
 acgacgctca gacttgaaga cttggtgtag taatcgtgaa gaaaggtgta gtccgagtgg 420
 cccgtagttg gagtacctct tgtacttgga gtaggct 457

<210> 20

<211> 577

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (121)..(417)

<223> Area matching *Drosophila* Positive transcription
 elongation factor b, Acc. No. AF027300

<220>

<221> intron

<222> (418)..(480)

<223> Probable intron

<220>

<221> misc_feature

<222> (482)..(577)

<223> Area matching *Drosophila* Positive transcription
 elongation factor b, Acc. No. AF027300

<400> 20

tggctaggtt atatcacttg gccagtgtat accaacaatc gaaaagttat tactaccag 60
 ctgtttgacc catcgatttc ttatcgatag gccttgacag tgtgtgcaca ccggtatttc 120
 tttagtcaac agctgtagaa acaccaattg ttgccgattt ctttcttttc gactgtcggc 180
 ttctcgcgaa actgtgattg tgaaaattgt acaaataagag gcaaatttaa ccatggcgca 240
 catgtccac atgctccagc agccttcggg gtcgacgccc tccaacgtgg gctccagctc 300

atcgcgacg atgtccctga tggagaaaca aaagtacatc gaggactacg actttcccta 360
 ctgcgacgag agcaacaaat acgaaaaggt ggcgaaaatt ggccaaggca ccttcgggta 420
 agtctccaaa ttggtgaaaa ctaactttaa actaaaacat acgaccctt tgattacaga 480
 agaggttttt aaggctcgcg agaaaaaggg cacaagaagt ttgtggcgtg aagaagggtgc 540
 tgatggacaa cgaaaggagg ccgtgcgtga aagcaca 577

<210> 21

<211> 577

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(577)

<223> Area matching *Drosophila* organellar-type

Ca-ATPase gene, Acc. No. X84681

<400> 21

agctgagcta aaaggtggga taataaccta ataattgccg ggactgaaaa ttcttaaaag 60
 ttggagaaag aggcagctct gcacaaataa cgtaactcgg acgatatacg ttttcagtca 120
 gccctgtctt gtgcgaataa tgtcgtgtca tagtgaggca gaacggcgat aggtagtaaa 180
 tcggcgcttg gtacttagtg caatagttat cagcacacat attcagaaaa aagcgccatg 240
 gggttatatta tatagagagt cagtggaaaa aagtacttaa cacacgcagt gcgtcgttta 300
 gcgagggttaa cgtaggagca gagcaccgtg attacggacc agatcccca atccccgca 360
 gaaactgaga atagaaaaac gaaaattgcg tctgttgtgc cgaagtgaca cgtgtgtgaa 420
 tctcataagc ggagcgattt ggccagggtg acaaccctca tagtaatgca atattccagc 480
 atattcttcg accccgatcc gacaattcgg atcctaagtt ggcgccgata ctgcgcgact 540
 ttatgggcaa tccgggcccg tcagaatgcc tgaatcg 577

<210> 22

<211> 534

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(534)

<223> Area matching Drosophila GTP-binding protein,
Acc. No. X71866

<400> 22

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gtccacgcga gagttttata tattttatatt ttacatgcat atttggtgat aactgggggtt 60
ttctgtgaac cgcgttaact ctcagccagc catgagcaca atattggaga aaatctcggc 120
catcgagtcg gaggtgagtg gaacttggag tacctgccga tcttacagaa actaacctgt 180
ctcgcatcca tttaccccg cggattcccc ctggattcta tctaaatcac cggggttggtg 240
gaccaccttc ttaactgaat cctagatggc ccgaacccaa aagaacaagg ccacctcggc 300
ccatttggggt ctactgaagg cgaagctggc taagctgcga cgcgaaactga tttcccccaa 360
aggaggcggc ggcggaaccg gcgaaggtgg gctcttggtg atacaattaa ggcaatcact 420
aaacattatg tatttccagc tggcttcgag gtggccaaga ctggagatgc ccgggtggga 480
ttcgtaggat ttccttctgt gggtaaatec aactgctct tcaacttggc ttgg      534
```

<210> 23

<211> 523

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(523)

<223> Area matching Drosophila genomic sequence

AC004351. Drosophila G protein alpha subunit gene
matches in ssame area indicating that NPS0027 lies
in an intron.

<400> 23

```
gctgtagaca gcaagaggag gagaatcgta agaaagtgtt tgcgcatga gtaatcaagt 60
taaatggcgc ctggcctcag ttatcgaaat gggaaatgtg ttaatcagcg gggagtgtga 120
aattgagcgg acccaccgaa aaagtaaaca attaaatcag atgaaatgcg gccccaaaac 180
ggaagcccc cacctagtag tgactttcac gcagatctct cgattatcat gaaatttctt 240
atatgtgatg tacatacata tgtacatcaa ttatttaacc acatatagta tattgacgta 300
```

catatgtata aggtcgctcg cttggcgata attttgataa gccaatgat actttcagtt 360
taaagtgtgtt ggtaagcgag ttcttaaata attgtagatt attaagttgc tgtgtgttga 420
cagtctgagt gcccgat ttt gatattgggtg ccccgacgagc atgacactat tttggttata 480
tattattttt ttccattttt ttcattttt tttttttttt ttt 523

<210> 24

<211> 305

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (19)..(215)

<223> Area matching *Drosophila* EST AA246996. This EST
matches *Drosophila* CD39-like NTPase gene, Acc. No.
AF041048

<400> 24

gttgattcca agacgccatt ccgtgcgcgt tggcttcctg atcagagttt atcattcggc 60
gggcgcggcc tcattagatt agatcgacat tagtgcggtc cgctcggcga tcggcagcaa 120
tcgatccgaa ataaacaaac gtcgcggtat ttacataatt taagtgaaaa gtaacgacga 180
cagaatgacg aacaccgatg tgcgaaagag aaaagtaagg aaaagggtcaa aagggcaatc 240
cacagcacia atttaatgcc aatttcattg cgctctctca cacacacacg cacacatgcg 300
aatc 305

<210> 25

<211> 473

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (387)..(473)

<223> Area matching *Drosophila* phosphatidylinositol
4-phosphate 5 kinase gene (inverted) , Acc. No.

AF071417

<400> 25

gtcggcggca tctcctatat atctttcctc gtgtctgttt tccttttttt tttaatatatt 60
atcgcacgca tgacacgtag aatagaacaa aaacaacaat aattgtacgt taacaacgga 120
aagttttgcc aaattcagtg aatgaaacta aactaactga aatgtgcgag gctagttgct 180
ttattagcaa taacgttgga tcttatttaa atggaagaag tccctctaaa gttaataact 240
tgccacttga cctcgttttt tgtggtcgtt gttgttgtgt tgctgttgct gtggctgctt 300
ttgccttggg accatttggt gtgaattatg agcttgcaat tatagcgttt tgccgggtttt 360
atttgtaatt taattagcgt acttacacag aaatgctcga gggaatagtt tgctagaggt 420
caaaaaaacc gaaagatatc cagcgaaaag agataattat ttgccctcgg ctg 473

<210> 26

<211> 319

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(319)

<223> Area matching *Drosophila* rbp9 gene, Acc. No.

S55886

<400> 26

cgtctttggg tttaaagccc ctctggcacc ttcccttcag tcagctgccg ttgttggtgt 60
tgcttaagtg tttgtttggg tgccgtgctg gctctctcag ctccaacaac agcaatgcgg 120
ccggcttacg agccccgggt ctcttcgcct cttttggagc tcgctctttg ccgaacggag 180
aacctaccgc aattcgtttc gtgttcacgg ctgcatttcc ttgtttatgt tttgcgaagc 240
caaagtgttag ggtacatcgg tttaagtgcc gagccaggaa gaaaggagag agcgagcgaa 300
ccgagtaccg tttatgttg 319

<210> 27

<211> 493

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(493)

<223> Area matching *Drosophila* manganese superoxide
dismutase gene, Acc. No. L34276

<400> 27

```
atttgaacaa tttactgcta gagatgagca gatgagaaaa tatcgaaaga cccaatcag 60
tcagtgatgt gagatcaact tatatatatt gaagttaaag agtaaaacta aaagaaatta 120
aaaactatct ttgaaggcca ctgaaacata ttcaaatcat attgaggatt tcttaaatat 180
ttcttatgtt taaatactac tttagtgaact attagcatat tttagctgca tacgtatcga 240
ctgcatccat tcgattgata cttgaattaa tcgattttgg cctctgtatg atgtcatggc 300
gctaaattgg aaataaacta tgaaattaac gtcataagtt taaaaatccg actggaacac 360
agcacacaac atgtctacat ttcaaatacc ttcccgaatc aaaatcgata taacaaataa 420
acgggcacag aacattcttc acaaatatct acatttaccg taagttgctt aaataagcta 480
aagattttat gat 493
```

<210> 28

<211> 571

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (233)..(377)

<223> Area matching *Drosophila* rab2 gene (inverted),
Acc. No. D84313.

<400> 28

```
cttcggccca ccgactccag gaatattttc ctgcgaagca attttgatct cacggatatca 60
acttttcact tgagaccacc tgaaaccccc attttttgat ttccgggtac gaccctacg 120
cctgcgatgc cctttgtttt gttgtgttgt ttgcaattac agattgtttc cctgacaatg 180
gccaaacttt cactggccat tccgtttcaa aggaagtgcg agcttgcaact cacctgtgtc 240
tccgataatg atgtatttga acaagtacgc gtaggacatg ttttaagctg acgggggtta 300
```

cggtaagcta gtttttagaa agtacgatct cgtaatgcca cagataatac gcaattcttg 360
 tacgttttcc aatctgttcg tatttatgat gactggctag cgacagtgtg gcactttgtg 420
 gccagggctg gcggaataac cgaaataccc gcaaggctgc aatcgctat cgatacga 480
 cgactggcg tggccaatcg atagtatatg tatgtatgta gaattgcaga aatttctcgc 540
 acaagcaaag tgtttgggag gataaacgcc a 571

<210> 29

<211> 550

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(63)

<223> Area matching *Drosophila myosin V* gene (inverted),
 Acc. No. AF003826

<400> 29

gttccactgg ctctctctcc tactccaggt tccgcttcgc gctccttctt tctctctct 60
 ccttcttctt actcgctgg gagtgagttg ggtgcataaa tcccgtagg tttaatttcc 120
 ttggtggtac gtttttttcc tggtcttgac agcctcttta aattaccatt ttcgtggtct 180
 ttttttgggt ttatgtaaat gtactgtcct aaattactta aaattagcca ggaataattt 240
 ataaaaacat tgataatttt tagatcgcaa cgccaaagtg tgagaaaaac aaacaaactt 300
 ccgtccctgt caccgctga ctgactgact tatgttttgt tgttgcaaa agggcagggt 360
 tgccaaaggg cgtgcagttt gggccaaatt agaaatgtgt ggttctaacc atggattaaa 420
 tttgaacaaa gtaaaatata ttgcaaaaag atttgtataa tgccacagta actgaatttt 480
 ttcttgcaaa acaccccaga aagcaccaat tatttggcgc gcaatgcctt gcagtttagat 540
 ttcagcactg 550

<210> 30

<211> 528

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (325)..(528)

<223> Area matching Drosophila

ribonucleoside-diphosphate reductase large subunit
gene, Acc.NoU09369.

<400> 30

```
agctggatta acatgcaatc atcccgacta cgccatcctg gctgctcgca ttgcagtgtc 60
caatttgcac aaggaaacca agaaggcttt ttctggtaag ttcatagctt gtattctgag 120
ttcttcgggt aatccaatca tgattcttat tagacgtctt cgaggatctg tataatcatg 180
tgaacaagga gacgaatcaa aaagtgcctt tggtatccga gtttcactac aatgtgggta 240
agaagaacgc cacacggctg aactcatcca taatctatgg atcgtgactt tggctataac 300
tattttggct tcaagaccct ggagcggttc tatctgctca aaagaaacgg gaaagatcgc 360
agagcgaccg cagcatatgc tgatgccgcg tgggcgatcg gaatccatgg agaggatatc 420
gatgccgggc cgtggaaact tataatcttc tatcggagcg ctacttcacg catgcatcgc 480
cacactgggt gccgctgcac aaccggccgc agttgtcgtc gggttcct 528
```

<210> 31

<211> 271

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (234)..(271)

<223> Area matching Drosophila Fzo gene, Ac. No. U95821

<400> 31

```
atatggacgc tttgtttaag cccgatgtct tctacaataa aacaaaaaaaa aagccaaaac 60
tggttctctt gttcttattc ccagcatgtg catgttccac agccagaaac tgtgtgtgtg 120
tgtgtgtgtg agccattagg aggaaggaaa aacaatctaa tcaagcaatt taaacagtca 180
acagcaataa aaactgctta aatttgcag gcttagattc tcgtggtacg aagtaacttt 240
aaagtagtga aagaccaacc gtttaattatt t 271
```

<210> 32

<211> 450

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (322)..(450)

<223> Area matching *Drosophila* mitochondrial
single-stranded DNA binding protein, Acc. no.
U00669

<400> 32

```
aatctggaat gggccttgaa atcacatctc ataggaggga aataaaaaag ctacataaat 60
gtagacaatt aagttagttc ttagccttaa cctccaagaa aatatcacgt tgagctgcta 120
attcagattt atgtaatgag ttattagaac atttgctgta tgtaattacc taatgataac 180
ggcaatagtg tacatttcct tgttcaatta acttcagtga tcaatttctt ctaggatcc 240
atgaaatgcc ggatttcata aagaaaatag ctaccatttc atttaaaaag cattcatgaa 300
gtcttaaata tttccccaca gatatgagaa cggcgactgg gccaacgca ccgactggca 360
tcgtgtagtg gtgttcaagc ccaatctgcg tgacaccgtg ctggaatact tgaagaagg 420
acagcgaacc atggtgcagg gaaagatcac                                     450
```

<210> 33

<211> 385

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (14)..(385)

<223> Area matching *Drosophila* RM62 gene. Acc. No.
X52846

<400> 33

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ccgtgctgcg tatgataaat ccgtcattag cataaccgca ttgaagctaa gtcttcggga 60
aaatgcttaa gcttgtgcaa tacatagccc cccgggtggg cggcgccacg ccccgaccga 120
```

ctgcctgcgg ctggggcaac ttgctattga tttccccgag aagtggcgcg agctccgaga 180
aatgtataac gcaacgtcgc cattttcttt tctcctccgc cagcagcagc ggcactttcg 240
cttcttcttc ttgctcttgc accgaacaac gacaacagtt ccacgggagt cgcaggaatc 300
gtgagacaat actgttccca agcacatata gtagtctcca agctcagtcg cagcgtgcgt 360
ttcgagacag ctcgaaacca gattc 385

<210> 34

<211> 442

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(422)

<223> Area matching *Drosophila* pterin-4a-carbinolamine
dehydratase gene, Acc. No. AF069297

<400> 34

gctgctggag aatacataac tgagatttgc gacaggctgc gcgaaaaata aagctcagat 60
ttaagtttgg tatttttggc cctccctctc cctccgcaca ttccaccttt tgaatacctt 120
cgtactcggt gctgttggtg cagttgtggg gaataaacca gctctgcggt tgctggcaag 180
caaattggcc actttctggc agttcggtt aatcacattc tgagcgcatt taattgttaa 240
caacattttc gatccaaaac tcgtttgttc ttagctgctg tttttgttgc tgtttctgtc 300
ggcgcggaac agctgacttt tgctgtatgt tagctaacat tgagttaaca tggagctggg 360
aaaaactgcc aacttgtttt tgacaacgtc tgctagcaac ataactgtta taaagtctaa 420
tgccgcgtaa tttgaattta aa 442

<210> 35

<211> 510

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (329)..(346)

<223> Area matching Drosophila cytochrome c oxidase
subunit Va preprotein gene, Acc. No. Y09065

<220>

<221> intron

<222> (347)..(414)

<223> Probable intron

<220>

<221> misc_feature

<222> (415)..(510)

<223> Area matching Drosophila cytochrome c oxidase
subunit Va preprotein gene

<400> 35

```
gcacgcgtca agttgaagat gcagtgtgac cgcaattaaa tcatcaaaaa ataccgcctg 60
gcagtagcca gcatcaatgt ggaccgttga aaaagaaaca aggtttgatt ttgatttttt 120
ttttgctttt tttgggcaag atagaagaaa ttaaataataa ggaaaatgat aaactaactg 180
tgatcttacc cgaatttgaa atatactgaa gcagaaacat tttaaataatc tcaactgttcc 240
gtgacagcga cagttataaaa cgtgtccatc cctggaaaag ccagtgtttg ccaaccatca 300
ctcagatctg tcatacccggt gttgaaaagt agcaagaaca agaaaagtga gttcaagctg 360
tttctttaac caaatTTTTG caattaacaa gcattttact gttttttaacg gcagcatgtt 420
gagcatcacg gcccgtaacc tggcaagcgc cctccgcagc agcctcgtcg gcacatcgtc 480
gcgcgtggcc gccgtgcgct gtctgcacgg                                     510
```

<210> 36

<211> 401

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(283)

<223> Area matching Drosophila Ubiquitin gene, Acc. No.
M22428

<400> 36

atcagtactg tccaaaatcg aaaatcgccg aaccgtagtg tgaccgtgcg gggctctgcg 60
aaaataaact ttttttaggta tatggccaca cacgggggaa agcacagtgg attatatgta 120
ttaatatatt atgcagggtt tcattactta tccagatgta agcccactta aagcgattta 180
acaattatth gccgaaagag tataaacaaa tttcacataa aaatggatta agaaaagctt 240
gtgtaagatt atgcgcagcg ttgccagata gtcctattta aaacacttca aaaacaataa 300
gttttagaaaa tatatacata aatagcagtc gttgccgcaa cgctcaacac atcacacttt 360
taaaacaccc tttacctaca cagaaatact tttttaattt c 401

<210> 37

<211> 445

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(213)

<223> Area matching *Drosophila* hnRNP gene Acc. No.

M28870

<400> 37

gtctgtctac ggcttttctt tccacaggaa aatatatttt cagtttttagg gaaggggtgc 60
tacagtgagc gtctttcggt cccagtgtcg ttatttctat agtattgctg agatatatat 120
cagagcagta aagatatthta aatataagtt cttcgaaatg ggtgggtcacg acaactggaa 180
caatgggtcaa aatgaggagc aagatgtaag tagcacacaa aaccgcgact gcacagggaa 240
aaaactcagt tcggccataa tcccaatata tatatatttt ggtgatcaac gcgcttttac 300
ccatgcggca actaaagttt gatgttgcta aagcatttcc gttgcggttt tgttacttaa 360
gactaagact aacagtagtt gtttcttaat aattgctagg gaattacaaa gcctgtcgggt 420
attggtttct cttttaactt tttag 445

<210> 38

<211> 380

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(380)

<223> Area matching Drosophila genomic sequence

AC006933. Drosophila Rhodopsin 4 gene(Acc. No.

M17719) also matches in this area indicating that

NPS0044 lies in an intron.

<400> 38

gttactggtg acagcgatat tattgtaact ttaccaccat tcctttccaa aggtactttt 60
tctgggtcac agtttacatg catattggat cacttttgtc attggcaacg catgtaaatc 120
tgcttataat tgatgaacaa attcggaggc aatatgttgt attacacttt tcacgctttt 180
tcctatttct caaaccaatg agctgcgagt taatagcact gaacataagt ttcatcatca 240
acatctatgc ctgcattcta tcaatcataa tgttgggata tcagatacca gcattgtatc 300
tgaataccac attctatacg ccaaaggatt atagatacaa tcaagggcta ctgggcaact 360
tcatggcctt catgggaaaa 380

<210> 39

<211> 449

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(449)

<223> Area matching Drosophila TipE gene, Acc. No.

U27561

<400> 39

gaatagccaa ccaaagcaaa aaagtgaaaa agacaaacaa aactgtccgt ccagcattcg 60
tttttctaca cacatttcga aagaatgtaa atgtaaagtg aagaaaaaca gagagtaaga 120
gagagacctc aaaactggcc attggcaggc caaacacata cacaggcaca ccaagcatac 180
aggacacaca ggccacacac gacacacacg cacgaacatc cagtgtttg ccgcagtcac 240
aaaataatca agaagcagct aaatcaggca aaagcaagac gactgcaacg tgctgatgtt 300

gacgaaacat ctccattggg acgaataaag caattagcaa aggttcacga ttgttgccac 360
ccacactgcc aggaggcgga agaagctgga agggattaag aatgcgggat acgttggggac 420
tcccactcgg actccgtgga gtttttagc 449

<210> 40

<211> 572

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (463)..(528)

<223> Area matching *Drosophila* EST AI405330. This EST
matches *Drosophila* mitochondrial ATPase coupling
factor 6 gene, Acc. No. X99665.

<400> 40

gatgagatag aataatttca aagtttttag ttcattattca tattcttcat attcatatta 60
gagtaataca agaatttatt attcatattc aatttagatc cgattttggc ttgtgtggga 120
ttttagatac agtttaggtg ttgttttggg atgaacgttt atggagcagt tttgatttaa 180
gttggacata tatagtaaga tacataaaca gacacagtgt ataaattagc ttttcataat 240
ttgtaatat tttattatag gcagtatttc gatagaggca actaatttaa gcggattggt 300
gattaaaatt cttgttcgca acgaatataa tttatatgat acagctaaca aatacaggat 360
taagccaaaa atcggcttag gaaataacct tactatttaa aaagcttaca tacgatagta 420
tcccatacac ccatcacgcy cacatcacta acaccaact gccattgtga actgacaatt 480
gtaacttttc cgcacgaaag ttagcatttg caaaggaaaa taagatgaaa acaagattta 540
aaatccttaa aatttattgg gggagttcca at 572

<210> 41

<211> 246

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1) .. (246)

<223> Area matching *Drosophila* heat shock gene at
87c, proximal end, Acc. No. K01294.

<400> 41

```
ctaaagccaa atagaaaatt attcagttcc tggcttaagt ttttaaaagt gatattat 60
atttggttgt aaccaaccaa aagaatgtaa ataactaata cataattatg ttagttttta 120
gttagcaaca aattgatttt agctatatta gctacttggt taataaatag aatatattta 180
tttaaagata attgcgtttt tattgtcagg gagtgagttt gcttaaaaac tcgttttagat 240
ccccgg                                           246
```

<210> 42

<211> 407

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (221) .. (318)

<223> Area matching *Drosophila* EST AA440389. This EST
matches *Drosophila* Fas gene, Acc. No. U73160

<400> 42

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gtctagacat atcaaacta accctgacct cagcaatggg caaataaaac cgcccatttg 60
gccaacatct accacatcta atctgctaata gagaatacac gcacatacca cacatatgta 120
tgtataggcg cgcgcacgca cacacctgca aaagctttta ctaatctaaa gctcacgagc 180
gagcttttgc tgaaatgctg caggttcttc gtcgtcggca atttttgcac atcagtttta 240
aaaccaagt taaccgaaac ggcttggtta tttctagctg cggcggtata aaacaccttt 300
ttttttggtg taatccaggt taaaacaata aacagtgggt ctcaaataaa aattccatcg 360
aactttgcgg ctgttcactt ttgctgaaca gtttgcaatt cttgttt                                           407
```

<210> 43

<211> 537

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (15)..(95)

<223> Area matching Drosophila EST AI297861. This EST
forms a contig with ESTs AA697916 and AI063366
which overlap 5'end of Drosophila 49KDa
phosphoprotein gene, Acc. No. M32141.

<400> 43

gtttgcagat ttacctgtta gaagagcggc tctcgagaac attttccagg cagttgcgac 60
gaatttatgc tactaaattc acccgaaatt gtcagttcac aatagtgaca ggttaagaga 120
gcgttgccag atcaaccgct tgtcagaccg gttttacaac actggcaaag tgagccctat 180
atttgaactt ttcaaaataa aaatttggtt attgaaattg tatgtttata acttttattt 240
gtattttcaa cttcttttaa acttattttt atgatattaa ttttatattt aatcgagtgt 300
ttggcagtat taaaccattt acgcaaactg tttacatatt taaaattcga agttggaata 360
taaaaagctt tagtagaata aattaataat taaacagcca aattgtatag ccattttaca 420
atgcttaaga ttaaaacgga aaaagatact cgtcataact ttacaagttt ttatttttaa 480
aaatattaca atttgctaga taaattgtgc cttaaagttat cagatttagc tgcgaaac 537

<210> 44

<211> 292

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (231)..(292)

<223> Area matching Drosophila Tcp-1 gene, Acc. No.
M21159

<400> 44

atccccggggt tttgtcaaca tctgcggtgc gtctgcgggc ggagcacgtt tcttactcat 60
cgcgggtcac gctctccacg aagaatgttc cggaaccaac ccgggggagg gcgatcttat 120
tttaattgga ttaacaaaaa aactcattga atccaaggag ctacaagatc ctgtggacaa 180

gcctatgcga agtgaggtta tgactacaac tcggctttta tatgctttca gttatggccg 240
ctctgtccat atcgaacatc gtgaaaagct ccttgggacc cgtgggtctg ga 292

<210> 45

<211> 349

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(349)

<223> Area matching *Drosophila* HSP70 gene Acc.No. V00213

<400> 45

cagtaaacgg cgcaactgttc tcgttgcttc gagagagcgc gcctcgaatg ttcgcgaaaa 60
gagcgccgga gtataaatag aggagcttcg tcgacggaga gtcaattcta ttcaaacaag 120
caaagtgaac acatcgctaa gcgaaagcta agcaaacaaa caagcgcagc tgaacaagct 180
aaacaatctg caataaagtg caagttaaag tgaatcaatt aaaagtaacc aacaaccaag 240
taattaaact aaaaactgca actactgaaa tcaaccaaga agtaattatt gaagacaaga 300
agagaactct gaatactttc aacaagtcgt taccgaggaa agaaagaac 349

<210> 46

<211> 241

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(241)

<223> Area matching *Drosophila* glutamyl-prolyl-tRNA
synthetase gene, Acc. No. U59923

<400> 46

cgtagcagc tggccgtact cgtgccgttt aaaagccgaa atttcatcag tttgatttca 60
attgcaaaca aacaacctgc gaacatgtca ataaagctca aagcgaacct taacaatccg 120

cccataagtg agtatcaaac ggatgccggc tgctgtgacc tccagtcccc ggaggatctg 180
 cacttagtga ggttatatcc gcatcggggg ctatttatgt acacaatata tccggcaatc 240
 c 241

<210> 47

<211> 499

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (225)..(237)

<223> Area matching Drosophila ribosomal S4 protein
 gene, Acc No. D16257.

<220>

<221> intron

<222> (238)..(333)

<223> Probable intron

<220>

<221> misc_feature

<222> (334)..(499)

<223> Area matching Drosophila ribosomal protein S4 gene

<400> 47

cgctggccac accgcccgc aatctgcctt ttccttttcc tggtgtattg cccgacggac 60
 ggtatgtgta ttttttgcag ctagccacgt gctaagtttt gtcaatggaa ggcccggcat 120
 tggggatttg ctggccacgg atgcggcact ggcagtggcg agcgaatgct ggcacaaaac 180
 taacgtttga ttgttctatt tgcagtgatc gcccgttcaa tatagtgaat caaacatggt 240
 gagtatctgt tgggtggtgaa gatatgggtca cgattgtttg tctttgcctt tggaataacct 300
 gactaacggc taaaaccac tcacactttg caggctcgtg gcccgaagaa gcatttgaag 360
 cgtttagccg cccccaaggc atggatgttg ggacaagctg ggaagcgtct tccgccccgc 420
 gtccccctga ccggtccaca caagctccgt gagttcctgc ccctgctgat cttccttgag 480
 aaaccgcttg aagtacccc 499

<210> 48

<211> 462

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(462)

<223> Area matching *Drosophila* Rl1 gene, Acc. No.
X73216

<400> 48

```
ggctgtacgt agctgtgagg atactagagc tggcaccaag ccgatggcac tatcgatagc 60
gatggctgca ttctggccgg caccatcgat ggacttgcaa tagcgattgc tatatgaaaa 120
ctaattctaaa gaggtggatg cacttcagtc gactttctat aatttgctta aactaataaa 180
tgatttgatc aatacagctt tctgtaaaaa ctggcagacg ctttctgctt ttaataattg 240
ttaatttaag ttcaacgggc tggcatcacc gtttcttagc acggactcaa gcctgagtct 300
attatttcaa ccaccactgt aacgaaaaca gcatggacag attgaaattc aataatttgg 360
taaataaacg attttattta aaattataga gttctaatta aaaagaactt ttacaggtga 420
tatccaacaa gaaggtcatt caaaaggcac gcgcccagac ca 462
```

<210> 49

<211> 164

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(164)

<223> Area matching *Drosophila* relish gene(inverted),
Acc No. U62005

<400> 49

```
atcgaaacga gctccgccga tggctgacca ttcgttttag gtacttcccc gatgttcggc 60
```

ggatgggaaa ttatctgcgg cggccacgtc gagatgactc acgggttttt caggcgcacc 120
actcagtgtg atttttttga tcggctatac tataagcatg tacg 164

<210> 50

<211> 207

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(207)

<223> Area matching *Drosophila* HSP2 gene(inverted), Acc.

No. X07211.

<400> 50

ccaggagcct ttgtagatca ccacactaaa atgagcatac atatgtatat gtatccgata 60
taaagtattg caactataat aaacttttaa agtcacttg ctgtatccct gacttttggc 120
aattttctct gcttccaaga ctcgatttcc cgaccggcag gtgaatatga ttggcgactg 180
cttctccggt ttcgatattc cgtactt 207

<210> 51

<211> 438

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (15)..(438)

<223> Area matching *Drosophila* MAP gene Acc. No. X54061

<400> 51

gggtgggtgt gcgcaaaaat tagtcggcaa gcaattcaaa agtaagagca accggagcga 60
acaaaaaagg gaataactta ctaaaatctc tgaaagaaaa ataaaaagac taacgggctc 120
ggcaagctgt gtttatttcg acaagtaatt atatacttgg agtgcaagca aaggcgaagg 180
aagtgaagg acaagcaacg aaatcgtgct cttatccggt cctgtactgt gtctctcttt 240

cgctgggaga gtgtgtgtat tgggtgtgagt gtagaaatct gcaagaacag caacgccaat 300
 aaaagtggaa tcgagaaaaa aaacgcagtg gcgcgtgaat cagcagcaat ctgaatcatc 360
 tctctacaaa aatacctggt tctgttggcg catcatttat acccaattaa atcctaaagg 420
 atgggaacac cacgaagg 438

<210> 52

<211> 554

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(80)

<223> Area matching *Drosophila* HSP68 gene (inverted),
 Acc. No. J01102

<400> 52

gtcagaacat tccagtcagt tcgtgtgtgt gcgagcgagt caactagtgt gcacttcgca 60
 ggggaaattg tcagttgaag gactgaaaag ttcaggaaat ttcgagaaat atattttttt 120
 tattgacata ggtcatcatt ccaagtggtc attaaactaa attcgtatgc aagctatttt 180
 tggttgattt gcggattgat acgttaagcc attcatattt ttagattctg tttttggttt 240
 atatctcttt tattatatgt gcaatacata tgtgtgtatt tttcttctga ttggaatatt 300
 tcctctgcag aatatgacat acaattacca taaaagtttg aacacacttt tcaaaaactta 360
 attattccaa ttaattattt ccaaaaattt aaagaatccg tactgctcta tatccaggat 420
 acataaatat atagatacct atataggaag tttcatagat aagatgtttt atagaatact 480
 tccgtagatc gggtagaatc tttaatgttt tttataaata ggggaatttta agaagccaga 540
 accaatgccc aaaa 554

<210> 53

<211> 450

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(450)

<223> Area matching *Drosophila* annon-66Da gene, Acc. No.

Y10015

<400> 53

```
gctcgggtggt agcatggcgt tagtgttgct aaacacagag ttgcatgtgg tctagtgttg 60
tgcagaaata ttagtgacag taaatcatat acatcttatg tggatatttt cgctatcaac 120
tgttacagtc aactaagcc aattcgatag atttcgatag taaaaataaa cattttggaa 180
taacataatt actttttagt aagttacttt ttacgggggtt aatttcaagc agacattttc 240
ccaacatggt ttacatacac ttccccaaca atttaaccga agaggagcaa atgctgcagg 300
ccaagtatca gaaactcaag aaaaagggtgg gaaaactcat gccacaaatg ttgattattt 360
atattaacaa gtttttaacc cgtagaaaaa ggcactgcaa ggcacaaagg cgccaagcc 420
ggaaccggag agctccttga ccttgaacgt 450
```

<210> 54

<211> 470

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (56)..(187)

<223> Area matching *Drosophila* RAD6 gene, Acc. No.

M63792

<400> 54

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ctctatacca ctgctgcccg agtttgccct caattaataaa taaattacaa aattcatcgt 60
taccgttcgc taaacgcaac gcattgcccga ggcgtccgag ttccaaatcc aacacaacac 120
gagtggtagt atcgtgtga aaaatgtcaa caccgcacg cagacgtctt atgagagatt 180
ttaaaagggtg agaagaaact aaggaatcga atgcgaatag aaaagaatac taactaaacg 240
aaagctaagg aaaacaggaa ggcaaggagc gaatggcaaa gttacacaca accgttggat 300
tttacgtttt acgtgtttct cgttccgaaa aaatgctggg gaaaagaaac ctgggggctg 360
cccaatacat ataagccaac acacggacac ccgttttata tgactgtgct ccacgtctgt 420
atgtagtgga aaagtttgcg ccagccaaaa tatttcgttg tgcattgttc 470
```

<210> 55

<211> 465

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (391)..(465)

<223> Area matching *Drosophila* Septin 2 gene, Acc. No.

U28966

<400> 55

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agctgtagac acatcagcaa tgcggacctg ccggatcgct tctgtgtgcg accagagatg 60
ccgaggcgga aacagttaag acatttaatt ttttaatacta attactttta attaataact 120
tatgcataat tatcaatgaa tgggacattt tattattagt tattaataaac tgaaacgcta 180
aatgatatgt actgaaatct taatccatga agtgcatttc actggatgat taacaatttc 240
gtttcactat ttgccattat ggcacatgta attcattaat taattgtttt ttaattcatt 300
gttaagctat aattttcttg ttcattcata tccacatact tctttgagcc gctggtattt 360
tggcctccgc cgttatctgg ccacactttg cagattccct ggcgacgcct ttgatccaaa 420
ctctgcgccc ggaatattgg attattttga cttgactatt ggaaa 465
```

<210> 56

<211> 564

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(514)

<223> Area matching *Drosophila* Fructose 1,6 biphosphare

aldolase gene, Acc. No. M98351

<400> 56

```
ggacaaacct agaaaaaaaa aaatgtgaga gagagagagc gaagagctgc agatatagag 60
aaaagcacgt tttccgtgca tgcgccttta atctcattca atcacccgct ctttgcacac 120
```

gaatcagctg tgaaatacac taccatgcaa agcattttatt atcttcaatg gaaaaatatt 180
 tttaaattgg aaaaaacacc agtgacattg acctgacact gaaaacaaaa ttatataata 240
 ccgcatcatt aaacaacagc atatgactca atggctctaa tcggttaact cagagttcca 300
 ctttaaataa cttgaccttt acaaatattc tttttatttt atggaaataa taattaggtc 360
 agttcagtaa aataatccaa cacttgattg atagctatct ctgtagcccg ttgttatctt 420
 tttcagtagg aacatatgta acttttgagt tacctggatt ttgggttgc agactgtgcc 480
 ggatcgata ccgaaattta gtccaaattt ttaagtttat tttttacctc ggaaatattc 540
 aaaatttggg gcttacgcat ggggt 564

<210> 57

<211> 251

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (46)..(251)

<223> Area matching *Drosophila* Bottleneck gene
 (inverted), Acc.No. U01035.

<400> 57

ccccaggttg aggcattaaa aagctaacgg tttcttgttt tccgcttcgg caaacaaaac 60
 aggtgcgtgg tggcatagtg aatatacgca tatgtatgca cacgaatata ggtgtggaca 120
 cggcggacag cgggagcacg gagtcttgcg tgattcagtt tacaacctgt ggtagtgtgt 180
 ggatttagca attctgtttt atcagtcccc tagaactgat atattggcta ttcggaattg 240
 ggaatttttg c 251

<210> 58

<211> 450

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (49)..(450)

<223> Area matching Drosophila HLH106 gene, Acc. No.
U38238

<400> 58

```
ggcccgccag tatttaatta cgaaccgttt ttgtctcttt catcagcagc attcgcaatg 60
gacacgacac tgatgaactt aatagacgct ccgctggacg agtccatgga tttgttcaaa 120
gcgaggagatg tcttcgaacc gttcgacgcc gacctgcact cggacatgct ggacatcatc 180
ctcaacgata tggacctggc gccgacgcag atgtacaaca tgctgctgga cgagcctcga 240
acgcataccc agcagacgca gtccgtggat cagcagccgc aatccgtcga gcaacagccg 300
cacgtgaaaa gcgagcactc ttgccagtgc cacatcaagg aggaactgca tcagcagcaa 360
caacaatcgc cgcttctcgc tacaacccag atccccctcat agccacaagc tacaattgtc 420
ccacaacagc cgacgggcct ttgaaggccg                                     450
```

<210> 59

<211> 581

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (328)..(581)

<223> Area matching Drosophila DAD gene, Acc. No.

AB004232.

<400> 59

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accacgccat agtagccatc caacggatgc tctccactct cagatgtctt ggattctttg 60
gtttagcact tgtagtagga atgggaatgt gaaaaatatg acgatatttt aacaagtctt 120
ttctaattaa taataaaact gaagttctta tacattgtta gaacgggaac tttatgtatg 180
attctaattt tacaatttct tgggtctctta attttctct ctctctctaa acctccctct 240
cccaggcgct ctctcaggcg tttctccac gtttattccc cacagctcca aagactatca 300
atccgcacag ttagcgcttc gctcattgcc ccaacaattt tcaaccgcgt cgcttgtgtg 360
ttcttttgcc gttcgagaaa tccaaatccg aaagatatca acgaaaagat gggatacttt 420
gacgtattgc cagcagaaat tttccgaata acgttatttg tgttcgagac tgctaaatga 480
ttttggggta attaaaatga caaaaaacgc agttctaaat atcggttttt tcgcctttcc 540
cgatcttttt tcgcacatta acgggttttg ttttggtggt g                                     581
```

<210> 60

<211> 436

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(436)

<223> Area matching *Drosophila* genomic sequence

AC005557. *Drosophila* Brother gene matches this
sequence 15bp 3' to NPS0066.

<400> 60

```
agttaaacaa tacaatacac aaactacagc tgtttaatgt gcccgactc tagagttgtc 60
acctgcttgg gctgccatgg ttggcaactc cctttgctta agtgctgtgc taatcaacac 120
tgttaaaatt accgctaaaa cgtaatttcg aatttaaact taaaattata aagtgcgttc 180
aatcgtttcg ttttatattat gatagcattg tacctgcaat ccacaaagta taatattcgg 240
agctgtaaaa accctacgga ttataagaca aacctcaaat aggataccta taagtgttat 300
acctgatcct tattgtgtcc agatgggttc catccttgat taccagacga caattagggg 360
attcgttagg tagcccaatc gcaaccgat tacctggtct acaactcttt ttttttggt 420
taaataaggc gggcaa                                     436
```

<210> 61

<211> 645

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (46)..(176)

<223> Area matching *Drosophila* Aef-1 gene, Acc. No.
M90755

<400> 61

aaccagccac agataatgct gtgaggaccc gattctgata ggcgagagca atacgcgaac 60
accctccgaa aggcccatat ccccaaaaaa ccgaatcgag tgcgaaaaaa tgatgtaaaa 120
cgggggaaat ctaaacctga aaggccccac acagcacagc cacaaaatgg aaaggtaggt 180
caatgtgtgg gcgcccgaag agagttcaag tgtgtcactc agtataccca attccgtctg 240
gaatcatttg gcaaaaatag cgtttataga cgtgtgaaaa acaatggaca tttgagctcc 300
aaaattaaaa gtatcctaac ctcaaaagag cttttacaca gtacgtgtcc gtgtgtgcgc 360
tagtgatgtc catacgtgtg tgcgactgaa agtggttgtg acttttagct gaagaaggga 420
gcgcgagggg cgatctagag gcaacgtgtt agtggaaaaa ctgcttttga aaaaagggga 480
aaatatcccc caaaaagccc gcccaaaaaa ggtcagttcg gaatcctgtc gatctgcct 540
cgttgagatg tatccaattg gtaaagttat cactaagttc ttaagttgcc agaaaaacac 600
atgtaatttg gcgagaaagt aacacgtgt caattcaaca caaaa 645

<210> 62

<211> 445

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (224)..(298)

<223> Area matching *Drosophila* EST AI292767, this EST
matches *Drosophila* serine/threonine protein kinase
gene, Acc. No. Y07908

<400> 62

gtctgcccc gacctaacc gtaagtgtgt gcgtgcgaga gtcgtttcat ttgcattctt 60
gttttagcgca ctccctctct ctcttcgtgc gtttttcatt cataagcaca tttttactat 120
ttggaactgc aattttttac actaagcttg aggacagaca agaatactgt gaaaatccaa 180
tgtagatgaa agcaggccgt gctttttcca tcaaagtaat cgcaaaaagt cgagattaac 240
acaagttcaa aattattcgt taaatttttag aacagaattt tgaaatgaac ataattcagg 300
tactgtgtca tccacatata aagaactttt attctaaaaa caaataatcg tccgatcggt 360
gtgggtctgtc caataaaaat tcacggcaaa ggcgttggct aaaaatacat agacaaacga 420
gtcgggtaaa aaacaaatac atgat 445

<210> 63

<211> 531

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(531)

<223> Area matching *Drosophila* Fascilin 1 gene, Acc. No.
M32311.

<400> 63

```
gtccgtggac attgcataat ttctgcggcg gccgttaatg ttaattcctg cagcccgagt 60
ttccgagaat tacgcagaat aaagaccaga gagaaaacta taaaatcgaa aacagaaaaa 120
agtgccgcag cagcgaaatg caaaggcgca taataattaa acacacagcg acggaatgaa 180
gaaaaaataa tacacaataa gcgcagcttt gtttctagtt aaattgcgtt tgtgttgtgc 240
ttgccgtttc ctcggtggtc cgtttttcgc ttgttgttct atgtgacata acggaactct 300
gggcaaaagc gaacaggaag cagcgataac cttgcaaaaa caaagaaaat accaaggagg 360
acaaaaagc atgccaagca tatatctgtg aaataatatt ttcttttccg aggaaatgct 420
gtttgtcgtc ggctaactgt tgtttgcctt tgaattgcag atcttaatcg tagagcagca 480
ctcacaccag cacacgcccc ccgcaaaaaca gcacacacag cacactcaca a 531
```

<210> 64

<211> 421

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(421)

<223> Area matching *Drosophila* HSP23 (inverted), Acc.
No. X03889

<400> 64

```
cacgaaactt ctcgggctga aaatatcgca gagttctcga atttgccgca attacgcatt 60
atctgccatt gaaagtgaga gtatcgctat ggaaaatgag caatctccta ggggagtgagg 120
```

aatgaaaagg cctggtggag tgataagtcg catcagcacc ggcaaatatt atgtgtatgt 180
atagatgtac gtatgtaagc acgtatgtat gtacatacat agcagatagg aaggttggag 240
tatattccac gaaggatgga agtaaattcg cgaaaacttc gagactgcag aacaagtctt 300
ctttttatgg cctggcattt aagctattaa ctttaattaa tatccaagaa tggggctctg 360
gtagtgggga aatctaatta aaatcataag tggttaatgc ccgggtaggt aataaccctg 420
g 421

<210> 65

<211> 882

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (548)..(882)

<223> Area matching *Drosophila* ATP sulfurylase gene
(inverted), Acc. No. Y12861

<400> 65

cccgacacta aaacgcgtta agcgaccgca tgttccaaga acttggaanaa tttccaagat 60
atgcagctga taaaacagct gatagcgctg ccaacttatt gcagtgggag atcttgcgat 120
caacggtgag atcgggtgtg agttgcgacc gtttggcgag aaattcaaat ttaaattttt 180
tatttaattt gttactatta ataataataa attaatacaa tacgtgacga tgacgatggt 240
gatgatcgtg cccaacggca gcagacccaa ttgtaaaaag ttgtaatggc agaagcataa 300
gtctaagtag agggctccac ctagcactgt ttgcgacttc tggggccccc tgatatttaa 360
aaaaatttta ctttattaac tcgatatttt tatgcattta attatcagga aagcatatta 420
acacgttctt ggatcagttt aattatttca ccgcacgcac tgatctttct tggatatactg 480
ggtcgtattg ttcatagaaa caatagctgt atgggaaatc ctcataaccg caaaaaatac 540
aatcagttca ataagtaatt ttctatttta ttatttatat atgtattaaa aaccgtccac 600
aaaatagctg cacgatattt tgcttaagat aaaaagaatt gggtgactta agttagata 660
caagtagatt gtacgatagc aacatttagt taggaggagc acaacattca cacacgggga 720
cagccacgga tttcggctta gaacaatgga aaaaagatgt ggtaagtggg aagcgccttt 780
agcttgaaat atttatgtat aataagcaca cgagctataa ctaggaggaa ttgcacgttg 840
cggatcagat gtgagcagcg gggtacgact gcggcaggtt ct 882

<210> 66

<211> 569

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (83)..(135)

<223> Area matching *Drosophila Nemo* gene, Acc. No.

U12010

<400> 66

```
ccccggcgcg ttttacttcc atctcgctcc cacaaaggcg gaagagttaa acacaaaaaa 60
aaaagaaaaa tagaaaagaa attataaacg aaaaactgcc accgccgctg ctcaataatt 120
tgtgcatttt ttaaggtaat ttaaagtga atggaatgct ttgtttgcat aggttagggt 180
taattagtcc ggaaagctaa gcgaaaccct gggaaatatt acatatcccc gggcggaattt 240
cttttgcccc gttacttttc gattttcatg cgagcgtttt ttgattgcgt tcattttctg 300
gcgacttggg ggtgctcgcc attgtttggg ttttgaaca tttgtaaatt tgcataaaaa 360
gtcggatttt aagtgatttt ggtgtctttt gagcggcttt ttgcgcagggc agcgcagtcc 420
gaaaatcact cagaatcgca ctcacatgcy cacacactta caattgtaat acacggacgc 480
gccccgggtc ggcacagcta accggcactt tttcatgtcc tctcgcgcgc tctctctcac 540
tgctctcttc tcttctttct ttttgatcc 569
```

<210> 67

<211> 500

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(357)

<223> Area matching *Drosophila* UDP-glucose:glycoprotein
glucosyl transferase gene, Acc. No. U20554

<400> 67

aacagggcca aaaccagctg aaaactggtg aaaagtaaaa catttggaaggaggaaagcct 60
 taagtctctc tctacgcttc gtacacgtaa tgtgcgtggt ttaatctacg ttaaaacaag 120
 tggaaacccat gttacgtgcc gtggctttgt gtgtgtcagt ggtgctcata gcactatata 180
 cgccaacttc tggggaatcc agtcagagct atcccattac cacgctaate aacgcgaaat 240
 ggacgcagac gcccctatat ctggaaatcg ccgagtatct ggccgatgag caggcggggc 300
 tcttctggga ttacgtttcg ggggtgacaa agttggacac ggttctcaac gaatatggct 360
 tgtgtttata agtcatggga gaaccgcgat taaagagctt ttatattctc ctcaatgtga 420
 atcgaatcca tataaaatca agtaatgggt cggaatataa aatccctatt cccaaagccc 480
 tataacgggg acctttccca 500

<210> 68

<211> 469

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(20)

<223> Area matching *Drosophila* Cbl gene, Acc. No.

U87925. This association is confirmed by overlap
 with *Drosophila* EST AA441040.

<400> 68

acccacacaa ttttttcgac tttttcaatg aaatctcggt atgaccgcgg ccgcaacgcc 60
 agtaaatacc aaacgagctc gcacggctgg tcacactgat cgaagggttg catttcgctg 120
 tgacgtcatc gttgacccat gtaaaatgcc gttacaaaat ggcgagcttt tgaaaaaatt 180
 cgttacaaat ttattaaatt aaataaacta atttttaaaa taatttgaat attcattttg 240
 ggaatatggt tagaaataat agacttacag aatataatct attggtaacg attttctttt 300
 tcacagtttt cctcctcgaa agggaagtat tttaaattgt tattacacat gggggaagtt 360
 gctgcttggt taatgaaatt gtgttaaata tatataggga aatgctttta atctactttt 420
 tgtaggaaac ctttcatgaa aatatgtgga atctcacgtt ttattaaat 469

<210> 69

<211> 539

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (468)..(539)

<223> Area matching Drosophila EST AA392994. This EST
matches Drosophila Guanylate cyclase gene, Acc.
No. U23485

<400> 69

ggcagcgtca attactgttc tcatatcatc tccgagagca cggaaatcag tgatggcaag 60
tgagaggagc aaatcttttg cggatagcaa aaaccgctaa gtgtgtggca gtcaacgcta 120
cttttcttag tatagtactt agttatacct tttatcgtgc aattttttaa tgaggactat 180
gtttttccaa aatggatctg ctcaatataa tttgactatt tatcttttaa tccatttaaa 240
cctagtttta aaaattttta aaaagtgttg ataatgtatc ttgatggata tctttcggat 300
atcctacact gagcgaaact aaaattgttt gataaagcgt cctcatatgc ctaccttaac 360
acagtgaaaa aagccaaagt gccatctctg ggagcatgcc ggtgtcgtc gcccgatttt 420
cgtttggggc tttcagtatt attctattcg cctgcgcccc aagttgtttt tttcggatcg 480
gcaaagcccc cgtgcgcccc atcgactct cgacacaca catacgcact ccagaaaac 539

<210> 70

<211> 547

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(547)

<223> Area matching Drosophila UbcD4 gene, Acc. No.
Y11349.

<400> 70

gacgtgctga gcgctgtaaa aagtcagatt cgtgttgaaa ttggaataat aagtttttta 60
ttttccgtgc gctggctgag ctggttgctt cgacaattcg aaaagcgatc gaaaggagca 120
acctttagg ccaacagcca ggcgtaattt acgcaacgca caacactcac aaaatccaaa 180

attgcacggg ggggcaacaa taaaaacaga ggcagaacag aacacagcaa gaagagcgtg 240
 gtgaagagga gcggcggaga aaggagaacg gtgaacaggg aacagggaga gagcagaaag 300
 gagagtccga gaaacggagg aaacatcatg gcgaacatgg caagtgtcgc ggatcaagcg 360
 gggagttcaa gggaggtgat gcgcagcgag ggaggggtgag tcccagcac caaggcccg 420
 aggacactca aacggcacct cggcaatgcc agcttgacc accggccctg gtcattgggc 480
 agggggcggg ggaaggggtg cgcgaacgt tgggtggcgt ttttggcgcg cttatggctt 540
 ccgtttc 547

<210> 71

<211> 563

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(163)

<223> Area matching *Drosophila* SNAP gene, Acc. No.

U09374

<400> 71

cacccgctga aaagccgaac aagtcttaaa cttagatgca attagtgccg aggcggacat 60
 aaatcctcga catgggtgac aacgaacaga aggcgctcca actgatggcc gaggcggaga 120
 agaagttgac ccagcagaag ggctttctgg gatcgctgtt cgggtgcgta tcaaatcaaa 180
 gaagtttcgc aatttctgtg ggagtgggga aatggaagct gtgtctggtc tagcctagca 240
 tctccacaac cccacaaggt actgagccct attccaagta gcacttgat gccaatcac 300
 tatgcttact actttgtttt tatgtatata ccactcacc ataatacgta tacgcagttg 360
 tggactctac gcctccaccc agaaaggaga agaaaatagc gcaaaaagtg cgacttacag 420
 aggataagtt tcagatatga agaacacaaa gtgtgcaaaa tgctgttaaa aaatatcccg 480
 tagtacataa tatatgtaca ctatgccatt cgtaccaggt ttcgatgaat catagtgcc 540
 aaaagtcaat cgtgtaaaat aaa 563

<210> 72

<211> 594

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(104)

<223> Area matching Drosophila Caf-1 (inverted), Acc.

No. U62388

<400> 72

gattgagtcg aatcctggcc gggaacttac actttaaacg gcgtaacgtc agggcaaaat 60
agaaattggc taatttcctt cgtttttttg caagcgcgtc gtcgatgata gagatgcaat 120
gctaaagatt gtcgagacga ctgccatatt cgattacgat aacgataaca gagttatgga 180
gatgacactg cgcggtattt ttataacttgt tacgttcctg cgtcatgatt ttagtatttt 240
gtggtttaca tcgatatatt tgggggtttta aaaggtatat tttaacgggt gcagttgcgg 300
gcacactaaa gtgcataaac aaagtttact acttaattcg ttatcagtgc gaatgattcg 360
aaaccagttt acgcgccaat gaccggcttt ccattcttat ttgacgagcc taacgtgcc 420
gttgagttta agttcccca cgcgaacgac ggtgggcagc cgtgattcat cctcaacgct 480
ttttttccaa ttgtgtatgc aaaatgtttt tgcacgtaac gagctgaact attgagtttg 540
ctaaatagtt taacaagcaa taatttggcc gacatgcagg ttgatgggtg acca 594

<210> 73

<211> 583

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (374)..(518)

<223> Area matching Drosophila Elongin B gene
(inverted), Acc. No. AB007692

<400> 73

ggttagggta aaattaaagc cgaatattat caatccatt ccaaagttca attttggtgc 60
ggaaccatag taaattaatt gttccttgct attaacaacg aaaaatgcat atttagctat 120
tgcagttgag acggcagcta ttgcttcttc accacgctgg gaagttgaga atcgagaca 180
aataaatctt cctcctcctt cgtccgggtcc gaccatcaac ttcgatttca atttcataca 240

ttctgtttgc gtgggacaag cgagcgacag cagtctctgg agttagcgga tttatattgt 300
 ctcgatttgc tgctgctggt gattttgatg atgtgtttgc tgctgtttgt tgttctcgta 360
 ggggtgattg actgactgac tgctgtggct gcacacctat gccacctgct cctgggtccgt 420
 tcgaggcctc ttgggttttt catgacttcg ggtaagtctg ggtggtgccg agtaggggtg 480
 tcattgtcca gtgtctcaaa gtgcgccacc tcgttcctta aagacagata gctatgttgt 540
 actactacgc tgaactgtaa gcttgtaagc ggaacacgtg ccg 583

<210> 74

<211> 589

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(231)

<223> Area matching *Drosophila* TAF110 gene, Acc. No.
 L06861

<220>

<221> intron

<222> (232)..(401)

<223> Probable intron.

<220>

<221> misc_feature

<222> (402)..(589)

<223> Area matching *Drosophila* TAF110 gene

<400> 74

gtccgtgcga gcacgcgcga gtgtgtgtgt gcgcaggaaa acccgccgat cgggaaaagt 60
 gtagaaaggc ttagcgggcg aaacaaaagg cagcgaatta gcgagataac acacacgcga 120
 caacgactgc aacggatgcg ccaggagaaa ggccgacgac agtgacggca aaggcgagtg 180
 cgagtgaacc agcgcagcac caattcagcg gagcaccgc ttttttggcc aaggtgaatg 240
 cgattacctg tgcgcggcat ccagggtgtac gcagcatctg gtttatggcg cacggccgcc 300
 aggtagccgg cggtcaggta gcacctccac cgctacctg tttctccacc gccttgagcc 360

gaatcttgta taaataactaa aagcgccctcc ccttgatttg cagttcgctt ctggagcgca 420
 caagcatgca acaactccgc caacaccaac acagggatgt gcgcaactag tttgatcgga 480
 acaaggatcg cttgcccaca ccaacacaca gaaagtcagt ggaataggag aaacacactc 540
 gccataaca taaacaccac acagcacgat gaacaccacc agacagctt 589

<210> 75

<211> 314

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(314)

<223> Area matching *Drosophila* genomic sequence

AC005641. *Drosophila* EST AI259618 matches this
 genomic sequence 40bp 3' to NPS0081

<400> 75

gtccagcctc gcactcttcc tccagggcgc acggtctcac agaactggtg gccggcggtc 60
 aactggcgc gcagcaagat ggcttggtta caccaacgcc tatcgatata gaatagtgc 120
 cgtttagact agccagattg tttgtggtat gagcacatat tttattataa tacataatag 180
 cttataactt atttatctag cttataattt gtttacagca cccaatacac aatatatcgg 240
 atttggagcg gtgggttatgc gatgcgattg tatagtggat cacggctatt ttaccatcga 300
 catgtaaaga attc 314

<210> 76

<211> 591

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (509)..(591)

<223> Area matching *Drosophila* EST AA202837 . This EST
 has sequence similarity to hypothetical genes from

yeast and arabidopsis.

<400> 76

athtagggcc tcgagaagga cgcacgcctt gcacggctgc tgtgaggaaa cgaagccaca 60
tcgggtgcat gtgccacgct cgggcttctt tacctgtgcc ttgaagcgaa gctgttcgcc 120
agagtagatg atgtccatta taaccgatgg tcgcactttc tccaaatcct tgagaaacgc 180
tcgagcgtgg ccgcgatacg cattgggggc gaatacgcac tccgttgaga agtagaccag 240
ctttttgtag tgggcgtaca tcacgatttc tttctcgtag ctgtacttga ggggcttcac 300
tcggggaatg gtatcctcgc cccgcgcggt gcggatgctc gtgcagcgtc gcaggcgcgc 360
cgtgtcccca cggagcacgt tcatcaagac agtctccgca atgtcatctg cattgtggcc 420
tgtggctatg ctatcaacgc ccaacagctt ggccctctta tccaaggcct gtccggcgaa 480
gacccgcaaa atgtgcagtt gttagacggg ccgatctggg caacaatgcg gtccatggtc 540
cagccgtaaa cttcttgtag gacaaggatc tttagtggca ttgggtaatc g 591

<210> 77

<211> 617

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (166)..(393)

<223> Area matching *Drosophila* EST AI293734

<400> 77

gcttagatta cgatctcaga actgagaacg tgggagagag agcgtgatag aggtaggatg 60
agggagtgga gccccgagag agactctctt ctcttgccca ccgatatcta atcaaaacaa 120
ataatgcttc agtccacggc ggctttactt gattcatata tttagttcta tactgcgagg 180
catgcagtac gcttgccgtg tgctgcgttt aaaaagtaat aagtaaattgt totggataaa 240
aatttaatca aaagacaaat aagtgaaga acaagaaact caaaagatat aagcaacata 300
actcgaaatt cagtacgcct gagttggaaa acaccgaaac cgaaactcaa atcgaatcta 360
catataaccg ataccataat gaagcacaaa cttctgttgt tggtagtaa atatttcagc 420
catctaaaac agtatcccta tcttatcgca catactttgg gctcagatag tggggatcag 480
agagtgtttt ccgttaagct cttttctgaa tgtgcccag tggggagacc tttttatgaa 540
gccatcgatg accttcttcc ggacgggcag ttggcccaaa aaaaaaccac caaattagga 600

tgccatatag gtatcga

617

<210> 78

<211> 396

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (261)..(377)

<223> Area matching *Drosophila* EST AA202757 (inverted)

<400> 78

```
gtacagaact acttcatgcg ctgggattaa cagcactcat tgcgcataac agcacgctgt 60
tagttttaac aggcgacaga ggtgcccaaa caaactcaac atttttgcat gcgcatacac 120
acaagcatgc atgtatgtat gtatgcgttt gtttgtatgt atgcctttct ctgcgccatgt 180
tacaaaaagc aagaagtttt tggcaacgac aatgaatgaa aaattgaaat ggcgaattgc 240
aaatgcgaat tgcgcttacc tgcgtcgctg cctggccttc ctttcgcgac agtggcgagc 300
gaaatgcccc cgtcgcgcgc actcgtagca cttatcgtcc ccacgaccac cgccgactcg 360
gaccgcgtcc tccgagttct ttcaccacca accgcc 396
```

<210> 79

<211> 586

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(247)

<223> Area matching *Drosophila* EST AA696498

<400> 79

```
agcgggcctt tctgcctctc tgtgtgcttt tgaaaaaagt ttgcttgaaa aatgtgtaaa 60
gaaagcggcg ccgccagtga gtgcgtgtgt gtgtttttat gtgtttgcaa atacaaaggt 120
aaaacagccc caaaggcaac aacaaagtgg cggcgttggc ggctatagcg cagtagcagc 180
```

gacgcagcgg agcagcagca ggcagctcca gtgcattttg gtgcaaacta attgttggtg 240
tgagaggtag gctatactcg tatgtgtatg tgtgcgagtg ggtgttagtt gcagggtgtgc 300
gtgcgatttg atttgcattt atgttggggg tttgttttca tcttttcacg aagtaatata 360
aactaaataa atgaactatg tgtggaaatc atttaataa tatataaata aaattagaaa 420
gtataatatg aacatgaaag ttaaagttaa aatccgtagg aaatcaacaa aattggtgaa 480
tattaaaatt aaacaaattt tccgaaaaac cgccacacaa ttccagcaaa agccaaagta 540
aaacttaaaa atcatattta ataaacagca ttaggggact ggttgg 586

<210> 80

<211> 646

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (100)..(646)

<223> Area matching *Drosophila* EST AA950073

<400> 80

gtacagggtgt ttttcgaata gccggcactt tgatccaage tgttattgcc atctccttca 60
aagttgccta tcgatagggt tctcaactag tccacgtctt ctacttgccg tttttctttt 120
tgtaaaataa gaatgacgt ttaatgttgt gttaaactatg caattaccta gagcgacta 180
actagtatag catcagttag gtcaattgtt acctgtaggt gtaaagttca agccgcctga 240
tgtggataac cggtcagttt gttttttttt tgctgggtggc acttggtgcc gcaaaatcga 300
aaacctcggc ggtgcaggat gacatcgccg agtataagga cttcaagaag ctgctgcgca 360
ccaagaacaa tgtcctcgcg ctctacgtga ccagtgcgaa atccgctgct gctgagctaa 420
agatattccg tgaggcggcg gaggcgatac ggggaaccgg gacaatgttg ctgctagatt 480
gcggacagca ggatcgcaag aaactgtgca agaagttgaa ggtatcgccg gaccctacg 540
ccattaaaca ctacaaggat ggcgacttcc acaaggacta cgaccggcag ctgagcgtcg 600
ctcattgaca ctttcatgcc gtgaccctcc ggcgaattgc ctggga 646

<210> 81

<211> 655

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(50)

<223> Area matching Drosophila EST AA695104 (inverted)

<400> 81

gttcggtgct ttcaacattt tccgcaatcc gttgaaaccg gcaaaggcaa actgattaca 60
tgaaatcata tgtttctgcc ggaatatcga taacggactc tgtcttttgg cgccgcaggt 120
tatcggagtt taaattgtga taaggatgca aagaaagttg gttcttagat gttacaatca 180
atttcacaac ccaatctttg cattgttgag ttaggatcat cctctagcct tacatctttt 240
gccatttagt tacatcatgc aattgttcat atcttcaacc aaatccatat agaacagatc 300
ccctgtttat atattttttt atacgtacag agttgtaact aaatcctctg agattctgtg 360
gaatggotta ttgctagcgc taaatataaa caggaaaatg gggtcattca ccagaattt 420
ccatcgaaat tgaggctgag acccattctc ccttccccac cagaatttgt ttaggaaccc 480
ccgtgcatcc actattacgt cgctttattt gtagacaact tttgaaatca agagtgttaa 540
gtacattagg cgggctgaag tggttatccg taatggatac ggctactact attggttaca 600
gcgatctaaa aactacaggc acgccctaaa tagcgaacgt atgggtcaatg aattc 655

<210> 82

<211> 601

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(427)

<223> Area matching Drosophila EST AA942153

<400> 82

ttttgaaaca tattcagtc tggcaatgg agttggtgaa acgcgggttc ctgcgtgcgt 60
gcaagaacca cagctacctc agcttcgagc tgatcgatga tatcctggcc ccgctatgtg 120
ccaaccacaa gactacaaag cccggcgaca aggaggcgat tagggcactg gtggcggaga 180
ttaatgacac catcagcgac ttgggccagt tgctggtctt catcaagtat ccggtcaagg 240
ccgaggagta cctggtttac gccaaagcgg acgctacgcc ggacagcgtg gccaacaccg 300

ggctcactgc cgaggagtgt cagtactttt cgaaactgct ggacaagatc gcctccgagg 360
 aggactgcca catcgcttgg aatgacgcct acaatgatat cgtcctacag gccagctcga 420
 agccgttgaa gaagagccgc atgcaggagc tgctccagaa gtggatccaa atgggctact 480
 tcatggaggt gaccgacaga atctacctag gtccacgtag cctcgtcgag ctcagtttct 540
 atttgagctt gaaccacgcc gatacataaa aaatgcacgc ttgtgcaagt gcctgggtgtt 600
 g 601

<210> 83

<211> 543

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (42)..(334)

<223> Area matching *Drosophila* EST AA540352

<400> 83

ggtcgggtct tcaatgtcac caatcactat cagttaaacc gtcgagtgga tcacttcaac 60
 atgcccagtt tcaaggataa agttataatc gtgaccggag ccagttcggg aattggagcg 120
 ggtacttcgg tgctcttggc taaactggga ggctgtctca ccatcgtggg caggaatttg 180
 gataagctca acgagaccgc ggagcagata gtggcagctg gaggagcgcc agcactccag 240
 gtggcggcgg acataaacag cgagtcggac gtccagggca tcgtatccgc cacattggcc 300
 aagcacggtc gcatccgacg tgctggtgaa caacgccgga atcttggagc taggcagcat 360
 cgaggacacc agtctggagc agtttgacct gcgttatgaa cacccaacgt ccggtcgtct 420
 taccagctga cccacctggt cacaccggag ctaatcaaga ccaagggcaa cattgtaaac 480
 gtgtcttagt gtgaacggca ttccgttctt ttcccgggag tttacatac aatggttcag 540
 tgc 543

<210> 84

<211> 162

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (115)..(162)

<223> Area matching Drosophila EST AI238523

<400> 84

```
tatccgcccc aatgaagaga agctactctg tatttttgtg ctctttgtgc ccgcctcttc 60
aagtcgcttc acgtcgagggc aagtcagcag ttcagtcaca tttagacatc cgcgcggtaa 120
accgcgtttc ggcggtataa cgagattttt tatttcgaat tc 162
```

<210> 85

<211> 526

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(69)

<223> Area matching Drosophila EST AI260872 (inverted).

This EST has sequence similarity to mouse
signalling factor U29156.

<400> 85

```
gcttggcgca ttgcggcccc taatttagct actctcgaat tttaaaaagc ctaaatttgc 60
ttttttgctc ggtggatagt gtgaccgttc ggataacgat taaaatacc gtacggctga 120
tgattaagta taccactagg taaatgcgt taaaataccg cataaattaa taccgttaaa 180
ttaacgaaca ttattatttt tttaaagtat aattttttta aattcatttg tctatattta 240
ttcctttaac actaaacgtg aagaaaattg tgtactttga aacggacggt gcagaacagc 300
agtagcttat aaaaatgcaa tgtttcccggt taccctaacy gaacagataa tgtttaaagt 360
ttaaaatttt taattctaatt tcttctttta atggagtata tttcctgtat gggatctctt 420
accttaagct aggaccttag agcagaccga aggcggcaat tggggggccc gccttgggca 480
gtacaacacc ttgcggcac cagccaact tcgtaattgg agttcc 526
```

<210> 86

<211> 568

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (5)..(77)

<223> Area matching *Drosophila* EST AA801728.

<400> 86

```
gtctgtttca tggcgcacag ccagttttcc gctctatcca tgtggcctca atggcgtaaa 60
tgtagtcggc tgggttttct ttccaccagt tttttcttgc gaccgggtat ttaaggtgta 120
tctaaatacc gttgaaggcg attgcatatt caaaagctat tacttccctt attaaaatac 180
atacgtgcat acatattatg tattaatttg ccgctcgtaa agtaaaagac gactcgctca 240
cttatcaact gttggtgcct ttatttacgt aactcagagc accaagcagt tgattcctcg 300
catgaagcgc tctccttgaa ctaaaactag ttgtcattca ttttgatagt gttggttgtt 360
ctatgtttga gtgccttaga gcttatgctt ctgatctttc ttttgccatt ttagctattt 420
tccctgagat tttgtgatcc cctatgtcta tgtattcgtg catttacgcc aaaagtgggc 480
ataagaaaaa atttaaaatc aagctttcgt attagcaata agtgccatgt ggacgtactg 540
gaacttgaaa acacagtctc ttcatttt                                     568
```

<210> 87

<211> 675

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (228)..(675)

<223> Area Matching *Drosophila* gene SMT3, accession
number AF053083

<400> 87

```
gtccagcacc agtttttttg gcgtgtagct gtagcagaag caaaaggaag ccgcttgtga 60
taaatttcaa cttccatcag caagcactga atttgaggaa atcaggtaaa tttttgcatt 120
tctacgcgat tagttgctgc cccgcggtat tgtgcttagt ttttacgtgt ggtttaccaa 180
tttccgcgta ctttaattgga cattttgcct cgtttttttt cgtacagcac gcccggcatt 240
```

cgacgctccg caaaagaaaa aaaaaacttt ttgaccact tagcagcttc aacaagcaac 300
 caaaaaatca acatgtctga cgaaaagaag ggaggtgaga ccgagcacat caacctgaag 360
 gtcctcggcc aggacaacgc cgtcgtccag ttcaagatca agaagcacac acccttgagg 420
 aagctgatga acgcctactg cgaccgtgcc ggactctcat gcaggtggtg cgcttccggt 480
 tcgacggaca gcccatcaac gagaacgaca ctccgacctc gctggagatg gaggagggcg 540
 acaccatcga ggttaccagc agcagactgg gtggcgctcc ataagaatac ttagttaagt 600
 tagttacttc tcttacaact accccttaaa acgaaaagaa aaaattcccg aaaaccccaa 660
 agcaaaacac accac 675

<210> 88

<211> 210

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(210)

<223> Area matching *Drosophila* EST AA439866 (inverted)

<400> 88

caacggcgga tccttaatac gaactaacgc gcacacgact ctacgctttt taccgctatt 60
 tcggctacac agcggtttct gttttcgttt tgcaataata ttctattctg aaagcgcaga 120
 tgcagcggac aaggagaatg tggatgatta ctgttaggcc agtgatctcg aacttgtctc 180
 caaatcggat tcgaagtgct aaccgaattc 210

<210> 89

<211> 590

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (31)..(590)

<223> Area matching *Drosophila* EST AA820803. This EST
 has some sequence similarity to to human aldolase.

<400> 89

ggctgtgcga gccaacagtt gtccgcgaag ctttcgacga gctggaacag atagagattt 60
gatcgcgaga aaggcgtagt agcactgggt tagacttaga agcgtccaat ttgcacagcg 120
ttaattatca ggcgcagaga caagatggcc aatctgggtc ccaccatccg gctgaacaac 180
gggcgcgaga tgccaactct gggccttggc acctggaagt cgttcgagtc ggacgcctac 240
cactcaacgc gccacgccct cgacgtgggc taccggcacc tggacaccgc cttcgtctac 300
gagaacgagg ctgaggtggg ccaggcgatc tccgagaaga tcgccgaggg agtggtcaca 360
cgcgaggagg ttttcgtgac caccaagcta ggcggaatcc accacgaccc tgcattggtg 420
gagcgcgcct gccgcctgag ccttagcaac ctgggtttgg aatacgtaga cctctacctg 480
atgcacatgc cgggtgggcca gaagttccac aatgacagca acgtgcacgg aaccctggac 540
tgacggacgt ggactatctg gacacctgcg cgagatggag aagctggtgg 590

<210> 90

<211> 478

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (30)..(478)

<223> Area matching *Drosophila* EST AA803545. This EST
overlaps EST AA697132 and has sequence similarity
to frog/human MSS1

<400> 90

gttcagtcac tctcgccgta aaacaaaagg aaaacatcgc ataaactcat tttttgcctt 60
aaaaaccgta caattgcaat cgaataagat gccggactac ctgggagcag accagcgcaa 120
ggtgaagcac gatgagaagg aggacaagga gatcaagtcc ctcgacgaag gcgacattga 180
gcttctaaag acttatgggc agagccagta tcacaaatcc atcaagagca tcgaggagga 240
cattcaaaag gctgtgaagc aggtgaacga gctgactgga atcaaggaaa gcgacacggg 300
tctggcgcca ccagcgctct gggatttggc cgccgacaag cagatcctgc aaaacgagca 360
accgctgcag gttgcccgat gcaccaagat catcaacgcy gattccgacg accccaagta 420
tatcatcaat gttaagcagt tcgccaagtt cgtggtggac ctactgactc ggggtggcc 478

<210> 91

<211> 574

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (76)..(178)

<223> Area matching *Drosophila* EST AA438591

<400> 91

```
ctctgaacag ttcttagact attgaagcca agccatcgat tgtgccccgg catatcgata 60
ctaccaacat ggccgtcgag aaaaattgaa gtgaacgcaa cgccgtgttt ttcatttgcc 120
aataaaacgt taacagctca cgaaatatcg taaagcgtgc ccgcaaacgt cgccaaatgt 180
aagcaaatta ttttagtgcc tgttttacat cgtttacata attgccagag ctgaaattcg 240
gaatttagtt gctgccgtcg ggagtatcgc caacttttgc ctcacactct ctctctgtct 300
cgctctgcat tcctctcgtg ctgacaaggc aaatatattg gtgctggtgt gagtgtatgt 360
gtgaaaaatg gaagaaattc aaaatgcata tgtgaaaaga tatacgcgca agccgattaa 420
aaatcggtc tctcgcacga ttttgattgg gaccacaggt ccccgacccc cgcggcgtga 480
atgggttaaa tgacagccgg agcgcgtccg cgattctctc tgcgttttca ggtctctcgc 540
tctattccat tctgataact ccgctcctga attg 574
```

<210> 92

<211> 169

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(169)

<223> Area matching *Drosophila* EST AA979551.This EST
overlaps EST AA567400

<400> 92

```
ggttgtgtcg tcgaacgtga aactacgcgt ctccgcgaat gacgcagact ggaagcttcc 60
```

actggcatga caatcgtcta aaaacattca acaatagcgg tgcacttgca aattactggt 120
gccgcaacaa caataacaac tgcttcgcta agcagtagct gcgaccaca 169

<210> 93

<211> 414

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (138)..(414)

<223> Area matching *Drosophila* EST AA439261

<400> 93

agctgaatga taaacgaacg attttattaa accgtcacct tggttatcct caccctgaca 60
gcgcccttgg gcgaatggca aacagctgac gccatatccg cggacgcgaa tggcacattg 120
ctagttctgt tttcttgctt cgcgtttgct gtttatcaaa cgccttttgg ctaatgggtcc 180
gcagtccggt ggcgttatca cggaattgac gaggccgatg cgtcacatgt gcgtgggctg 240
catccggaca ccatgaacta ctcgactcc gcgctgtcgc ccggcggtag cggaggattc 300
gggtggcgttg accagcacia ccgatgttgc ggaaacaagg cctgggtgcgt caaggacatc 360
tgcggcattg tgtgcgtgat catgacctgg ctgcttatcc tgttcgccga attc 414

<210> 94

<211> 354

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (7)..(354)

<223> Area matching *Drosophila* EST AI107509

<400> 94

gtttgtcccg tttgctcgag cacttgttcc caacgtaagt ctgaaaagac ttattttccg 60
agataataaa tcgccgtggc tgcgcattat gtaaagtgga gtgggtccgt gccgatttcg 120

ctgcgttggg gccgttccaa acatatggaa tctaaacgca gcgtatttca ctctgcccg 180
 tgtgtgtctg tgtgtgttta tggttgtagt ggggcttccg tgtcgcaagt ggaaaacaaa 240
 tgaaattgag ttctcgcttt gagtcatatt cgagtgcaca ataaagcgcg ttatgcgttg 300
 tccatcgaat taccctttaa tttgattacc agctaatttg gtacccccca agac 354

<210> 95

<211> 48

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(48)

<223> Area matching *Drosophila* EST AA540348

<400> 95

gtccgtcgac tacttgtgcc atttgttttg aatattccga gcgaattc 48

<210> 96

<211> 577

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(311)

<223> Area matching *Drosophila* EST AA735555 (inverted)

<400> 96

gacacagctt ttgagtgtt ttatttcgtt tttgttgtt ctctgcgtgt acttgcagct 60
 ttagctctca attgttgctg ttgttggtgt gtgcgaggtc atcgacgcgc attagccgaa 120
 aaaatcgata tttaacactg gtcgcactag ataaaattgg ttaatgggtt agcttatggt 180
 tgtcgattga caacgacaat gacaaataac tacagaaact ggagtttttc aacgcacaaa 240
 cgcataata aattcaataa ccgggccgcg aatcgaaaaa ctttccgctg acttggacgc 300
 acgttgtgtc gcgagacgca atttttccaa atgggagctg caccgatgtg atttttggag 360

cccaccgaag eggcgctcgc tctcgctctc tttatctttt tcttttctcc ccttctttcg 420
ctctgtgcgc tctctctttg cgcagactct ttatcgcttg aagtttttaa ttcggattcc 480
tttgcattaa ttatccaata gccggcttat atgccgtctt aagaggtctt ggatgatggt 540
tcttcggggg gaagtgtgaa tggggccgtg taacaag 577

<210> 97

<211> 582

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1) .. (582)

<223> Area matching *Drosophila* genomic sequence

AC005646. ESTs AI064020, AI542218 and AI25740

match this genomic sequence 26bp 3' to NPS0118 and

have sequence similarity to Human SEC61

<400> 97

ctttggtggt ggcaccgctg ccgataggtc gtgacgctga ggtgacagct atcgtgcact 60
tagacagctg gagatgacag gctaaggcaa ctcaactatc ggctgctttg gctctaaaat 120
gaactagtaa aaaaaaacg aagaaataat atattcaagt tatgaattta atagataaca 180
ataatagata aaatattaat tctacaaaat gaattgttta aatcaatttg aatgaatcct 240
attaatataa ttggctatta ttaaaactcc gataataaat gctattattc ttgatttccc 300
ttgatttaat tatataatac atacttaata actatataat tatatagaat aaaaacttaa 360
tcacgcattt aatagatcat atagatatag aatatataga aaatcaatga aatcgatttt 420
gatagcgata atgtgcaacc ttgcatgtaa gttattttta gatttttagct gggcaagcgc 480
aattttcttg gcgcgcacca aacaatttgt aaataatatt ttgctcaac tggatttggt 540
tcgactgca atcactaaaa atattaagt acttaagccc cg 582

<210> 98

<211> 297

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (7)..(170)

<223> Area matching Drosophila EST AA263700. This EST overlaps EST AA978721.

<400> 98

gtccagggtca tggcaacaca accgctgttc accgatcagt ttttattggg tttcaggaat 60
aagtaaattg gattattgaa ggcttcactt ggcacgtatt agcttggatt tctatacgct 120
caagctgcgc agtcttcacg ttgtgttatg agacaaaaat agatcgaagt gcgtgtgtgt 180
gttattaccc aaaggagttg tggtctttaa acttcgaacg ccaccgacat catcatgttt 240
ttcatctcac cgaattataa atagttgtgt gtcgtttgtt ggtgccataa tgaattc 297

<210> 99

<211> 583

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (364)..(583)

<223> Area matching Drosophila EST AA941785. This EST overlaps EST AA695548.

<400> 99

ctggtgaata aaattcgcgt cttgtggaaa gtgaccagag tcacgaactg ggaaaacggt 60
agaacggtaa actagttcca ttctacgatg attatgatgc gatacatcga actgctttgt 120
tacatatcgc ttaaaatcgt gtcaatagaa aataaacggt ggatggcatt taaaaaatcg 180
gatttgaagc aaaaaaattt aatgatttca ttogtttata tcatcaaagc cagaaaatag 240
atgaccttac aaattaatct aatagcaata ccgatataac gtgaccaccc tcacacgtga 300
cagctgtgaa catctgttgc acgaatcacc cactgctttc attcgtcgtc atgcgtcatt 360
cagtcgaacc gtgctgtgac aaattacgca atgtctaaca actgatgtaa aacaagcaat 420
ttaccaaaaca gttggccaaa ttccgtgtgt acacacactc cgatcgaccc agcgaggcac 480
tttaaccagc tcttgaccac ttcgagatgc tgcgcaaaac ggcaacgatg ggaatcatgg 540
cggcggttgc cgtaaagcg gctcccgagc ccagaacca gct 583

<210> 100

<211> 675

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(260)

<223> Area matching *Drosophila* ESTs AA802928 and
AA817115.

<220>

<221> intron

<222> (261)..(561)

<223> Probable intron in gene represented by EST
AA802928

<220>

<221> misc_feature

<222> (562)..(645)

<223> Area matching *Drosophila* ESTs AA802928 and
AA817115.

<400> 100

gtcacactgg caatttggtg cccgaagttg aattgccgtt ttgtgaagcg gatagttacc 60
tgccgataat cttaaataaa aatgttttaa ctggcccgtg tgctcctgcc gcagcagcgg 120
atcctggcca gcccgctgcg cctgcaacgc ctgatctcta ccagcgacga ggtcaacgca 180
gagcccatca tcaagtccat ggacaccatt ggcggcctcc ccaccgaact ggtcaacgaa 240
cagaagctga agaagactag caggtaatca atctaccggt tttcgcaact gacctttgcc 300
ttgcctgttt gttttgttta catttcgacc ggtatgggca tgggcatggt atgcatgtat 360
cggaggcctg ttttgggcgt gattttcgaa aaggagtttc ggggtctttt tttcttgatt 420
tcaagtgggg gagaaagttt gtatcgagcc gcttatgcag tcacgtagac catagatgcg 480
tgcattgtgt tgtgtatgta tttgtgcctg cctggtggtg tcagttatgg gctctattgg 540
tcttgacttt tggtttgtcc acagaacctt atcgacgctt caaaatcctt cggttcccat 600

tgccgttcgc gtcacggtgt cgaaagatga aagtcgact ttatggcgg ttccaggtga 660
aaattggtta ttatg 675

<210> 101

<211> 395

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(395)

<223> Area matching *Drosophila* EST AA539001

<400> 101

ggtcaacgta aaggccggag agcacaaatc cgccgagttt ctcaagttga atgcgcagca 60
cacgatcccc gtgctcgatg ataacggcac catcgtgagc gattcgcaca ttatctgcag 120
ctatctggca gataagtacg caccggaggg cgatgattcc ctgtatccaa aggatccgga 180
gaagcggcgc ctggtggatg cccgtttgta ctacgattgc ggatcatctat tcccgcgaat 240
ccgtttcatt gtcgagccgg tgatctatctt cggagctggc cgaggtgccc agcgattcga 300
gtggcctacc ttcagaaggc ctatgatggc ttggagcact gtctggctga aggtgattac 360
tttgggtggg cgacaagctg accatcggcc gatct 395

<210> 102

<211> 58

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(35)

<223> Area matching *Drosophila* EST AA735863 (inverted).

This EST has sequence similarity to human death
associated protein 3, Acc. No. X83544.

<400> 102

ggcgaggac tcgcgacagg ctgccaaagc gattccggat cattttcata gagaattc 58

<210> 103

<211> 621

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (68)..(195)

<223> Area matching Drosophila EST AA941860

<220>

<221> intron

<222> (196)..(474)

<223> Probable intron in gene represented by EST
AA941860

<220>

<221> misc_feature

<222> (475)..(621)

<223> Area matching Drosophila EST AA941860

<400> 103

gtccgtccct accagcaacg cgaaagggtt ttgtcttget ttcttgttgc tttgtgtgat 60
tctcgagtct ctgttctgcg tctgcgtccc gttctcgtgc caacgaactg atttcgcccc 120
gcgttcgtgc tcaatcgtaa attcgaaata aattaaaaat gtctcgcagt tcgtacctgt 180
tgtgtgtgct gtttttaggt gagcgaaaga gagggagaag aaatgaagaa atcgtctcgc 240
gatcagattt tacggatacg catctcgtaa ttgcaggcgc cagctgcttg attttcagtg 300
cgagtgcagc gcggaacaat cgaaggggtt acaaggccac ggagccgccc accaccaccc 360
agcccccgca gacggccaag gagtatctgg acagtcgacc cggaatctcc acattcggca 420
tcatcgccat catcttcacc gtaatcggtt tctgcctcgt cttctactac ggcataat 480
gctaccctt actctgtcgc gatgagaaga aatcgcgggt tatggaccgt atcttcaacc 540
attactgccg cacattgcgc ttcatthaat ccatagagaa ctattccgac ccgaacacca 600
tcatacggtg gctgattcg g 621

<210> 104

<211> 534

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(210)

<223> Area matching *Drosophila* EST AA246460 (inverted)

<400> 104

ggtgtgcgct tggcgtgggt gtgcgtgtgc gccgatgtgt gtgcacgcgc cccgtgtgac 60
gatgtgcagt ttttgcaatt aaatttataa acaaaacact ctttttcctt caatataatt 120
cacagacaca gacaccactg aacaaattcc ttagtggtcg tgcttctcgt tctctgacgc 180
catcttgtgt gtgcgcaggc cagggttgtc gaggtgccgc aactgtctaa catgggcggt 240
cggaggtggc aacgctgtta gggctaacta atagtgtgac ccaatcgctt ggtattgtta 300
aattttccct caacggtcat gctttgcata acaattcaca ttttctgatt gaagaatcct 360
tattttatgc caaaacttgt attagatata taaaatatcg agatgtctct atcgccagcc 420
agtggcattg gtcgtttcta tgccaagtcg gcaaaaatca tacgtttcgt acgcctggga 480
tgcaccaatc ggccttttta tcacattgtc gtcattggagg tgccgtactt tttta 534

<210> 105

<211> 593

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (66)..(593)

<223> Area matching *Drosophila* EST AA141928

<400> 105

accatcctt aacatacaaa tattatcgag aaacttatcg actaatcgac tcgccactct 60
gcagagagcg cggcagtcag tcgctgttga accaagctaa aggacagatc aaaaataaaa 120

gagacacgtg aaattgtatt agaataattaa cttctgtaaa cggcgggctaa aatctcagaa 180
 gtgggattaa taatccaaaaa tggacgataa aatcatcctg aacgactttt cgctgacaac 240
 cctaaaagat tggctacgta ttctgggcca aaatacggag ggcacaaaaa ccgaattaat 300
 cgcgaggctg caagacatcc caacggcagt tcggggcgat tgtccaccgg agcaccacca 360
 gaaaaacgct ccaccaggaa acgacatttt ttcttcactg ggattttcag aattgtgaaa 420
 ttaacaccga tcacgtaaag tgtgaatggc gatgaacaga aaagaatcaa ccgaactggg 480
 cagtgaagg gagacaaaca tgttcgagct acagcaacta cgcgagact agcagaagcg 540
 aaggcatgct taacggacac gatcgacttt gcagttccag aaccaccacc acc 593

<210> 106

<211> 332

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(332)

<223> Area matching *Drosophila* EST AA979014

<400> 106

attgcgtgcc tggaaatcga acgtgtgtga atttaattta cgattcgat aattatcagc 60
 aagagcaaac aatataagtt gcaaacgacc gttaagccct atgacactaa gatccaaagt 120
 aagtggctac caccgaactg ttccatttgc atttgaaacc agtttccagc gattcgagtg 180
 catgaaattg tccaaaaaag tgcaacggtc gagttcaaca aaccgatcga ttgagataac 240
 accgcaaata tatagcagtg aaactcgcaa ataaatacct acatattctt ctgataagtt 300
 caagaacagg ctagccattg gttaccgggt ag 332

<210> 107

<211> 475

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (52)..(475)

<223> Area matching Drosophila EST AA817254

<400> 107

ggatatagtt atacgcgact tcaactgctcg ccgcggcatc tttccacctg cccgcaacgg 60
tcaactttgtt gttgtcaatc gtttcggtcg catcgcgctcg cggaaaatcg agatataaat 120
acggaaaaca aagatataac tccgacgagg cgacttccgc agcaagcaac tgcaatgcgc 180
tcgagttgag ggcgcgccga taactatgtg cgtgtgggag cgagtgcgag tatagcacac 240
aagtgatcac catcagcaat tagcaagtga ccaaccgacc gaccaatgag cacggggcat 300
tggcagcagc agcagcagca cggagggagc agcagcacct gggaactgag cgcggtattgg 360
aaggcgtgct ccctgcttgg cccgcagacc cgtcgaacgt cgataccggc aggacacgcg 420
ctaagcagcg actcacttga acgggaagcg gcgccgcagc ccgatgtcg ccagg 475

<210> 108

<211> 36

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(36)

<223> Area matching Drosophila EST AA536262. This EST
forms a 1209bp contig with ESTs AA948897, AA539274
and AA392320. Sequence similarity to glycogen
synthases.

<400> 108

cggctgccca tggattttct ttttgtttcc gaattc

36

<210> 109

<211> 614

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (475)..(581)

<223> Area matching Drosophila gene for Aspartate
ligase, accession number AF113612.

<220>

<221> misc_feature

<222> (35)..(86)

<223> Area matching Drosophila gene for Aspartate
ligase, accession number AF113612.

<400> 109

gactgcaccg cgctggtggc atgtgcaata gtacacgacg ctcgatgaaat caattcggttt 60
gtgtattaaa agggcaagat ctagctggta agtcgagtgac actcgaatgc accattgaaa 120
taaccaatag gggaagagac aggaagtga tagaatcggc aaatgatcag ataaaagacc 180
gcaaagttaa gggtatgtgc gagccgctag acaaggagtg tttctctgtc cccggaaata 240
tttgtggaca tatggctatt ggaggaggag actgggtgac tgaactgcag tccggaagac 300
aatgtcactt attcgcaaat ggggcacttc atcagccaag tgctatttat aaaaccatga 360
cgcaacgcac acaatactcc tccttttttcg cctggttgcg gcttatcgaa actgtgtggt 420
ctacgttctg gttttgtgac cctcttgtaa aatatacaac ccttccttct tacagccggt 480
tttgtgcatt ccaagatggt cgaggacaaa gagcaagtgg ccacgggaag cagggtcttca 540
agaagggacc caaaagctgg ccaaggccgt taagtgagaa tctttgtttg gggacctggc 600
gttttgggtt tctt 614

<210> 110

<211> 636

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (368)..(636)

<223> Area matching Drosophila EST AA390587

<400> 110

caagagacca ttcacttttt tcgttttgaa gcaacaaatt tgaaaagaga aaactttatg 60

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tttttccgc gggcttggtt gttttttttt tctcgctctc cgtcgaattg actctacatt 120
ttgatgtgat cttattatta ggtgaatcag ctgtcttcaa aagaacagtt ttaatttaaa 180
aaaaaatccc tcaattccaa ttcaaatttc atttagaaca caacgaagat atttctcttc 240
ttgtacgaac aaaatgctct cttaactcaa gttggaacgg ccgttcgggc aacatttaag 300
ttggcaacat tgttgcacgc tgcacgtatt tgagcacaag agtgtcattt acgattagca 360
actcgcgggc aacggacgtg tgtaaaaaat agccgggggag aaaaaacgaa gtgacgattgc 420
cgaagaaaaa cagagagatt tcaaataata aagaaatgca aatgaaacag aagaaaataa 480
aaataaagca aagtgccgtg agttccatct cctcagtggg gtgaaatttc cagcagagtc 540
taacggcgat ttgcgaatgc cgctcaagaa gtgcgaaacc aaaacggggc ccggttaaat 600
attctcaagc gaaaatcatg gcttttttga tacccc 636

```

<210> 111

<211> 342

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (55)..(110)

<223> Area matching *Drosophila* EST AA979454 (inverted).

This EST has sequence similarity to human REC1L ,

Acc. No. X57303

<400> 111

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aactcacca tagtactcgg cgaactctc cattgctgac atgcgaatcg attagattaa 60
attcaattaa taatgtaccg ctcatcaatt tgcggccgct ttccgtgctt cacataacca 120
ttctgcgcga aaccatgtgt tttgggcata aaatcacttt tccacgcaac acaggcacat 180
tgccagtgca gctgccgctc tctgcattct gtcatttgcc atgaccgcag gcaaaagggg 240
gaagcacctc gttgaacat tttaaataag tgttgctgca agcccaactt gaaacctcta 300
tttagacacc taaaaatata ttggatttta aaactttgaa aa 342

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<210> 112

<211> 575

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (31)..(460)

<223> Area matching Drosophila EST AA941359

<400> 112

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caacgaacgt ttccacccac aatgaaaaca aaacgtgcaa ccggccaacg aaatgccgcc 60
aaagtcaagc agcaagaaaa accaggttac ttggtaccac tgcgagtcct gcggcggtcca 120
cattccctcg aaagcgagag ataaccacga gggcttatgc tccgccatca gccaggatga 180
tgttggggccc gattccgagg cggagtagct tgcagtgga gcaatctata cgagaagtct 240
tcaacagcgt aatttcgagg tggagtctct gaaggatctg cccaccaagt atgccaatat 300
gctagtcttc gtctccgagg gtgcgatgca attggcacag ctacacattg gacaacatgg 360
tggtgctgga agctccatcg acggcggagc agcgcgtggt tagggattgt atggcccaca 420
tcagagcaat tctcaccac agtatttgct agcgaagggg gtattgtgtt tcacactata 480
aaaaccgctc tcaacaataa atgatcatac ttttaaacag atttcaaact tcattgcacg 540
caacttcagg aagctactca agactctgct tgcatt 575
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<210> 113

<211> 299

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (65)..(299)

<223> Area matching Drosophila ESTs AA201303 and
AA541066.

<400> 113

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ggacagtatg tgcgagaacg aaaatttcag cacatcgcta gcgcagcagc cttgttgttg 60
ttcgtctgtc tctgtcctac aagcgtttct ttttgtttgc tgagaattaa acaaaagcga 120
tttgttcgcy ggcaatgcga atgcatttgc aaagcagggc acaaagcatc ggctgttttcg 180
actgtgattg cacaaagcca tgtagtagag gtcgagctgg cgattcgcaa ttatccacag 240
gcgacgcaac acggtgctaa aaattgcgta gccaatat ctcgaaatcc ttcgaattc 299
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<210> 114

<211> 581

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (538)..(581)

<223> Area matching Drosophila EST AA698119 (inverted)

<400> 114

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atccaatggc tttctgccgc gcttttttac agctgatgcg agcttttgcg taaagctttt 60
ggccaactat cggttcaatcg gaatccgaat gtgtgttaaa tcaatactgc ggcggccaga 120
taatgataca gatatgaaac ttgggatccg gaatactgga cacaaaacag aacgtaatcc 180
gcacagctgc gtgctggacg cactatttga gtgactcaaa accgattcgt ttttcgtttt 240
gattcgatcc aatccaatcc aacccgattc gagtagaatc gtgaccatgt ttacctttgc 300
gcctcagcaa cagactgaat gcgaaacaca gaaaagccga agtcgcccga tttccgacca 360
gcgagaattg gaatgagtat gccaatggca atgcgaacgg aacgatttta gcggcggccg 420
taatggcatg tgaaaatgat tacatcagag tttgagtcac ttttccgcga cactcgccgt 480
cgttttgccg ctaccgcgat ccgcactcgg gcaaggcaaa tcggttattg agtcaccta 540
gtgctctgga tgctatctga tccgattccg aatccgaatt c 581
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<210> 115

<211> 632

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (111)..(549)

<223> Area matching Drosophila EST AA696174

<400> 115

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gccacgtctc ttctccgcca cctcggetag agttgccaac gatttggatt aatcgattca 60
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tcattgtcgc acaatgctca ctcgataaag ttactatcc aggtgatttg aactaagtta 120
 aatgttaata tgttttaccc aaaaacacca tttttggtga acccgttgct ggaagccgat 180
 atccttaaag tgaatgtatg tactttcaat gtgcacaaat acgtatttac aacaaaaact 240
 ggcttgcaaa ttttattaac tgtaattcc tggttttgtc aagtctgctg cacttgctcc 300
 gctgttgga tggctgtgcc ttactccaa agtcaccact tacaggggtga acactcttag 360
 gtgttcggt gacgactttc ggaaaaagtt agaagaaaaa ctgccattc gctacggtgt 420
 aaaatctcca aggattttact gcttgccaaa cctacccgag atgttggtgca ttgatccgct 480
 ggactcacag ctcaccaaag ctgtggccga ctccgactca aggaggtgag tggttgacac 540
 taactgcgga gctgcactac tgcgaggcgc ccacatatac gcccccggtg tttactatgg 600
 agtcaaact gaccgggagg aactcgcaat gt 632

<210> 116

<211> 243

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (107)..(243)

<223> Area matching *Drosophila* ESTs AI064230 and
AA263288.

<400> 116

ggttgccgta cctgcgacag ctaacggtga agccgatagt ctgcattatt gctccaacag 60
 aagtacggtc actctacaag taggcaacga attttggttg tcatcggcac ttgcattca 120
 acgtttccaa ttgtttttta aggagcttta agaatggctt tagctgaaat ctgcaagata 180
 tcgaatgctc cgtacatgcy gcccaatgcc tggatcatcg cgatgtgga ggaagagcaa 240
 aaa 243

<210> 117

<211> 445

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(212)

<223> Area matching Drosophila EST AI106957. This EST
forms a 1756bp contig with ESTs AA391125, AA567307
and AA735971.

<220>

<221> intron

<222> (213)..(275)

<223> Probable intron in gene represented by EST
AI106957

<220>

<221> misc_feature

<222> (276)..(382)

<223> Area matching Drosophila EST AI106957

<400> 117

gtttgtagtt tcagttcact ttctggttgg tttttagtg ctccttgctt ctccttggtt 60
ccttacttat gcatttttcg ttctcctttg ttccattaa acccccaccg aagtaagcga 120
atccagcgcg atgttggtga aatcgctgat tgcgttggtg gtcattgggg ctgccgtggc 180
ggaacaaacg cccgtctttt tgtgggggag caacaggtgg gtgagcgctt gcaccagttg 240
aatgtgagtg taacgagtg cttcctcctt ttttcacagt gtggcgaaac cctccctgaa 300
gacggtgtcc caagtggagt ttgccgagca gttggcttca ttgctggaag atcacatggt 360
cgtggccttc gaggaatatg gcgtaagtgc ttgagcacc acttagatag ctagggtttg 420
tgacacatgt gtttggtccc aactc 445

<210> 118

<211> 107

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(107)

<223> Area matching Drosophila EST AI820473 and
AA820473(inverted). Sequence similarity putative
cytochrome bc-1 complex core protein [Haematobia
irritans irritans].

<400> 118

ccctagtttt tcaatgcgct ccaaaatggt cacaccgagt accagctgtg acttatggta 60
agtcacggga ttttcgaaat atcgtgatct tgaataattt gactaag 107

<210> 119

<211> 546

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (19)..(102)

<223> Area matching Drosophila EST AA978449 and
AA940834.

<220>

<221> unsure

<222> (103)..(114)

<223> Gap of Unknown length.

<220>

<221> misc_feature

<222> (115)..(485)

<223> Area matching Drosophila EST AA978449

<400> 119

tgctggagaa agcagtagaa tgataagttt aggccgtatt tgcacaatta ctgagtaact 60
agtgcacgcc gaacaagcgc catgtattca taagcacctg ccnnnattcg aatttaaagc 120
ggccccggag cagaagcgac gcatttcttc gccgagcgtc cgcagagccg tcggatcgga 180
tcggatcggg ttgattggat tgggtgactaa aacagttgga caacaacagc ggcttgatta 240

gttggcagta aacagagcta ccgaacgcac eggtcattca ctccgcaccg ttttgaccag 300
aagcagttcc agtattggta gccataaagc cacagcaatg gggctctccg ttccagcagc 360
tgaagaagct ctggctgctc taccttttct gctcttttcg cgttcttcat ggtagccatc 420
agcatcaacc tggtagcgtg gccagcattc aaggcggggg acgcggagat gccgtgaagt 480
agttggcccc gtaattaaca atgggcccc taggaccccc ggttggaatg cacaactttc 540
ctggggg 546

<210> 120

<211> 546

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (182) .. (362)

<223> Area matching *Drosophila* EST AA802905

<400> 120

aacccccgcg agaaaaaaca tttttaccat tatgttggtg tcctcttctt tcattttatg 60
aatgggctgt gtgaacaaga gatggatggc gcagtagtgt gacaaaaatc gtgggtaaaa 120
agacgcagca aaatactgaa acactcatga aacggccagt cggcgaaaaa ttttcaaate 180
gcgggggtcgt acagcggacg attttcaatc ggaacgggtc agctttggag cggagcgcgg 240
agtttcgcat tttttgtgtt ttagcggaa aatcggtatg aaaactcaa atgtttacca 300
aatgagcggc gacaaatagc cgaccaattg acgagatcgt gtgtgttttt ctcaattaaa 360
cggtagtgtg gcgatagaga tggagatgta aagtatgcag tcaaattaaa gtgcggcaaa 420
aaaatcaaag gtgaaaaagt cattaaaaaa gtaagcaaaa tagaattgct ctgtggaata 480
taaaaatggt acatatacc atacatccat aaataaatat atatatatat atgaatatct 540
gcaagg 546

<210> 121

<211> 572

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (235)..(279)

<223> Area matching Drosophila ESTs AI259166 and
AI296787. Sequence similarity to Dihydropyrimidin
dehydrogenase component of pyruvate
dehydrogenase (human).

<220>

<221> intron

<222> (280)..(375)

<223> Probable intron in gene represented by EST
AI259166

<220>

<221> misc_feature

<222> (376)..(452)

<223> Area matching Drosophila EST AI259166

<400> 121

gacagtcccg tgtccaacta tttagcatat atgtcgtatt ccccaaaaac actctcacac 60
atacccatgc gatttgctg tggtgtgctg gctccactgc tnnccaagg tcgaatacac 120
gctctcctat atcgcatgat gcgtgatagt gtttcggctg gctgataagc tggaaaattc 180
cgtctaata ttaatgggtc actctttttg ggttccattg tttacatctg acgagtgggc 240
gattgaacgc ctaaagtgt agatagtaca ggagtgtggg tacgtaaaca acaacaaact 300
aacagctgat cgagcgtcca taaattaacc catccaaaat gctttcatta acatgggtcat 360
tttgtaatta taacagggtc tacaaaaatt acaccgttga gaatcagaag taaaaatagt 420
ttccaaggat actatttact catattgcaa gtaatacacc tatactattt atgcaatatt 480
accaaattaa taatttatga tgaattatta agttttttta taagtggata ccaccaatg 540
caaccactt taataaacta gttttggtg aa 572

<210> 122

<211> 492

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(238)

<223> Area matching Drosophila EST AA951193 (inverted)

<400> 122

```
ccccgaaacg gcaatggtct gcaccgaatt tattcacttt actcgccgcg cgatttactg 60
gctttttcttc gcatttggac ttgccaccgt tgttgctcagc tactttttca cacatatgtg 120
aacgacgcga ccgggttcgt tgcgagttct cggcactagc actgaatact gtatatatgt 180
gggaattttc ccacatattt attacgctcg ccaacagagt gcactgcgtg agtgtttgtt 240
tgtactcatg cctcagaatt gtcaaattgg agagtcttgg agctgctaaa acatcgctgg 300
ctgccacgat agtatcggtc gctaggtgcc agccggtgcc agcgatggac acacaactaa 360
atatcgaaac tcctttttat taaccctata atgcctgaaa ccaaattgtg acatgtcaaa 420
agctaaatat gttggcccat cttagacaaa aaagaaacca taaataaccc tctggatagg 480
taacgtgaat tc 492
```

<210> 123

<211> 605

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (326)..(482)

<223> Area matching Drosophila ESTs AA696743 and
AA803977.

<400> 123

```
ttcccaccta cgaagattgt ttacccttca tcttcggttt catctattac gtttcatttc 60
tctttttatt tattttttta ttttgattga aaaccttta ctgcatttgg aaacataaaa 120
aaaacttcag aagtatttta aatgaaataa tagaatatat ttataaacat aattttaatc 180
aagcctttac aataaataac aaaaacacct atttagcctt tttaaggctt cgcattgcgga 240
cccagtggag acaagctata actgatttga gatagaacgg ccacacatcc accggtggcc 300
agctggattg ttactgttgc ttttgttttt gttacaaatt ttgatttttg tcttgtttaa 360
caaaaaatga taaaatcttg aacagtaaag ataatccaca caatttacta tgagcaccgc 420
```

cactgggaac agcagacgga agacggaggc gttgcagtca atatacgagg gcgacacgac 480
ttcaaggaat agattagcgt ccattttcag taccaagtaa gccacattgg ataaaaaaag 540
ccacaattga taatttgtat atataatgaa atttttagtat ggcgaaaggt actaccagcg 600
tcttg 605

<210> 124

<211> 539

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (11)..(512)

<223> Area matching *Drosophila* ESTs AA990758 and
AA246427 (975bp contig)

<400> 124

gtcgcggttg tttgacgttt gtcgctttcc tccgttgcca atataatata ttacgtagct 60
catttttata caaacggaat tacgagcgca acgacgacag caacactagt agcactaatc 120
gtaagcgagc gggccaaaaa ttaaattgag tttgcggccg caaagatttg atgacgtcgc 180
atacgccgtc ttctagggcg taaaaagcaa agcaaagcaa acaaacgcca aagcgaaacg 240
tgtaaacggc gtagaagcga taaacgcgac tcaaatacgc agcagataaa atacaatacg 300
cgagaagagg aaaagtcacg ggaaatattg ttcataattcc ggcgtctttc tgcgagcgta 360
aacgtgtggt gcgtgggctt gtgctttgcc agtgtcgtgt gtgttaatgc ctgtgtggtg 420
tgtgtgatta agaagatata aaggatataa cggtaaatgc acgccgaaaa atgtgcagct 480
gacgccaaaca catggtaaac gtacgcacag nctacaccga ctattgggaa cttcaaaaa 539

<210> 125

<211> 563

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(406)

<223> Area matching Drosophila EST AA697797

<400> 125

```
agctgcgctc tgtgcgtgcg tgtgtatgtg tgtgtgcgag tgagtgtgtg tgtgctggcg 60
cgtctgtgtg agtgcggtgc tttgtgtgca gaataatttt tgcaaacatt atgtaaatgc 120
gcaaattaaa gttcaatoga cgcccgtttt gagtacgaaa ccagatcgcc ttgctttaag 180
tgccacggag ctacagtttc ttttcgtacc caatttttca aagatatact ccctcagtag 240
gcaggcacgc acacaaacat acacaggatc tcaaacgac ccccgatat acctttaccg 300
ttaggaaaat tcaaaatggc cacgacagcg gccgcaatgg cgcgaacgag tgtagttggt 360
ctggatcgcg gaaacaatac aacctgcacc atcaacttgc acggtgagca gaatgtcttg 420
aaacaatgat aaacaacaaa tgaatagctg gcgaacaatt aatcataatt aagaagacac 480
caccagcact ttgccaaaat tttgttggcg ttatttttag cggatgattg gcgcttagac 540
tttccgaacc gaaccggttc gcc 563
```

<210> 126

<211> 522

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(29)

<223> Area matching Drosophila EST AA802206. This EST
forms a 1341bp contig with ESTs AA02662, AA801949
and AA942041

<400> 126

```
cttccaacaa accacgtttg aaaattgacg tttctctggt gacgtaaaaa aacatcgccg 60
atgcgataca tcgatacatt tcgtatagag ttgcttnnnt agctaaaaat ataataaaag 120
ttatacatct gagcttatac acgccaccga caatatacat tagatctaca tgcaagtcca 180
tcatcttttt cgcttcaatt gttatatatt attttaataa acatcgagta ccaccagat 240
agttcggtaa aattgtaagc tgtgatcact gcgaataagg tattaataaac taaaaataga 300
taaattttat attattttct ttatttatgt ttcttgtaga taaaggaatc gaaggataaa 360
ctataattaa cacaggctcc tgccccggct taggattttc taaatgtaac tcttctgcaa 420
ggtccctaag gaatgtttta tataaaaata taaaagaatc tttagtgatg cgactaagac 480
```

tatgtaataa acaaaaaaaaa ccaggatgga atgctatagc cg

522

<210> 127

<211> 592

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (344)..(592)

<223> Area matching *Drosophila* EST AA978904

<400> 127

gttctgagcg cagcaatagc agcaagaaga ctaccaacaa agagcagagc gacaaatcag 60
cggagagcag gatggccacc agcggatttg tcgagtcatn nnctgggtgcc caaggcggag 120
acgggagtc tgaactttct gcagaagtac ccggagtacg atggacgcga cgtcaccata 180
gccatcttca tccggcgctcg atccccgggc aacgggactg gaggtgagtt ggcacttttt 240
cgcactctct ataccggtta caaagaactt gtacagttat tcttccaata ttacaatat 300
ttcgtcttac ctattctatt acgatttaac ctttctactg tgtcacgact gcttcttact 360
cccgtttctc attataaccg atccaatttc aatctgctcc tacgcaacag acgctgtgcg 420
atggaaagga ccgttaaagt aatagagcgg tacgactgtt ccggatgcgg cggacgtgga 480
catgaagaag aaggtgacgc cggacgagaa cggcaacatt aagggcctgt cggaaactcg 540
ctcagctgaa tccggactga tggctctgac acagatccgg aaaagcgggtg cg 592

<210> 128

<211> 551

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (101)..(223)

<223> Area matching *Drosophila* EST AA202366

<220>

<221> intron

<222> (224)..(291)

<223> Probable intron in gene represented by EST

AA202366

<220>

<221> misc_feature

<222> (292)..(551)

<223> Area matching Drosophila EST AA202366

<400> 128

```
ccctggagtt gcgaatttta acgtttttgt tcggttgctg aacgttttgc gcttgaaaat 60
gccagttcgc agcgccctggg cgcgagaagg tatgatgnnn atgtacctct tcaccaaggc 120
gaatctcata cgcttcctag ccggcgcgat atgcttggtg ctggtgctta actttgtggg 180
cttcctgtag cggaggttag gccacctccc tcagcaagct caggtaacta aatctatcat 240
attgccttgg cagagggttat cttatcaatt atttttggga acggatatta gcattcggcg 300
cgtgcacaag tatgctcata tctacgggaa cgctagcagc gatggagccg gaggcagtga 360
agcatccagg ctgccgcttc cccgctcgcc ttatcaaaag acagagagcg ggaccaggag 420
ctcaatggcg gacccaactc taccataaga actgtgattg ccacggcaaa ctttactttc 480
attccacaag acttaacgcy ctttctgctg ggacaaaaga aatttttgcc cccgcgacag 540
aatccacat t 551
```

<210> 129

<211> 492

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (103)..(468)

<223> Area matching Drosophila EST AA950164

<400> 129

```
gaatattgca aacaacacca acaacaacaa gaacaacaac aaaaccaaaa gcgaaacagc 60
aaaaaataaa taaatacgag gaaccagttt accttgaggn nnacactcac actcgcactc 120
```

gcattcacac aaatgaaaca gcccgatctt actcttactg cgagtacgga cacatagtgc 180
 acatatagtgc catatagtgc acagcacaga gcacagagta gacatagtga ccaccacata 240
 atttcgtgat aaagccacag agaatcggag cgctccgcct tatcggcaac ccaactgccac 300
 tgggtccggct actatgctcc agcggggatc gggacatcat cgctgggata gagacacagt 360
 ggacaccaga actgggatgg cagttgcagc ggccccaac gcattgaaag atgatagcta 420
 agcccaacca ggccaccacc gaaccaccat taagcttgcg ccccggaac agtgccaaac 480
 gggtttcagc aa 492

<210> 130

<211> 602

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (23)..(98)

<223> Area matching *Drosophila* EST AA952159

<220>

<221> unsure

<222> (99)..(101)

<223> Gap of unknown length

<220>

<221> misc_feature

<222> (102)..(602)

<223> Area matching *Drosophila* EST AA952159

<400> 130

cagcggccct ataaaaattg ctttttgtgg ggctgtcagc tcagtcagcg gctcattcat 60
 cactttccga cgcgctctag agtagctagt agacctttnn ntattacgcy tccccccgaa 120
 attgccccgc cgcccgaac gcaatagcat tccgcaaaaa caatacgata agcagcaaca 180
 agtgttcaag attcccttga aacatacaca gaatctaaaa ctccattgaa attggttctc 240
 agttgttttg tttaccagc aatcagtgcc caagaacgtg gcacatttcc aactgtgggc 300
 gggtaaacia ttgctgcgca acaattaaga aaacttggtc gccctgtctg tgtacacgcy 360

aataaatctc gggagtacaa ttccatacca gcccggtgac gggcacggaa aagcagctct 420
aactgtgcaa gatgattcca ggctatggac ccgtcacgca ggctctgctg ggcaccctgc 480
ttacctgggg actgaccgcc gctggcgccg cctagtgate ttcgtcgggg taaccagcgg 540
aggtctctgg acgccgctg ggattcgcag ttggcgtaat gatagcagcc tcttttggca 600
tt 602

<210> 131

<211> 558

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (102)..(512)

<223> Area matching *Drosophila* EST AA392519. This EST
forms 758bp contig with EST AA695318 and AA441243

<400> 131

gactaacggc tctccgctct cgccagtcgg atcggtata aaagcgggtgc gatctcagcg 60
agcgccgttc atttgagttt cgcggttcga ggtgtttnnn cgggtctttcg gctctggaga 120
aaactactcg catcgaattg aattgaatct ggggaaaatc agtccgagtc ccagctacac 180
agttagtttc acttcccagt ccaactataa aagtgcgctg cagtcccagt caaa~~a~~caactg 240
cattcagata caaactattg ccaattgcat ttcatgagc taactgtctc gcatcgcgty 300
tgaaaagtta caaacaacac aaaaacaatt gccaacggtt aatgtttaat gtccaggcaa 360
ttataaaaag caattcgatt gtctagctta cgcaaggcca actacaatta ccaataaata 420
cgacgaataa agcagcacag aaatcccaat ttggatttat taatagccgc tggataaaaa 480
aatcataaaa caccaacggt gcttgtaaat accaaccaat ggtaagtatt ttttcggccc 540
caaaggtaac ttcaaaaa 558

<210> 132

<211> 541

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (304)..(541)

<223> Area matching Drosophila ESTs AI515517 and
AI404462. ESTs have sequence similarity to Ras
related proteins

<400> 132

ggtggtacta agcgcgtctg ggaaatgcaa ttagtgatgg gcgatagttt tgctatcggg 60
tggcatcttc caagcggtaa tcggggctgt gatttttcta gtagtcatat tcctgattgg 120
aatccttgct aaccaatcaa actaacacat aaatatattt tttagaata tatttacttg 180
tgaaacaaag ttatttcctt gcaaaattct actctgcaag accagctatc gctgccagca 240
gcaactatcg cacctcgtgt cagccctggg aaacagctgt tcgcgcataa cataacacaa 300
taacaacaag ctttcaaatt tattaaatct tttatcttta ctgctgactg cgcgctttta 360
atcgcagcgc ccgctttgaa aacccccacc gactccgata aattcagttg tgcccaagaa 420
atcagacgca gcaggccgcc aaagggccaa ttacgcgctt cccaaccact ggctctacaa 480
gcaacaacaa caacagcagc acaccactgg accacacaca tcattctcatc cattttacaa 540
a 541

<210> 133

<211> 494

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (191)..(387)

<223> Area matching Drosophila EST AA698481

<400> 133

gtgcatacat acaaatgcag atatgcatgg caacaagagt tacatgactt tccggtttta 60
caggtttgct gcaaagcttt cgctctctca ttcggcgctc tctctctctc tcacacactc 120
tggcacctgc ctaattcgat tagccgcacc gtcgaacgc tcagtcttca aagagatctc 180
gaccgagcaa caagtgaacg gaagaatccg agcagtgaag aatcagaaag accgaggaaa 240
cactcgagaa ctctttaata acattgtgaa ccaaaaaacc agaaacagcc actgaaaata 300
cacggaaagc agagtgattc gcatagtttt gctagtgttt tcaagggcac ccatcatacc 360

agctgtgctg caaattttgt gccaggtagt gaatttaaata gaaaggccaa gaaaccacga 420
attatattga aaatttccat tatctagaga tcggtcgaga acgtacgcct gcaagacgta 480
ttctggcaga tttt 494

<210> 134

<211> 606

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (451)..(606)

<223> Area matching *Drosophila* EST AA803082. Forms

2166bp EST contig with AA941565, AA820668,

AA978815 and AA697381

<400> 134

gctcagtggg aaaaaggata aaaacgaaga caaagtaaata cggagaaaag tagcaacgaa 60
aaaagaacca gagcgccact aaaccgggtc gcttttcttc tcttttctctg ctgctccaac 120
tctcttcgct gattctctcg gtctccagtt ctcgctctct ctctctctct ctctctatcg 180
ttgcgggttaa ttaaaactcc gagaggcgtg cgacagttgt aagttgtgta ttaaaaagt 240
gtaacaacaa caagtttagct agcgtggcca attagcattc attttccgca aagagcagcc 300
gcggcacaca gcttttctga ttagaaattc acagtgggca ctogaagtgt gtctgttgta 360
aacggatcct cttggatttt atacataatt cattagaccc ctttggtgct gcgttagctg 420
tcccattctt cgatttcgg tacttacaat ttttgccaac tgcgcgggtg gtctctttct 480
atctctctta aataggtgaa aactaactgt ggtaactgtg caattaacta gtgagagtaa 540
tagtttaatt ggttggcact tcgcgtcttt tatttggtgta tgcaggctgg aattaaatcc 600
cacgag 606

<210> 135

<211> 570

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(570)

<223> Area matching Drosophila EST AI405762. This EST
has sequence similarity to hypothetical proteins
from Arabidopsis and C. elegans.

<400> 135

```
gctgggcggtt tcacaatttt tttgggaaac acaacaaagc ttcacaaagg acacgatgct 60
cggtctggta ctcggcgacc tgcacatccc gcaccggtgc agcagcctgc cggctaaatt 120
taagaagctg ctggtgccgg gccgcataca tcacatcctg gccaccggaa acatctgcac 180
caaggagtcc tacgactacc tgaagtccct ggccaatgat gtgcacatag tgcgcggcga 240
cttcgacgag aacctgacgt atccggagca gaagggtggtc acggtaggcc agttccggat 300
cggctctgtgc cacggccacc aggtggttcc ccgcggagac ccggaggcgc tggccctcat 360
ccagcggcaa ctgggacgtg gacatcctga tcacggggca cacgtacaag ttcgaggcct 420
acgagcacgg caacaaattc tacatcaatc ccgggatcgg ccacgggtgc cttcaaccca 480
tggacaccaa tgtggtgcct tcgttcgtgc tgatggacat tcagacacca cggtggtcac 540
gttacgtgta ccaacttgat cggcgacgag                                     570
```

<210> 136

<211> 236

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(38)

<223> Area matching Drosophila EST AA391495 (inverted).
This EST forms a 1135bp contig with ESTs AA439145
and AA949325.

<400> 136

```
agccgaaaga tgacttattg acgagcggat gaccatattt cggatttggg aaaaatccag 60
ctgtgctgca aacgaaaaat accagctgtg aacgtttttg gtattaatat ttaccaaata 120
aataaattta tatttatctt gaaaacaatg aaaattcctt aataacatta cattacttct 180
ttattaggag tgcttaagta ttctttttaa taatgaatta taattaatat tataat      236
```

<210> 137

<211> 526

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (353)..(476)

<223> Area matching *Drosophila* EST AA942305

<400> 137

```
gctcaaactc ggcgctcaca ttacgcacag tggctcgagaa aatgatagat gctgcttaga 60
tggcaactaa atattttaat gggaaaaatt atgtatgcta gtgttttggt ttaaatttct 120
caaccaataa agtaatataa agaatgtaaa ttaataaaaa cattgtattg aacgaagtgg 180
ttcaataatc gtatttgaat acagaataat ttgtacgaaa atatttaagg tgtgaactac 240
tgtgcggaat caacttggtt gttccactgt gactctcttc gacgattggg tgttgccaga 300
ctgaagtcgc tacgactatc gcatcaacta acgtagagca ctgcagccct ggttgactag 360
tgccgccttg gtccgattgc cagaaaaaaa caagacaagt gaaaaagcaa gataaatcaa 420
attaaaaata ttgtaaaaaa ttggagttaa cacgcgctga gcacggtgac tgaaaatgtg 480
atgaaaccat catagagaga gacagcgaga ttggtggccc caagct 526
```

<210> 138

<211> 391

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_difference

<222> (72)..(391)

<223> Area matching *Drosophila* ESTs AA951839 and
AA979603

<400> 138

```
ggctagtgtg tttatttttaa tattagcttt gtgacgttcg ctcaccaa at cagtattttt 60
```

cgtaccatcg gcgttaaaac acatgttcag cgatttagtg cgaggagtga aactaatctg 120
 agtaacaaca acagcatcgt cggcaaagca acaacaacgg cagcagaaaa ttttaacacg 180
 ttgacgcttt ttctagtgtt tatagcgagc ggaaaagctt actaagcgcg taacaagcga 240
 gaccccgaaa tcttttttca tctcggtctt ttcgcctttg cgtctttgag tgtgcgtgcc 300
 aaaattcaaa tacgtcatcg acgcgcgcag ccttaaactg aaaaggaatg aaataattga 360
 tatacacaaa tgccagcgaa agattgaatt c 391

<210> 139

<211> 458

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(112)

<223> Area matching *Drosophila* ESTs AI386817 and
 AI404737

<400> 139

cgtcagtgtg agcgcagctg ataacgggag gcggagtggc gacctaaaga cgcattggacc 60
 gcgcaggcag atggaaacag ttgcacccgg ttgcctcgag tgtgcagtag atgatccagc 120
 ggcaggaatg gcggccacga tccagaacac cctgaagggtg gcgctgcgaa agcgcattgaa 180
 ggatgcactg aagggcatcg acgcggaggg catcgcccg cagtcgcagg ccgtcacggc 240
 caaggtaaca ttggtttggc tgggccccaa ggttatcaag ttaatcccca atcctcctaa 300
 tcggctcgat cgcacagggt ctgcaaagcg agaccttcg gcaggcgcag cgggtaagca 360
 ttacctgag cacagcctcg gactggacac cagcgcttg tgtcggagat gttccgctgg 420
 agaagatggt ctttgtgccc actacgaggg acaggatg 458

<210> 140

<211> 527

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (435)..(475)

<223> Area matching *Drosophila* EST AA438658

<400> 140

```
gccacaatcg tgcgaaaatc acattttacat acatatatgg gttatgagta gaaaacgaag 60
agcaactcgt cgccgtatta gtcacgaaac atcgcagtcg gggaaattcg ggtagaatg 120
tgctcatcca tagttgtggg aaaaataact aaatataagt ggtatctgtc tataaaaaag 180
accaaagttt tcacatagtt gtgtgggttt tgagattaaa catatatcat atcacatcaa 240
ttgaactcgt ttttatccac tgtacagcca agtatcaaca actcatcatg cgtaacattg 300
ggcaacgcgc gatgagcaag gccaggcaat gagtagccgg ggcaaataaa atttccaaac 360
cttggacatt gtggagtttc aactccgcca acattgtttg tgtattttat ttaatatacc 420
tatctatcta tcccagcacc tcgggcagac atattccttt gtgcacacca tggcgattcg 480
aatggcgctc ggctttgtcg acaggatccg cggacgacac ggccatg 527
```

<210> 141

<211> 483

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (31)..(212)

<223> Area matching *Drosophila* ESTs AI106794 and
AI107315

<400> 141

```
ctccagagac tggcgacact cttggttccg ccttggtga gcacagaggt gggtagagt 60
gctactggct ggcagtgcg agcgcttcc tttgtgtgct ggcgtaggcg tgaagccatg 120
ttgtgaaaag tgtctgacag aaagtggaaa attcgcacgg aaaactgcac tcgaaagtgc 180
tggaataaaa gagcattgtt aaaacaatcc aagtgcgttg tgaaaagtgc aaactttttg 240
gccagtgcgt gtgtgtgtgg cgaaggaatt acgcaaatgt tgcacaggat tttccgtttc 300
cattgatttc gctgggggcg tgtgtgtata tattatatac atatatatat ttttaattgc 360
tgaggaggac aagcggagcc aaaatatttg cgtacaattc atttgcaact cccgggattc 420
actaattgga catggactga tgaattggtt gtgggcctgt tgaacaaagt acctcgggca 480
ttt 483
```

<210> 142

<211> 430

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(228)

<223> Area matching *Drosophila* EST AI403747.

<400> 142

```
caataaacta attgtttaaa atgtgacaac agtgaaccaa atgcttgctg agtaataaac 60
caaaggatgt tttgtttttc taaaacgtgc caattgaatc ggctccacgc aaatgagagt 120
gtgggagtggt ggtctgaaaa caatggagct gccgtaaaga attgattaaa caaaatagtc 180
gagaagagag cgcaaaatgc acaaaatggt taaattatc ctcaggtaat ttcagtccca 240
acaaaaacaa catgtgccag attgctttcg tgctcttatt gctgttggtg tagttctaga 300
ctctctcttt gcgctttaat attatgaatg acgtaagcgc gcctctttgg tagcaataca 360
aaagcaataa caacaatttg gttttgttgc ttttgtaaac aaggaaaata acagaatggt 420
tttgtctgtg                                     430
```

<210> 143

<211> 272

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(272)

<223> Area matching *Drosophila* ESTs AA802791 and
AA390699

<400> 143

```
gaacagaact agcaaagacc cacttgatcat agatgcgtac gagatcggtta accaaacaac 60
aatcacgttc gcaatcgacc agaaagacac tgaaaatcga accgaaatca ccccgagctc 120
```

ggcgagcggg tagagttgtg taacacggac ggacggggcc aaaaaaaaaa gaaacgtgaa 180
 ctagaactct gtgtctcctc cgctgggttt gttgagtttt tggcgagcag gtgaaacaaa 240
 agcatggcgc ttgaaacgga ggcgaagaat tc 272

<210> 144

<211> 489

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(190)

<223> Area matching *Drosophila* ESTs AA949990 and
 AA246423

<400> 144

gctccgacgg attggtgcgt cgctcgggtga aaccccgcca aaacgggtggg gcggaggggtg 60
 ggttgaatgc caacacgccg gacgacaacc aggatgcact ggacaaccta aaggaccagg 120
 aggacaatat cgacgatggc gactccaagg aaacacgact aacgctcatg gaggaggttc 180
 tgctgctggg actcaaggac aaggaggtgg gtgtgctcct tatctcatat ctgcttggga 240
 tgcactaatt aattggtttc ttctgcaaca taagtgttcc ttcttcacct gttaaccgga 300
 cgtctctctc tctctgtcgc tctcagcatt tctctcttcc gcaacctctt gcttggccca 360
 agtgcaaccg cagtccatct tccagcaggg gccgtagtga aaattggata caggggggta 420
 acttatcact ttcagttatg gggcaaccaa tggttatctg tctacagata acatttatga 480
 actttcgat 489

<210> 145

<211> 463

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(202)

<223> Area matching *Drosophila* ESTs AA201161 and

AA438658

<400> 145

```
gtcgaaatcg aaccaatgac gtcgcgaatc tgaggcgaca aagagcagcg ggaggaaagt 60
ggtcgcccaa acgaccgtat tgtgtcagcg taatcagtat tagaagcatt agcagtccgg 120
attggacaca ccagtcaaac gaacaccccc cactgaccga cacagaaaca tgtgctagac 180
ctcctcgaaa tgggatcgcg tatcaagtga gtatgcccat gccgccagc gccagttcgc 240
agcagcagtg ggcgttgcg tccactggtc gctatcgcg cgctctcact cccgcgactc 300
atcgcccatt cctcccgcgc ctccccccag aaatggacgt gaagaagctc ttcgagttct 360
ggtgcgaggt cagccgacg ccgggattag agaggggcac gagttccagg agcggcggcc 420
agctgttccg ccggcggtga tcgtggagag cttcccagg gat 463
```

<210> 146

<211> 506

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (202)..(472)

<223> Area matching *Drosophila* EST AA978927. This EST
has sequence similarity to human PCF11p homologue

<400> 146

```
gtgcagccta agatttcagt gcatcacggt ttattacaaa taaaatgggc agagatgaag 60
atatcgctaa caaacatcgc aaccttaata cattattcat ccaaaatata ccgacaaaat 120
cccattaata gtgcaaactt tttcacacaa attacctttg cttttcatgt catttaatta 180
ctttgttata ttttccttg cagtcgaaac atagcaactg cgactacttc aaaccгааata 240
acttgatcaa tatccggatc aagatctgga atacagagtc cacaatggag cagctatttc 300
agaattaccg cgacgatgag cgaaggatcg gcgaggagta tctgtcaagt ctccaggacc 360
tcaactgcaa cagcaagcca ttgatcaata tgctcacgat gcttgccgag gagaacatca 420
actacgcca cttcatagtt aaaggtggtg gaatattaca tcagcccagg ttaacaaaca 480
aaagcgtatt tacttaaaac caagac 506
```

<210> 147

<211> 445

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (84)..(318)

<223> Area matching *Drosophila* ESTs AA541084 and
AA538937

<400> 147

```
ggttcaccaa aactgagctt ttctccatgg cgccgccgat caaaggcggc gagtgctaag 60
tagtogaatc tgaatcggtt ttgtgagtag gcgctttgaa accgttaacg gagactgcgt 120
atatactcaa tggtatttta tattgcacta taataaaaac cacgtgacgc ccaattcacc 180
gcaaaaatct gtttttgaag tgctgctgtc agacaccgct tatttgtcgg tgcttggtt 240
ccaaaattaa attacaaaaa ttaaaatacc ataaataaat aagaaagcga aggacaatgg 300
ccaccaacct gcaaaaggta agaaaggata ttogagactg gtatcagtgg catcgcttaa 360
caatgcttca ccaaggtttt aaaagtttgt gtttcgccaa ttttgcccct tacctttcgt 420
acaatgctct gtattggtgg ggctt                                     445
```

<210> 148

<211> 509

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (390)..(509)

<223> Area matching *Drosophila* EST AA951890. This EST
has sequence similarity to mouse RIR2 gene.

<400> 148

```
ctcaaaacta attaagtggc gtttcatcag ctgttttctg gattagtcta gggttgtctc 60
attgcatgaa atatcgatga taaaaaaatt tcaaaattta tttagtattt gaaactatta 120
atattaatat ttttcaagtg acaagctggg aagctaaaca taaaattgtg cagtaaggat 180
```

tcgatttatg gtttaagaaa agaaaactac caccaccataa ttgcattaga tttaccctaa 240
 atttataaaa agtgaattga cgactcgcac agccctgatt ttcccatagt tttcccatca 300
 ccaaaaatgg cggcaaactg aaacagtttg ccgcccggca taaaacccaa tgtagctgta 360
 tttcccagat catttgccac acaactttca aactgtacac ttaatacacg tcgtgggttta 420
 agtgaatttt accagagaat cagagaagcg cccctacctg ctaataataa tccattcaaa 480
 acatctcaaa tggcgtccaa ggaaacatt 509

<210> 149

<211> 490

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(140)

<223> Area matching *Drosophila* EST AA439230

<400> 149

acccaaccca aaaaaaagag aaagaaaact gaacgaaaaa ctcccggaga aaacaacaac 60
 acacaacgat aaactgcaaa agtaaacaaa ttgcgccgaa actaaacgaa tttcggaaaa 120
 ctgcagccaa cggaaaaaag gtcagtacac agcgattgat tggccggaaa attaactaaa 180
 ttaaagtaaa aaccctcgag tgccaaagtg gtgttgagca gcaaacacct tttaatagtc 240
 ccccatTTga ccttcaccca tggacaccct cgcaaattgg tagcaccaaa gtcgggctag 300
 cagttaaccc ttacccttga tcaccgttaa ttggaccccc ctctcagac tatcatggtc 360
 atggtcagca gggttgtgaa aacgggtcat ttattggagg gtgcgttacc ctttgcatta 420
 tataaggcac gaaactcttc aatgaaaatc taatttcaaa gggattttta cccctgtaag 480
 aaaaaaagta 490

<210> 150

<211> 522

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (3)..(522)

<223> Area matching Drosophila ESTs AA948907 and AA92191

<400> 150

```
cgccgaattg aacgcacgta ggggaccgga cggatatcgc atcttccgat cggaaaaatc 60
gtacagtgca gccaatcgc cgtctacaga aatctattag cgcgctgtg ttggtgccag 120
tgcggtggca aattaaaaca aaaaacatct gcgaatttga atacgcaaat ctcagtctca 180
ctaagagcgc aaaagtcata gagtgcagaa tagtgaattg aagaactttt ggacgcgcta 240
agagtcgctc tccatcccca tctctctctc tctctcttgt gtgtgcagtg ctagtgtgtg 300
cgagtgtgag tgagacgggc aaacaatttg ccgctaaata caaaaagcag ctgagaccag 360
ctgacgcattg tgtatgttcg aaatacaatt aaagttaaca ggctataaat aaattgcaaa 420
tgtttatgta gccgtcaagc agcaacagta gcagcgcaac aacaaaacca cgtggcacag 480
acattttggc cagcatagta agcaaatacc caaccgatt aa 522
```

<210> 151

<211> 590

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (25)..(76)

<223> Area matching Drosophila ESTs AA802379 and
AA246624 (inverted)

<400> 151

```
gtctagttta gagagcatca ttaccttcga ctttaaatta tcaccaattt atattccaac 60
gaaatacgcg tccgttcaag tcgaacagct ttctgttagt cagtgtgacc gtggcggagc 120
gctcttataa cctccgattc gccaaaacaa gccctaaata tgccagcaaa agtcagcaca 180
gcaagagaac tttgataagg agcggaaactt cggtaacgcg ctttcaattg cacatttcca 240
ctagatgagc taacaccttg ttccaactga gccacattaa gcacatcttg cagataatct 300
ctaaattcct ttaaaatcgt tatattatta agttttacta cacattattg ctaagtgatt 360
tagtatatcc gatgttatcc aactagtttc tcatattatg tatgggttcg ctttaaactt 420
gtttaatatg aaattaataa ttttttatca atagacctca aaacctacta ttcaatttga 480
acctaggtac tttttgggaa atctctacca ctgcagcaac gcttttctta tcgccgctaa 540
```

attcagagct taaatctacc agacttttctg cgataggaat gccctataaa

590

<210> 152

<211> 411

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (9)..(100)

<223> Area matching *Drosophila* EST AI404485.

<220>

<221> intron

<222> (101)..(178)

<223> Probable intron in gene represented by EST
AI404485.

<220>

<221> misc_feature

<222> (179)..(411)

<223> Area matching *Drosophila* EST AI104485.

<400> 152

ggcaagacag tttatattaa ttgtttacct gtgcaacaat cttttgttcc gcgaacaaag 60
actatatttg caattgatcc cgccgacata atcataaaag ggtaagcaat acgctgcaag 120
gccactggca ttgcgtcctc cgcttactaa cgtttcctac taactttctt cgctgcagct 180
ggagtcgggc cctagacatt tcttaatggg gaaaacagca tagccttcta catatgccac 240
cggctctcca tgagcattat caagatgagc ttgcacacac gggcgtagt gttctccacc 300
ttctttggca gctgcctggc tattggcctc ttgctcgtca gcatgaccac taatcactgg 360
gtgcgggcca ctccacgccg caagaactcg tcggacgccca aggggtgaatt c 411

<210> 153

<211> 561

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (60)..(449)

<223> Area matching Drosophila EST AI108647.

<400> 153

```
ctgcgcgtgc taagctccga gttgctaggt ccagaaccat actttttaga tactgtatcc 60
aaactccggg caatccgctg ccgctttata aacaaacagt taaacaaacc gaccgctcga 120
acgtcgccgt gtgtgtgtgt gcctgtgtgc ttttcgccct cattgtgctc tcgtgcaaatt 180
gaaaatttca ttgagcagaa agtcgcagca gcagaagcag cagcagcagc agtagaaaag 240
tggaatatcc taaagcggcg ccagcctcag caaaaaaaga aaataaatta aaaatctcgg 300
ctagtgaatt ttcagtcag aactagacgc cgcaattaag ccaaatacag accgaaccac 360
gacgagtcaa tcgctggaaa actgccaaaa cagccacgcc aatcgattgc aggcgttccg 420
caaattgaag ttcaaccggc gcagcttgta ccgctaaatc gatcgacaaa gatgcagtgc 480
ggtctggagc agatgaacga ctgtgagcgg tcggcgaacc ggacgaacct acgggtcaac 540
tttaacgaaa agggggcgga a 561
```

<210> 154

<211> 49

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(49)

<223> Area matching Drosophila EST AA951902(inverted).

This EST matches other EST including AA949796.

<400> 154

```
gtccgtcaca caacatggac gcactctcgc cacacacacg ggcgaattc 49
```

<210> 155

<211> 489

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(489)

<223> Area matching *Drosophila* gene RanGAP, accession
number AF143860.

<400> 155

```
gtctgaagcg tcatccagag ttctggaagg cgctgtggaa gaacatgttt actggtcgtc 60
tcatatcgga gattccggag gcactcaagc acctgggagc cgcgctaatt gtgcggggcg 120
ccaaactgac agtcctggat ctcagcgaca atgccttagg accgaatggc atgcgaggct 180
tagaggagtt actgcgatcc ccggtctgct actcgtgca ggagctgctg ctgtgcaatt 240
gtggccttgg tcccgagggc ggtagtatgc tgtcccgggc tctgatcgat ctgcatgcca 300
atgccaacaa ggcgggcttc ccgctccagc tgcgtgtgtt cataggttcg cgcaatcgtc 360
tcgaggatgc cggtgctacg gaaatggcaa ccgcattcca aaccctcaag acttcgagga 420
agattgttct ggagcaaaac ttcatttaca tcgaaggcgt cagggccttg ccgaatcttc 480
aagcataat                                     489
```

<210> 156

<211> 450

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(278)

<223> Area matching *Drosophila* EST AA940865. This EST
has sequence similarity to *Xenopus* chromosomal
assembly protein, U1367.

<400> 156

```
attggaccca atggcagtgg caagagcaac gttatcgatt ccatgatgtt tgtgtttggc 60
tgccgcgcca atcgcatccg ttgcaagcgt gtctccacct tgatccactc ctcgtctagt 120
```

tatcccaatt tacgcagctg ctcggtcgcc gtccacttca agcagatcgt agacaagggc 180
gacggcacat gcgaggacgt gcccgactcc agcattgtta tcgaacgcac tgccatgtcg 240
gacaactctt cctactacca gatcaacgac aaacggggcgc agctcaaggg atgtggctaa 300
gctgcttaag aagcatcatg gtgggatctg gagcacaatc gcttcctcat tctgcagggc 360
cgaagtggga gtccattgcc atgatgaagc caaaagggca gactgaaatg aaatgggaat 420
gttgggaatac tggaggatat tgtcggaaca 450

<210> 157

<211> 349

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (117)..(263)

<223> Area matching *Drosophila* ESTs AA803314 and
AA941391. These ESTs have sequence similarity to
Human B-cell receptor associated protein.

<400> 157

cgtgagagtt tcccaatttt gtacgtcgaa aaatcatacg tttattatca caaaatctat 60
agagagtgtc ctgcgtttac cgacatttaa tatatTTTTT aaattcctcg tcgcagaaga 120
caaacaagat ggcacagagc aaattgaacg atcttgccgg caagctgggc aaaggtggtc 180
cgccgggatt gggaatcgga ctgaaggtcc tggcccgccg tgggagcagc cgcctatgga 240
gtcagtcagt ccctgtacac cggttaaggat aaagccgata ggataaagcc acccgatttg 300
agggctaaaa gcataaacac gggcaatagc ggcatgtgca catacctca 349

<210> 158

<211> 511

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (209)..(405)

<223> Area matching Drosophila EST AA201448. This EST
forms a 856bp contig with ESTs AA438721 and
AA247046.

<400> 158

```
ctttgggctc tcacgccttt tctgctctct cctctctcga tttaaaactt gtaggacttg 60
tttcttgagc ttttttgca aaacataaaa accggtaa at tttttttcga aactgcaggc 120
agagaaaaga gagcgagctg tgttggtgtt cctgtattgg cattttttac cttaaccata 180
tttttcacac actttgcttt ccttacagtt ttctaaacac acacacatac agaaacgaga 240
agagccaacg aactcgcagc gacgccaag aatgaaagag agcaaggcaa catgaaaatt 300
acagcaacaa caactggctt gccgaagaag ttgtaaaaga cgcaagagca gaagaagaag 360
cagccacaac agtatttttt attagcgggg tgtttttgtt gtcatgtatg tatgcacact 420
tttttcgctc cacactctaa tataagttga tcgttggtgt gtgctggtgt aattattgtg 480
atgcttgat atattgctgg tgtgctatcg t 511
```

<210> 159

<211> 492

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (37)..(243)

<223> Area matching Drosophila ESTs AA696343 and
AA696180.

<400> 159

```
ggaccgcctt tcataacgta gtaagttttc gttgcgaacg gacgtagccc aaccaacttg 60
gccttaaccc ttgcgctccc tccgatttat tccgcggcaa acacattcca gtggacagtg 120
gtgcagttca gcccaagacc aacctacatt ttagctccct gcaaaccctg ttcttcatca 180
aataactatg gcgtccaacc gtgcagcgaa gtctggtttt gccgcccagg ccagcgcaa 240
agtaagtacc aatagcaac aacaaccgca cccccaccc aaaaaccgaa gagcgccaaa 300
caaaacaaca caataaaca attgcccaaa aaaaatcaac ttttgacgg gtgtgtgctg 360
gagtttagag ctgcattgac tttatttggc gctgcgttgt caagatttta tcttcgcgcg 420
ccaaatgcca aaaattagcc aaaaatggtc ttgaaattgc cagcgtctaa caaggaatga 480
```

<210> 160

<211> 580

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (261)..(580)

<223> Area matching *Drosophila* EST AA540783 (inverted)

<400> 160

gtttggcgt ttgcaggcg ccaactacga cgggtggcata gaagttgatc tgggcttgca 60
gttgggtgggc tcgaggacc agttccttaa ccgccttctg ggtactttgg cagatgaagc 120
cgaggaaggc gggattgctg gcggctctgt taataatagc agtcttggct agcggaacgc 180
caggacgctg caacgggcgc agccagtacc agtcgccatc cgatgaccgg agcctcatgg 240
tcttaacgat ctggacaaag atcattgtct cgtgataggg cagaatcagg gccataactt 300
cgctacggtt atactcgtga acctggaatc gtcgcagcaa ccattcgaag gccatgtgtg 360
cggggcggag cagaaggtag ggcgaaagaa ggcgcagaaa ctttgcaatg gccgcgtcca 420
gcatcttggt aatctccggc agctccacgg aacgctccac gtcaatgtgg cctcatcgaa 480
caacgttagc tggaactcct tgaagccgga ttaaagtcgg tcaactcctgc agtcccgtac 540
ccgactcata aatggaccgc catccttggt ggccgctctt 580

<210> 161

<211> 494

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (26)..(267)

<223> Area matching *Drosophila* EST AA695850. This EST
overlaps EST AA698310 and has sequence similarity
to Rabbit FKB4 protein.

<220>

<221> intron

<222> (268)..(335)

<223> Probable intron in gene represented by EST
AA695850.

<220>

<221> misc_feature

<222> (336)..(459)

<223> Area matching Drosophila EST AA695850.

<400> 161

```
atacggtctt tccaacgtgc ttgagcttgg tcaactctgcc atcatcgtgc gaattaaagt 60
tcagcagcca aaaatgccgg aaggggaataa aatcgacttg tccggggacg gtggcgctcct 120
aaaggagatc ctgaaagagg gcacggggcac agagacgccg cacagcggat gtactgtgtc 180
cctgcactat acgggtcgcc tggtcgatgg cacggaattc gattccagcc tcagccgcaa 240
tgagcccttc gaattttcgc tcggcaaagg tgagtgtgtc gccggcaaact tcgcgaaact 300
tctatttaat gtactcctgg ccaccggaca cctgcaggca atgtgatcaa ggccttcgac 360
atggggagtt gccaccatga agctcggcga gcgcttgctt ctaacatgtg ctccaaactt 420
acgcttacgg agctgccggc agcccggcag ccattccgcg gatgctactt gattttgagg 480
taggaatgaa attt
```

494

<210> 162

<211> 224

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(224)

<223> Area matching Drosophila EST AA441346. This EST
forms a 1677bp contig with ESTs AA390646 and
AA696470.

<400> 162

gctccagcga taacggtact ccaatgtgct ctctcgacg cacacagaag catccccgac 60
acgtacacca ccaccactgc caaaaagcaa atcctgccca acagccgcac ctataaaaagt 120
gggcgtgggt agaccaagt tactgtaaca aatttgcaaa aagtgatgca tgctaattgt 180
ttaaacaat cccagcttct ctaatcaaat acctttgcga attc 224

<210> 163

<211> 541

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(514)

<223> Area matching *Drosophila* EST AI0643375.

<400> 163

gcacagccaa aactgaagat tacatacaat ttacaatggc cgacgagagc atcacgcgaa 60
tgaacctggc ggccatcaag aagatcgacc cgtacgccaa ggagatcgtg gattcgctct 120
cgcacgtcgc cttctacacg ttcaactcgt cgcagaacga gtgggaaaag accgatgtgg 180
agggagcctt cttcatatac caccgcaacg cggagccctt tcacagcatc ttcatcaaca 240
accgactgaa caccacgtcc ttcgtggagc ccatcaccgg cagcctggag ctgcagtcgc 300
agccgccgtt cctgctctac cgcaacgagc gctcgcgcac ccgcggcttc tggttctaca 360
acagcgaagg agtgcgaccg catcagcggc ttggtgaacg ggctgctcaa gtcccaagga 420
tcagggaacg aatggccagg cccacgtcac gtcttccgcg cccagcagca aagcaggaca 480
gcagcagccg gccagcatat tcaacatgct tgaccaaggc cagaaggact acatgcccga 540
g 541

<210> 164

<211> 497

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (181)..(299)

<223> Area matching Drosophila EST AA540197. This EST
forms a 723bp contig with ESTs AA695503 and
AA941503.

<400> 164

```
atcgagttgg cataaaagaa tctggtcttc gtgtcgtgtt attcattcct taattgcgcc 60
ttgtttaatt tgtgggtgac ggaaatcgga gctcggcgac atcgccagtt gtgcaatact 120
gactccagcg gtatctgtta atccccaacc acttcgcaaa cgtattttct ttgccttgca 180
gatttgctga ctttgtcgtt cgagtactca gcgtttaacg accacaatga atcggcaggg 240
gaaattccta atcttgtgcc tctttgtggg cctcttctcc gcgaatttgt gcgaagaagg 300
tgagtctttg atcaaattac accgaattaa aatcgaattg aagacacgcc gaacactcat 360
ttctcaatta tgactcggga cacacacaca cacacgcttg catgtgcatg cgtaccgtgt 420
gcgcaaacc ctcgcgtgtg tgccgcctg cgggcatgtg ggtgtgtgtg tgcataaatg 480
tgcggtgtgtg tggatgt
```

497

<210> 165

<211> 523

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (167)..(212)

<223> Area matching Drosophila ESTs AA979442 and
AA392418 (inverted).

<400> 165

```
gcccgagaa acaccacga atgactacca aatcgggatt attgggtgat taggcttaat 60
tggtggctat ctactgatg aggcgatggc cgtcagttgg gcaaggtagt aatgcaacac 120
ttttcacaca tctttggtgt tttctcgcgt tttttgttt aattacctgc tcgaaaatga 180
aatgtatcgt attttataaa tatcgataga tatcagtggc ggtgtgcccg ttgatgggta 240
gcacaaaaac accatccggc taagagatgg cattttgcgg tataaaaata ccagataaat 300
gctctagtgc ctagttttaa aaacattgcg taaaatctta aatattatta ataagtaata 360
aattagtccc tgaaatatat gatcattcac aattacaata ataacaacaa aagggatata 420
```


taaaagggca ctgtaagaaa agtcgatgag taaagtctga aacgccactt atcgatatca 480
ccatgactat gtggcagcac ttaattcaaa aaaagggcgg cct 523

<210> 166

<211> 414

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (89)..(159)

<223> Area matching *Drosophila* ESTs AA536378 and
AA392418.

<400> 166

tgtggaaaca tttatcgata attttacaaa ttagagggat ataaaacaat ttggtatatt 60
ttcatttcat acctggaggt atattgcgtt gcacaaaagc ggtcacacta attgatagac 120
gcaaagtttt aagtaaaatt tgggttttagt taggcaaagg taattaaaaa tgataaagga 180
gcgaaaaatg taacaaaaaa tgccgatatg ttgtattcta cgctctttta tcgatttttt 240
aaaatgcatt tctcattgtc cattcgatga aacacgtaag cggttgtaag caaactgaca 300
agatggcggc cacatctgct taattgaaaa tcgaaattaa atacgatata actagcctgc 360
cgacccaaat tgcaaacggg ttgggagctg gtgtaatcat aataatttgg aagc 414

<210> 167

<211> 570

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(570)

<223> Area matching *Drosophila* genomic sequence

AC004345. ESTs AI515537 and AI062109 match this
genomic sequence 50bp 3' to NPS0219.

<400> 167

gtcgagtggt tgctcaaaag aaccgaaagg acgaagggtc cttcaaacag gataaacaag 60
ccaggcaaac acgattgtca ttggcgacag gctttaaaat ctatagcgac aagcttcgct 120
ttgctgatcc tatattcatg gcaaattcat ttaatttaat ctccttaaag aggaatgact 180
taacatagtt aattgaaaag taaaatgggt agagtataac ttacacttaa ttatgtgtac 240
tttcacagag ttaataaaaag tactaatttc gaaatatattg aatatttggt tattcagact 300
gatcagtttt aaaattttta aatcgaaata ccagctagtt gtaaatttcc aatcataatt 360
gggagatctt aaatgcagat ctgcaatagc agataaccat cgtcacttag acttcctata 420
aacaatacct ttgcaaggat tataataata agagaggcat tcggtgagac ttcaaacgag 480
agataacgct cttgacagtt gctcgactgc tcggttgag cccgaatcga agccgatgcc 540
ccggcttaag tcgatggcgg ttcgagaact 570

<210> 168

<211> 601

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(184)

<223> Area matching *Drosophila* EST AA390646. This EST
forms a 1705bp contig with ESTs AA440523 and
AA696470.

<400> 168

cacataccta agtagacgca cgagagctct cgtatcgca aaagcgtgtg ctttgttgtt 60
gctcttccac tccctcgctc taagaggcgc tcccggtgtg ttttgttgt tattgccgct 120
gagcaaatgg cagaccctct aagcgggcgc cgctggtgat aacatgtcgt aatggccaga 180
gaggtaagtg caaacgtgct aaaagcaaag caaagccggc aactacggct taaccgtttt 240
agttttcccg atcaccacgg taccgcaagt tactttgcca aaatcagctg ttctcacttc 300
atcaccatcc cccatcattc acatctgcaa ccaacggtgt tagcctctcc caacattaaa 360
acagttaacc ctatgtcata tttttccaaa aaagttaaac ccaacactac aacttaataa 420
taaaaatgct gcgtgtaaca aatagttatt ctctgtagga atgaattttt taattaagca 480
gtagaaacaa aataatcaaa aataatacta ggtaatagat tttttttaat aacatgcaat 540
ttgaccaagt aaaatttata atatattcta atatttcttt gacttggtt tgtagaaatt 600

<210> 169

<211> 467

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(104)

<223> Area matching *Drosophila* ESTs AI064169 and
AA816652.

<220>

<221> intron

<222> (105)..(309)

<223> Probable intron in gene represented by EST
AI064169.

<220>

<221> misc_feature

<222> (310)..(467)

<223> Area matching *Drosophila* EST AI064169.

<400> 169

```
gttaggacga aatgagccga aagaacggaa accaggacac ctttcccaag acggagaaga 60
tgcagcgcta ctacgcggag cgcgagacca caggaccoga gttcgggtgag ttttcctcgg 120
ttcgcaatcg gtacacaatg gattcagaaa tggaatctga gtaaccgggg ctgcgagaat 180
caacccccaa agccaaagga tgtgtcttct gcgcttaggg gttgctgttt ctgcggcgaa 240
gaaacgtaga aacggaatta gaaaaccgaa acagatttta acgatttttc ccacaaatcc 300
ttgctcccag acgatcgctt gataaagctt gtgcgcgcca atccggccat ctatgatgtc 360
agccatccgc actatcgccg taatccggtg cgggtggaca tatgggatcg cattgccaac 420
gaactgggcg cctcctgtga gtatattgca tttttatcca ctgcgta 467
```

<210> 170

<211> 288

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(288)

<223> Area matching *Drosophila* EST AA439345. This EST
forms a802bp contig with ESTs AA949877 and
AA439626.

<400> 170

```
ttgcgaaccg aacagaacgt ggttgaaaat aatcgtagtt tttatactgt tataacggct 60
caccatgggtg cggcccaaca acaaccagct gccggagaac cttccgcagt tgcagaacct 120
catcaagcgg gatccggagt cgtatagcga tgagttccac atccagtacc aacactttct 180
cagcttgctg gaagtttttg cgctgaatcc cagcgaagaa aacaaatccc tggatgacat 240
cgtcatgttt gtcgccaggg tggctcagtg ctatccggcc gtctgcga                288
```

<210> 171

<211> 350

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(350)

<223> Area matching *Drosophila* genomic sequence
AC005452. EST AA979503 matches this genomic
sequence 181bp 3' to NPS0227.

<400> 171

```
ggcttgctgg tcagctgcc atggcgatac tatcgtcgga agtgcttggtg cagcactgga 60
cgtttgctga aacttgtttg aaatatttcc ggtcctttac gcatttaatt ctcttccgta 120
atctatattt ataatttaaa tgttcctttt tgttctttcc cttaccattt tccctcaaatt 180
ttgtttacaa tatgtttttt ggggagccgt gcagcactgc tttctagaga tggtagtggc 240
```

gggaacgtat tggaactggt tcacctaata ttataccttc aaaatttaca gggctagaaa 300
tccagtagct aactattttac ataaccaat aatattatTT taaagaattc 350

<210> 172

<211> 446

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(93)

<223> Area matching *Drosophila* EST AI293141.

<220>

<221> intron

<222> (94)..(169)

<223> Probable intron in gene represented by EST
AI293141.

<220>

<221> misc_feature

<222> (170)..(446)

<223> Area matching *Drosophila* EST AI293141.

<400> 172

cgccgtacag cgcacggatt gcagttgggc caacaacaag gcgcgagcat aaacagcgat 60
accaacatgg cgggcttcgt cgcggtgcac acgggtacgt atcttggcca tggcggttcc 120
gatccgccgg gcagacagcc agatgattga tgaccgctac ttgctctcag gggctgggaa 180
ctgcatcgac gaaacgaagt accagcgggt gattaaggag gcctgcctgc gcgccacgga 240
gatccttcgc aacggcggat ccgccgtcga tgctgcgag gcggccattg tgcggttgga 300
gaactgcggc tacacaaacg ccggctatgg ctccaatctc tgcattggac gctctgtgca 360
gtgcgatgcg gctataatgg gatggctcaa cgcttaactt tggcgctga cgaacgttag 420
tcggtgaaga ccccatagac ttggcg 446

<210> 173

<211> 478

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (12)..(244)

<223> Area matching *Drosophila* ESTs AI107445 and
AA390813.

<400> 173

gtgcagacag agagagacgc gaatgtgaat taacaaacaa acaaaaatat tttgcgaaaa 60
agacaaacac aaaaagtgaag agccaataaa gtgtattaca taaacaaacg gagctccgat 120
atctaaataa atattatgga aatcgcacca ctgatcaata acgccgtcgc tgcgtcaca 180
gcctctgcct ctgccgccgt ctctgcctct gctagcgtcg gcagtagcag caaggatgat 240
aacggtaggc gggctctctag atgataagcg gtacacttcc agtgggttca taataaacta 300
taaaaataat aaaatatatg taaatacaaa gcataaagtg tagatacgtg ctcgaaagag 360
tcacactttc tcgttaaaga acttcacgtt ctatccatat tatatgatta ttatgtttca 420
aaatccttta ttaatcaaaa agccgaatta gacaatcagg aatatcttcc acccagca 478

<210> 174

<211> 528

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (12)..(478)

<223> Area matching *Drosophila* EST AA390942.

<400> 174

gttgcgacca gcactcgatg tagacgtacg cacggatact cgatctccca gttgtatctg 60
cgttaggggcc tcgcatagtt tttcgcgtaa tattttcggc ttcgcaattt tgttggatac 120
ttgatgaaat aacgtcagtc ggattgtata taacccaaag cagcggcaaa tcaatgtcgt 180
cagttgtata aataccacaa ataaacaaac acattcacia agagtttttg tgctttcatt 240

gcatagtgac caagtgtggt agtcacccat acagttttatt tatgtgctaa aatgcaaatt 300
 caaaatcaca agaccaaaca agttgctaaa atgtggcaga ggaagccaat aagtgcgaat 360
 aaaaataaat aaatacgcg agcgcagcaa aaccaaggcg cacaaaaagg attacaccag 420
 ataaataaca ctgaagccgg cgtaaaaata gcaaaaacgc aaaaacacat ttcattgccca 480
 acgagcgcag aaagcagcag caacaagaac taagccaaca gggccaag 528

<210> 175

<211> 539

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (11)..(103)

<223> Area matching *Drosophila* EST AA802688. This EST
 has sequence similarity to 10Kda HSP protein
 genes.

<220>

<221> intron

<222> (104)..(295)

<223> Probable intron in gene represented by EST
 AA802688.

<220>

<221> misc_feature

<222> (296)..(389)

<223> Area matching *Drosophila* EST AA802688.

<400> 175

tcccgcatct agcgagaata gttacgccgg cacgtgtagt tgagtaaaaa gttcactcat 60
 taacttttat caaccgctcc agtttgcatt taagaattaa aatggtaagt taaaagtgca 120
 ttgccccata tgaggtttag aagacagttt gaaatcgaag gatgatatcg gtttttcgag 180
 aaggttccac ggctttcggt ccacatccca ttcgccgggc tgttgtgtaa tcaatgagag 240
 aaacatgaaa cattgaaaca tgggttaatt gttgggtctt ttttaatgat cctcaggccg 300

ccgctatcaa gaagatcatc cccatgctgg accgcatcct aatccagcgt gccgaggcgc 360
tgaccaagac gaaaggaggc attgttttgc cggagaaagc ggtgggcaaa gtacttgagg 420
gcaccgttct ggccgtagcc ctggcaccgc taatgcccg gagtatttcg ctttatcaat 480
gcagagatgg tcatttaac actgaacatc ccattctccg cagtccatgg caaccacat 539

<210> 176

<211> 541

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(414)

<223> Area matching *Drosophila* EST AA392415.

<400> 176

cgtggtccga aagcaacgaa gcaaatacgg caagaggcga gcgaaaaagt gaaattgaaa 60
taattccaaa tcaaaaatca aattcgaaat cgaaaatcgc aaatcacaaa gttggaagtt 120
gagtgaagcga acgcgtgtgt ttgtgtttgt gcgtaagtgt ccctcagtgt gtgcagtgcg 180
acggtatcgt aagacgaaaa gtaacggtaa ccgagcaatt ggggtgtaag ctgtcagaat 240
ctgtgcgcag agaaaaccga aagttttggc ttgttacctt gccgtagtaa tcaaaaatca 300
aaaccgaata ccggaattcac cgatcgccat cctggccgc ccttcgactt tagtttaagg 360
cgctctgccg gcggttcgcc ggaacggtaa actccccca caccctgctg ccgctcgctg 420
ttagcatacc gataccgata gaccaccgcc gatagcgata ctttcgaaat tcagcaatcc 480
gtgccccatt tactaggatt ctgttcggtt ttaaccctac gaagaaggag caccgcggc 540
g 541

<210> 177

<211> 66

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(22)

<223> Area matching Drosophila EST AA695619. This EST
has sequence similarity to human cysteine rich
protein.

<400> 177

gccacgtgca ttcttccact tcttttttttc gctcaaaatg gacggtcgcg ttttctgctt 60
gaattc 66

<210> 178

<211> 542

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (399)..(542)

<223> Area matching Drosophila EST AA142132.

<400> 178

ctttgtatgt atcgctgac gtatgcgcag tgtggccgaa cagggctagt gagaaatacc 60
agccggcgagg tagatatact aaaagtgtat tatttttagt taaaacagtg cattgtcaca 120
taaattttta tagcctcttt attaaactat atgagcgcttg attgccacta tgaatatcta 180
agcaatatat tacattacaa tatggcaatt atattggcat ttggtactgt cgaataaaat 240
accaaaccctt gcagtgctgc ccatcagcta taccaaaaaa aaacttggca gcattgcgca 300
tcgtgttcat ttgaaatttc gaaacacaaa acattataaa taaattcaaa cgaaattagc 360
tcgccatgga aatgcgtacg ataaaaacag ctagacttta ttaatcaata acatttatta 420
tttacagctg aaggagtttc gattgctctt gcagaccgcg cttgaatgac aaaatgcatt 480
agttggtttc gaaatattaa tgattggcta acaattatga tccttattat ttatacccca 540
tt 542

<210> 179

<211> 519

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (366)..(519)

<223> Area matching Drosophila EST AA536537.

<400> 179

```
ctccagccac actaacagct gatagggctg tcatcaccgc ccaattagtg atgagcgtct 60
ttttttaaga aggtgacgca aaaacggaaa aattactaat taaaattaaa tgaaagaata 120
atattgtctt aaaaatatgt gctttttaag gatttaatta tcaactgttg ataaaaaggg 180
ctcaactttt taataagtat tatgaaatta cattttgggc caagaacgtt acctttaaaa 240
ttaaacaata tgattcaata aatttgtttc actactattg gtgttggtca actatcgaag 300
gaacctcaac tatcgattaa tgtgaccgct caccactgac caccactagc tctgcagtac 360
aagcaacatt tggcatctct actgggtatc attttcttga tccgttaaag tgatggattt 420
gagtgataat agcccagtgaggaggatcaa tacttttggt tacaagcatg ataagctatt 480
cggcgaaagg ttcccctggt caaggaaatc cgcaggatg 519
```

<210> 180

<211> 480

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (26)..(303)

<223> Area matching Drosophila EST AA264253. This EST
has sequence similarity to SNF7 genes.

<400> 180

```
ataggggacg gcaatcggta tcgggtgacg catacgaaca acagctccca gacaaccaag 60
aaacgcaata gcagaaaaaa cttacttggt cgctaaattc gggtgaaaaa acagatcagc 120
caggatgagt ttcttcggga agatgttcgg cggcaagaag gaagtggccc ccaccaccgg 180
cgaggcgata cagaagctgc gcgagacgga gaacatgctt atcaaaaagc aggagttcct 240
ggaggccaag atcgaggacg aactgaatat agcccgcaag aatgcgtcta aaaacaaaag 300
aggtatgaga ggagtgcgcc gaggtccttg gcttcctagt tggtcactca aatgggcca 360
ggggaaatga ctcatgctt tggttttggt gcggccgcga agcctgcttc cagttaatca 420
```

agtattccca tactggccag caaatagaaa actcaataaa caatatgtat ctcttttggc 480

<210> 181

<211> 593

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (186)..(593)

<223> Area matching *Drosophila* ESTs AA441247 and
AA820771.

<400> 181

cagtggcctt tattgtttat atatatcttg ttgcaatac atgaacaata tatgagtcac 60
tattaaatta aaaaaattta tgggcaagcc agagcttatt taaagaccat aacaattcgc 120
tcgatctttt aaaataccaa attgacagtc cgaatataaa cggtcactta attcacttgt 180
ttacaaaata tttaccgcat attttcagag aaatttagtt ttaattacaa atttgaaaat 240
ccacttagcg tggagcctta aaactatgca acgcggtaaa atttccttcg ggaaaatcaa 300
attgaatgta aacgtgccac ccgcggagcc aaaatccaac gaaaccgagg cggaagatgc 360
aaaggagtcc actgaagcca gcggaaatgg cggaggattc aagaaaatgg acaaggagca 420
gatgattcgg cagatcgagg acgtggcccg aagatctgga gagccagcac ctcaggaagt 480
gatgggcatc agtggctttg gtcgcaaggc ggccaaggtg ttcgacatca cgagcagata 540
gaaaaggcga agagtaccgc cccggaatgg ccaaaaaagg gaggagtcca gcc 593

<210> 182

<211> 446

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (318)..(431)

<223> Area matching *Drosophila* EST AA202196. This EST
forms a 1942bp contig with AI108811, AA950029,

AA202752, AA440491 and AA697007.

<400> 182

```
atttgaacca tcccttttca ctgttctcgg tagaggggat gtgaaaaaac cagcgactac 60
atcaacaaaa gcgtgtgtgt gaatataaca atctcgttgt tccctagttt agttgctaag 120
aagcatttta ataattgtga aatcccagta ccgaggacga caacaaatgt agattttttc 180
aaagcacaaa caactgcagc acgacgttcg tcgcccttcg ggagcggttg tattggtggt 240
ccgtgctggt gtgtttgtgc taccaccttg ttcgatttta atgtgttggt tctgtttttc 300
acatcaaagc tccgtatttt cgtgcggaaa gtgtaaatgg ccgtgtttta aatattattt 360
cggaatggtg tctccgctat ataatcaagc tgtttgcaac gttagcgttg acgcccacat 420
ttgagcccac ttgtgtgccc gaattc 446
```

<210> 183

<211> 553

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (83)..(319)

<223> Area matching *Drosophila* ESTs AI064123 and
AA263284 (inverted).

<400> 183

```
gccccaaattg tagcgccctt gccactgcaa tttacccaat gttttatatt aaactgcggc 60
gcagtttgga actcggaatc ttacttttca caacgggcag gaagcggcac aatttttttg 120
caattttgcg aaccctgct ttcgatgacc gcttagcgcg cgtctccttc gaatcactgc 180
actatggatg ggattgatcc tgtccagcta tttacacatg ttcggttaca agagtctttt 240
tcggtgctta tgttgtaaaa aataagcaaa aaccaaggag cattttatgg tggagtgggc 300
accgccatta atccacgcat gaagcgtgc cagaggtttt ttgggaaagt gtgggccaga 360
ctcttcgcag aattagtaca tgattgcatt ttcagctgat taccttaacg tgttggttgg 420
gtgctagcga ggagagcgga agggggttgt atcacgaaat ccggatatat aatcggaatg 480
aaatcgggat ataaataact tattaaactg ggattataat ttacttaaga acacttttga 540
gatcatgggt ggt 553
```

<210> 184

<211> 89

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(89)

<223> Area matching *Drosophila* EST AA441173.

<400> 184

tgccggctga aataaattcg attgtgtgcg cgcgcgtttg tttgtgtgtc ggcattgtgcg 60
tgtgagtga cagacaacaa aaggaattc 89

<210> 185

<211> 414

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (65)..(414)

<223> Area matching *Drosophila* ESTs AA440852 and
AA541034.

<400> 185

tgacagacca atttcagacg tatgtacctt catacatatt ctatacgtat gtatatatttc 60
gtaccttctt tcgtcttaaa tcagcggatc tctgttttgg tttctggttt tctcaatttc 120
ttgcacacca aaatcaccga tatttgtgtt atttgttaaa ctgttaaaca ctttagcata 180
gacactttgc aatgctaatt attaaagcgg ttacaataaa ttgtaattga atttgattat 240
tttagcggga tttgtgttag ctggctctat tccattcatt gaacaaaaat cgcgtctggc 300
tttgatttac ccgttgtgct gcgacgaatt tcactttcga ctgcgaacg atttgaattg 360
gatggatttg ggtttgtgga ggggcctatg taattcaatt caaattcccc gggt 414

<210> 186

<211> 131

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (2)..(131)

<223> Area matching Drosophila EST AI062640.

<400> 186

gacgccaccg aaaatcgacc ggccggaatt ttctgcacta gtgtgcaaaa agtttcattg 60
gccaaacgag agggaaaaaa gtaaattgtct tccggaaaat gttatatcaa ctgaagatta 120
tgaatgaatt c 131

<210> 187

<211> 536

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(77)

<223> Area matching Drosophila EST AA695507 (inverted).

This EST has sequence similarity to cytochrome C
genes.

<400> 187

gtcttaagtgt gtgaacacca aaaattcttt cgtaattttt cacacagcta tggatcagtg 60
tgaccgcgggt aaagtaagaa aaaataccac acgctgcaga aaatatgata ttgatacttt 120
caaattgcttg agtagaccaa ataaaaacaa acaaagtgtc ctattgttat tcgtcgtaat 180
aattgggaaa taaactctag cttaaacaat aaagttctta aaataataat aaacatatat 240
ttttgttagc aaccgatata ccacatttaa aaaattaatg tacaacggtc accctacagt 300
gtgcaacaat caaccgactt aagtgttggg aaacaccggc ggaacactgg gtatcgaaac 360
cacaagaggg cgccacttgc gttgccgggc aacaaaaatg taaaaacaaa aaattttatt 420
aaaaaagttt attggaatct gcatgaaaaa tgtcaagcaa ggccggtaat ctgctttgat 480

actcaaaaat gaacgatttc aaatatcgga cactacaaat gatgctcgca atgaag

536

<210> 188

<211> 589

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (89)..(251)

<223> Area matching *Drosophila* ESTs AA736186 and
AA801973. Thses ESTs have sequence similarity to
Thioredoxin genes.

<400> 188

gtctatccat tcgaaattca ccttcaccaa acgcgacata cacatatgca aaaagagagc 60
gtatagcaat gagaagcgtg agcatcggag taaaaaatct ataaaagcaa ctgcgacgtg 120
ctcatttttg taaaaaattt agctgtgctg caaagagctg cccgagtggg aattaagtaa 180
cttttgtaca tttctaccgg ttccgtctcc acatctccca tccaacatgg tgtaccaggt 240
gaaagataag gtgagtcact tcaaccggat ctatggacgc atcacatccg tcatctattg 300
ggtaactcga tagcgctacc ctttgacccc tcagttccag ttacacgttt attttttcgc 360
tccggacttt gaaaatatgg cattggaagc ggcatccaa ttagcctctt actttgaatg 420
attggattcg ctacgctttt tgccatacgc tcgcccgcga atagaaggaa ctcattgttcg 480
gtctagacga cgagaaagcg gagagcaaac gaagaaagtt ccgaatagca gcacagcgaa 540
atggataatg atatcattcc atggaccgca aaacgggtct taacggaac 589

<210> 189

<211> 533

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(417)

<223> Area matching *Drosophila* ESTs AA697603 and

AA801716.

<400> 189

cgctagacca cgtaacgcca cgattttcgc eggatccacc gattcgattc gattcgccgc 60
gatcgtcagt gcctatatat acagttccca acggagccga gcgataaaga taaatgtgca 120
aaaacaaagc gcacttagat aaagatagcg aagttctccc atgtggaagg cacagtgcaa 180
gtgaagtga acgagaacgc agttttgaat aggaaatacg aaagtactca catatataga 240
gaacccgaga cttggagtca gaatgcaaat gtggcgagca taaagtcgca aagcgtgaaa 300
atctacgata tatacgagta tagtcgattc caagtgtcag ccaagtgaaa cccagtgtgc 360
agccgaaacc aaaccgaatg actatgactt ctacggtgct ccaacggccc attcaagcca 420
agccagagaa gaaggccttc ttcaaatcga ccagcttctt gagagccgtt cacgatggcc 480
tggtccaatg agaactgcgc ttctctgcat cgacaacatc ggacttaaca gct 533

<210> 190

<211> 528

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(528)

<223> Area matching *Drosophila* EST AA950741.

<400> 190

ctctagcagt atgctgcgca agtcaaagaa acagccacag acggtggccg agaaggtcag 60
caagctgttg cccatccgaa cagagcgaca gcgcagagga ctcggaacttc gatgtggcca 120
cggggccacg tctggtggac ttcgaggagg aggagtacga cctgccggat gcccggagca 180
ccgacttttag gaagaggaac gtcaagctgc tctcgagca gaggaccgc taaaaaggaa 240
agatcagcag tcgcaaggag ttggatgacg atgaggatga ggatgatgat gaacaagagg 300
tgtcctacga agaaagcgat gaggatgatg agaacttgac agactttaag cagaagttaa 360
atgctggagg agctgaagac tccgaggagg aaacggctgc tggacattcc gaatctggtg 420
aaggaagtga agagattgag agcaatttga cagactttaa aaaaaagttt gaggctggag 480
attttaagta tgatgatgat gaagaggagg atgatgactc tgaggaag 528

<210> 191

<211> 52

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(52)

<223> Area matching *Drosophila* EST AI063204. This EST
forms a 887bp contig with ESTs AA697347 and
AA201878.

<400> 191

cttccaagta cttttcacat attgcaagag cgatttaata tcgtaagaat tc 52

<210> 192

<211> 531

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(44)

<223> Area matching *Drosophila* EST AA441029.

<400> 192

gttcagagcg tgaaaaatac gttatatgct gcaaaagttg tgaaacgaaa cgtatccgag 60
agatacaatc ccattgggag agcgagagcc aagcaaagtg cagtttccag aagcagatac 120
catttaaaca tatttataac ccaaccgaaa ccaaacaat aataaaggct gaaaaattcg 180
aatacaccca aaaaaacaaa tttccaaca actcaacctc gacgacgacg attcgcaaca 240
caaaactattg ttggattaac atttttttcg atcaaggtaa gtcggtttac atatgctgtt 300
ttcatttttt tttttatggc catcattaac actcaaaagc attccgaagg tttaagttga 360
ctcttggett ttatagttgg tatgtagctg tcttgcagcc caaaaaccga caaaagttgc 420
tgtcagtttt ggatgtgact ctggctaatt gactcaagct ggtgttttca taattaagct 480
aaatgaaccg accggtagta caattgaagg ttccgtagat acatatttca a 531

<210> 193

<211> 560

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(157)

<223> Area matching *Drosophila* EST AI114266. This EST forms a 1141bp contig with ESTs AA949325, AA735675 and AA391495, and has sequence similarity to GMP synthase genes.

<400> 193

```
agtgtgtgcg tgaggaagga aaacggggga ccgcaaaca cggatcgca atttcgtctt 60
aagacaaagt cttgcgctgc ttatgcacgg tattccacgg ccttgccgac ggacttcccc 120
gttctggaaa accgcagcca ggctaaaacg agagaagggtg agagtcgcaa tatggcgaaa 180
aagatccccg atcccagcca aatcgccatg cgggtgctgct ccgcccacaa ttccgaaccc 240
cgcccgttga attcagcaaa caaatgtat atttactgat gttttagaac tttgaatatt 300
cctctataaa agttgcacat atttcacacc ccaatgcatt tcattttctct ctcgtccata 360
aaacattcaa aatgtattcg cgcattcgat ctaacaaaca tttattgctt tcgaatattt 420
aaaattttatt tattttctat ttcaagaata tcatatatac atacatacca tatttgcaga 480
acatttggtt acttcccagc taatttggtt agatatccca taattgcata taattcctat 540
tcgcaacgga cttattaataa                                     560
```

<210> 194

<211> 562

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(562)

<223> Area matching *Drosophila* EST AA951648. This EST forms a 1340bp contig with ESTs AA539581, AA802940

and AA263326.

<400> 194

```
atccacgcaa ggaaagctta attcgagcga aaaaaaattt acttagctct taatattttt 60
aaaaacaacg ccctcgctgg gccagtggtc ggttaactag ttagctgtaa gatgacgcgc 120
gtaacgagaa gtgaaatctc cctggacatg gagttctggg tggaggagct gtcgccggca 180
caattggcgt actacgagaa gattactaac gagcacaacg cgggaagggt tgcactaaag 240
aacgcggtta gcgccaacga gggcaaggag ctgtttaacg gccagggtgt ccaggcctac 300
tcctttaagg gcaaagtgtc gcaggagctc aaggaggcta cgctgcccaa aaaaccaccc 360
aagccgacgg actctccctc aacacccgcc gcccaaagcg gtggcacagg gcgggggtcgt 420
ggcccgccca ccacgacaac catccaacat cgctacctg gagtcctccg atgagggaga 480
cgacgatatg ccgctggcca agcgactggc gctgtctgca ggcaaaaaag cagtggccgt 540
ggccaatgca tcttcttggt ca 562
```

<210> 195

<211> 528

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (26)..(137)

<223> Area matching *Drosophila* EST AA391135. This EST
has sequence similarity to human SEC61.

<220>

<221> intron

<222> (138)..(359)

<223> Probable intron in gene represented by EST
AA391135.

<220>

<221> misc_feature

<222> (360)..(422)

<223> Area matching *Drosophila* EST AA391135.

<400> 195

```
gttcattcgg tttttgaaat ttgaggcggt cgctgtgcag tgaaaagtga gactttctac 60
tgttcgcgta gaaagtgata accaagccac ccactcagtg cccagactag caacacaagt 120
ccggcaaaat gggaagtaag taaccgtcat cgccagacat cttccccaaa atcgggggagt 180
gcagcggttt ttgtgtgaag tgccgccctt gcaatgccgc tcgcaccctt gtgcgtcatt 240
gcttacgtat acaaaaaaga ttcggcggtgc gccgctcggt gtgtccgaaa atcgcaatta 300
attaaaaatg gcctgagaaa cgtaactaat tcggttgcct taattcacta tttgcagtca 360
agttcctggg aagttatcaa accgttctgc agtatactgc cggaaatcgc aaaaccggac 420
gcaagggtgtg tataaaaccg taattaagat gtaatcaaag tgtagctagg tatcccaatt 480
gctgctgtac catggaatgg tcgaattttc caacaattgc ggctttct 528
```

<210> 196

<211> 535

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(124)

<223> Area matching *Drosophila* EST AA696531. This EST
has sequence similarity to *C. elegans* pro7 gene,
Z66519.

<400> 196

```
ggccagtagc caagtaaacc gcggcgcggt ataatacatt ttagtaciaa tctcactga 60
aaaccgcgca aaatggccga ggttgaagcc gtgcagataa ttgcagagtc tttgaagcaa 120
caggtaagag gatcacctgg tcgtccagtc atttgtccga cattttggca ctgcactttt 180
ctgcacttgg gatattgccc aactactata tatctcattt gtgaacgggg gccgcggaat 240
ctgtggcgct ggcaagaaca atggagtggc ctcttatctt gaggcacctg tttgttgtgc 300
aaagttcaaa aacacttggc aactgtaagt gtggttgggt ttgttttgcg ggtgagaatg 360
tcccccgatt actccggtta ataaaagacg gagcggattt gataaagacc atgttccaaa 420
ggtttgggac caccgaccaa accaattggc gcttgcagct gcgaatatcg cgggggggca 480
gaataaaatc aataatactt taaccgggat tccgggcaaa tcaactaaga acggc 535
```

<210> 197

<211> 549

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (442)..(549)

<223> Area matching *Drosophila* EST AI124332.

<400> 197

gtagcgcggt tgcacttgta atccgctctc tcacgtactc tctctctccc gctgtctctt 60
tttgccgcag cgaattacat tggcgcgcgc atttttcaaa tgttttttta cggcgaaaat 120
aacgattttc gtcgctgctt gttttgtgtg ctgaaaatat acattttatg actatgtaca 180
cacgcacagg aagttgagag gggatttgga tgcccttgat caaggagatg tgtggggttg 240
agttgggcgc gtaggaccat ttcgctccgt aattctccct aatatccttt agtttgtttc 300
tcagattaat atcaaaaatg cataaataat agtgacgggc cccttatttc tgttcaataa 360
acttgcttgt aatacagtaa atcatcagcg gaacaaaaac caaaggaact ctactaactt 420
ctctcttttt tcgcttcag gccaaatccg cagaatcaaa gaaggccaag aaggccgcgg 480
ccgccgatgg agattccgat gaggaaaagc tctggaggaa atcatcgagg gcgacagtga 540
aatcgaagc 549

<210> 198

<211> 667

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (52)..(382)

<223> Area matching *Drosophila* EST AA949873.

<400> 198

gccggcagaa aaggaagaag aagaagctca taccattgcc gattgctgtc gcgttgcgct 60
ttcttcgttt ttttcggctg ccgaaactta tattttgtcg ttgtaatatt ttgcataaat 120

atataaatta aaacgcgtga cggaacaaca aacaaataac gaagacagca aaataaaagg 180
 gcgaaaaatc gaaacgaaaa cgagtcgaat tactttcaag tgcaaatagt gtgcgtgggc 240
 gtgagattgt gtgtgtgtgt tgtgtttgtg cgactgtgag tgcgtgtgtt tgtgtgcaaa 300
 aaaaaacaga acgtgcaaca agaagcaaga agaagagcca tcagcagctg acaaaccagc 360
 aataaaacga aattttcaata agtaagcaac atttaggcaa agctaaaatc caaaagcaaa 420
 tcgaacaaga ggaaaaacta cttttggaag ccccgcaaag cagacgtaac aatgggcaaa 480
 agcaacaaat ttgcggctct cagctaattg aaagcgaatg gtggtggttt agagcaatgc 540
 actcgataaa aaatactaaa gcaatggcat aaaaatacaa attagaacgg gcagcacagc 600
 agacgaaaac catattccac tgggaaaacg aaaagtcaaa tgagagaaaag agagagagac 660
 cataatt 667

<210> 199

<211> 498

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(498))

<223> Area matching *Drosophila* genomic sequence AC006562

(1848-2353). This sequence also matches EST

AI133902 which has sequence similarity to

phosphate transporter genes.

<400> 199

gtttactcta aactcgtaac gatcccaaaa attcgacatt cggagtgcta agtgctcgga 60
 tttttgaacc aaaacataat tgtgaaaatt gagaaacttg cttagtgtca tttttggatt 120
 tacacattcg gatttgtact gaacacacat ttctggcgat taaaaggtaa tggttttaac 180
 ttactgacc tatctatcca tctattctat atctatatgt taataacggc gtgcaacttc 240
 cgttcaatat cgggccctcc tttctatttg ccacttttct atgaacacca cttgcagttc 300
 aatggatttc cactagtaca agtattactt aattttcttg cttaatccga tttgcgtgca 360
 ttgaactttt catctttggg tatttttccc tgttgatgtt gtagtcgctg gtattggttt 420
 ttatctttcg tttttttttt gtgttcgact ttattttgca ccaacttctt gtggttgaat 480
 ggtttttttt tttggttc 498

<210> 200

<211> 550

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(550)

<223> Area matching *Drosophila* Genomic sequence

AC005129. EST AI403609 matches 420bp 3' to
NPS0269.

<400> 200

```
gtctgcagtt cgcgggcgctg catttttccg ggatgttttc ttttggggag gaagtataca 60
atctgtatat ctgatatcg attaagcata taagttatcg gatgcagtag ctgccaggg 120
gtgacatacg ttagtcaaca tatcgataac attagtagca ctttaccatt attaacaatga 180
ggggattttt ttaaattaaa ataattttat ctttgaaata atttatgtac ctaagtatta 240
tttttttttg gaaataaaat atacaaaact ttgtcgccga ttttttcttc actatacaat 300
gtttacatat attagatatc aacctatttg tcttgataaa aatctatacc ccaccaaact 360
aaagatctat ttacaaaaca atttactcct cgtcacaaa gagtcctccc agttccaaat 420
cttctccggc agttccggtc aactgggtgt gctctgaata ccgtaagaat tttccgctgc 480
ttttcgaact ccagcctgct catccgactc ggcggcgatg tgcccggcgt ctgggcccgtg 540
tgaaatgggt                                     550
```

<210> 201

<211> 527

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (299)..(375)

<223> Area matching *Drosophila* EST AA391470.

<400> 201

ggcaagggaa ttgttaattt tagtacattg cttagcactt catttaaacg cgcaaattgg 60
 tgacacaaat atcgatttat taaggtttga actatttaat ttgtcgcgcc tttcagcttg 120
 caaatagaag tatttacttt agacaatcgg atgacgcttt tgatttcgca tttgtttgcg 180
 actgtgtgtg tgcgacgagc cttctaattc cgacaaaaag aagaagagca ccattcggtg 240
 gcctaatttg tttcacttct ccggaatcaa gcttttccga tgcctgcttc tattaacctt 300
 tatttaatat gactcgccgc gttcgacgat atttttgcag tagttatttt ctttttcgtg 360
 cttgtgggag tgcacctctt ttatgccgcg gtttgaagaa gaagcacaac gtagtaagtg 420
 tttggaatgg actgcggaat ttaagggatg gggaatggcg taactcttgc aatcgatagc 480
 tcgataggtc cccttttcgc gtttcgcaac acttgggccc ggatttt 527

<210> 202

<211> 77

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(77)

<223> Area matching *Drosophila* EST AI062013. This EST
 matches *Drosophila* gene NURF-38. Accession
 number AF085601.

<400> 202

attcagatag aacggaagcg cacgaaatca cactgagatgg ctctgtacga aaccgttgag 60
 aagggcgcta agaattc 77

<210> 203

<211> 562

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(76)

<223> Area matching *Drosophila* EST AA696584 (inverted).

<400> 203

```
ccttggttat tagtttgcaa atttccaagt aaatacgacg aatttggcga atcagcgaat 60
cactcgcttc ccattgctgcg gcacacactc acacgctacc acccacacga acgcatacat 120
atgtttgtcg ccggcgggtcc gacaacgctg cggcaatgca actctgcctg gccacttggc 180
taattttggc tatttaccag ccaactactt tatagctagc tgcttatatc ttttcttttt 240
gattgttcca gtttaataat aataatataa tacaattata tttagaaatt taaatttttc 300
ataaattggt ttaaataatgc ttacgatttt tattcttatt tatttcttaa aatattaggt 360
gactgggatt ttagcaataa aaacaagcta tataatagca cagcctgcat atgaaagcat 420
ctctgctcgt gttttttgcc ttgactgggt ggcaactccc ttggttttct cggctgacga 480
aaaatttgac ccgaaataaa tcaattaaat tgaaagtgga gtgaaaagca aattccagta 540
aaaagggtgcc aggtgggagg ct 562
```

<210> 204

<211> 416

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(319)

<223> Area matching *Drosophila* EST AA439099. This EST forms a 1132bp contig with ESTs AA9493425 and AA940848. ESTs have sequence similarity to GMP synthase genes.

<400> 204

```
tttcggcttt aattcgcgaa aaaactgcag gaaatccaaa aggaaagtcc ctggaagcgg 60
ccataataac gcagccggtg aaaaccacag ggatttcacg gccagctgtg tcgagcagcc 120
ctggatactc ggaaaagaag ctgcagcagc cgaagaaatt ttgagtgtgt gcgtgaggaa 180
ggaaaacggg ggaccgcaaa caacggatcg cgaatttcgt cttagacaa agtcttgcgc 240
tgcttgtcac ggtattccac ggccttgccg acggacttcc cggttctgga aaaccgcagc 300
caggctaaaa cgagagaagg tgagagtcgc aatatggcga aaaagatccc cgatcccagc 360
caaatcgcca tgcggtgctg ctccgcccac aattccgaac cccgcccgtt gaattc 416
```

<210> 205

<211> 550

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (21)..(377)

<223> Area matching *Drosophila* EST AA695424.

<400> 205

```
gcgcggacgg tcggtttttg taattttgcc ggctaacaca cctttcgaac gacgcgtaac 60
ggtggccggg ccattaaaat cgccacaacc acgggcaatt cgagtgcggc gcgctaatta 120
tgcaaggctg agaactagcc acaaaaattt ggggggcagc aataaaccag ttgatttaaa 180
ctagttttgtg agtgcgtgtg aaaaggccaa ggaatttggc cgaaagtagt agacaatagc 240
taggaggctg cgactgcgga ggattcaagt ccagaagttg tccgaccagt ttccggtgcc 300
cgtgtgctcg tgtgtgtgtg tgtgtgtcgg gattacttgg attacctttt attttatggt 360
ggccggtgcc ttcgaagcgg agcgaatgag ttggagcagc tagtggccgc agagagatca 420
agagtgcgag agccagcgag agatgccctt cgtcagcgcc gtggtgcaac ccgtcaatgt 480
ggcccaagcc acgcggccag tttggggccac gcattcggac gattccactg cacgccgggc 540
aagtgccgga
```

550

<210> 206

<211> 590

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (152)..(590)

<223> Area matching *Drosophila* EST AA440949 (inverted).

<400> 206

```
caccacccga tctggcgccc gatctttggc gaagcgagct acgtgttaag ttctcggcgt 60
gatgactata acaatgagac agtttactta tctggcttac acttcaatag gaaaacaata 120
```

cttttatata gcttctataa cttcgggggtg cgataagaac atgaatacag atacacggat 180
 tgcaacagta cccaagccac ttgtttttaa caaatacagg ataatgggga gtaatgtaag 240
 ctattgactg ggttacaatc aggggtctga taacaatcaa acattgtcca gttgcctttt 300
 gcgaatatca atgaccactc acgagttgca actgataacg attatcgccg cacaatgcag 360
 tgggtgggta tttcactggg gggaactttt gggtccttag aaccagacg gattactcaa 420
 tgaatatagg cgatatgttt gggttttacag cgaaagtgct attaattgtcg acccgatatgc 480
 tctctttcga tgtgccagct ctctatttgc gggaatgaat gactatttta tgggtctggc 540
 cgcgctgcta caatgctgca ttgctgcagt gggacatcct ttgacaggcg 590

<210> 207

<211> 312

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (132)..(312)

<223> Area matching *Drosophila* ESTs AI062455 and
 AA440915.

<400> 207

gaacgcacaa tcacaagcgc cgctcgcgag aacgagaacg ggaactcgaa agaacggaga 60
 tcgctgggtcg gagaaccgtg gaaccctggg aaccgtaacc gtgaaagtgg ggaatcgaag 120
 atagaacgga gaggggtgta ggccgattcc ctctccccac tgcccgttga aattcagaat 180
 actaagctct cggttaaacg cggcgaaaaa gaaagcaagc tctgagcggc tgaaaaaaaa 240
 atgaagtga ataaaactgg ggatcgcggc accagcaaca agtttttagtg gctcttcttt 300
 gtgcgttttc gg 312

<210> 208

<211> 311

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (68)..(311)

<223> Area matching Drosophila EST AA816432.

<400> 208

```
ctcgtgtggc tctcatttgt ttgatttct cggttacata ttacttaact aattagaatt 60
tattatgaat ttttcattga atttcacaac gagaaatcta gtgccacgac tgcaccgatt 120
caccagcaag attgccgtgg atgttgaacc agctgtggtc tctgccctgg aacatgccac 180
actgaagccc agaaaacatc ccggagtagt gagaccaat catatggaac tgccgaaaca 240
attgaatgat acgcttaagc gccatcgtgg ggggatcatc ccgtcaaaaa actaatccac 300
gatggccagc c 311
```

<210> 209

<211> 359

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(258)

<223> Area matching Drosophila EST AA979191.

<400> 209

```
tggtgaacaa tatttttaaaa acatccaggc aggtgcttta tcccgtggca aggactttca 60
gccgcagcag caaccacggc aatgtgggga ccgaagctgc tgcgacagtg ggcgcacctc 120
cggcgacaag atcaccctt attctgccgc aagattacac agattgcttg ccggtgagca 180
ggaacacggc gcgccaggca tggattgaga acacggatgc tgtggcggag cgaaaggttg 240
gcctgattga actgctccgg gatgtctttg ccgccagcc gcgcgtggac atcatcagg 300
aagaatgttg gaagtgggca gagcaagtat cgttatgtaa gcatggcgca caccaaact 359
```

<210> 210

<211> 415

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (2)..(318)

<223> Area matching Drosophila EST AA391495.

<400> 210

```
tttcggcttt aattcgcgaa aaaactgcag gaaatccaaa aggaaagtcc ctggaagcgg 60
ccataataac gcagccgtga aaaccacagg gatttcacg ccagctgtgt cgagcagccc 120
tggatactcg gaaaagaagc tgcagcagcc gaagaaattt tgagtgtgtg cgtgaggaag 180
gaaaacgggg gaccgcaaac aacggatcgc gaatttcgtc ttaagacaaa gtcttgcgct 240
gcttgtcacg gtattccacg gccttgccga cggacttccc ggttctggaa aaccgcagcc 300
aggctaaaac gagagaaggt gagagtcgca atatggcgaa aaagatcccc gatcccagcc 360
aaatcgccat gcggtgctgc tccgccaca attccgaacc ccgccggtg aattc      415
```

<210> 211

<211> 89

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(89)

<223> Area matching Drosophila EST AA441636. This EST
matches ESTs AA820540 and AA817484. Evidence of
alternative splicing.

<400> 211

```
gccagaagct tggtgctttc tccactcctc ttctacctc gtcagtgtgt tgagtgtgca 60
agtgtatgtg ttgctaggc ttagaatc      89
```

<210> 212

<211> 488

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (59)..(488)

<223> Area matching Drosophila EST AI295363.

<400> 212

```
caccggacgg ttgaaaagtg ttctgtgaaa aaatccaagg aaaattttgc ttgtttcaga 60
ttttgtcaag tcatggagct gccttcaatg gtggagcggt cgggtgatcg cttggtggtg 120
cgcagcttgg ttagtggtgc tccactttat cagtcactta ttgaggcgag agcaggtgct 180
gtgcttcta tgtcccaaag cgtgcagccg ctaataggtc aggacttttt ggagcaacaa 240
ctggagcagt ataaggcgaa taactttatg ttccactat cgatggccgg gtttgtttac 300
gcagactctg caccaccggg ggacttgcc aaggaaaata tggagaactc actgccagat 360
ggtaatccgt gcaacaacaa caacgacgat gagctgccgc agtgcaagat accggcgtaa 420
ctacagctgc aaccagtgcg cattcttcac gcaaaatccg cgcagtcac tctcgcatct 480
gcggggac
```

488

<210> 213

<211> 170

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (51)..(170)

<223> Area matching Drosophila ESTs AI114059 and
AA941565.

<400> 213

```
cgcgacgtaa ataccagacc cgagcggaca ttttttattt gtggagcgcg caacaagaac 60
gagaaaagaa accgaaacgg aaagcagaca aaaagagctg ctgccagtgt agaatcgcaa 120
agcaaagaaa gaagcaagtg cgtgtgtttt taaaccgaag ccgagagaat
```

170

<210> 214

<211> 480

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (3)..(355)

<223> Area matching Drosophila ESTs AA801691 and
AA441008.

<220>

<221> intron

<222> (356)..(442)

<223> Probable intron in gene represented by EST
AA801691.

<400> 214

ccttagcggc gttccattca aaaactgcca ttaaagatta aaactctgga ttaaattggcg 60
ttatcagtcg aaattgaaag ggtaatggac cagggcaact gcctgatgcc cgacatcaat 120
atctgccaaa gcgacttggc caatcccacc gagcccattg tcaccaagat catggtgcac 180
tatctgcgga gtttcggctt tcgcctggag ccgccctata aaattggcac cgaactcggg 240
cactcgtcgc gggaggcgcg cgtctttctc atccgagtgt gccgccaagt ggagcgcac 300
gtccagatca gctttcccaa caagacctac agctatatgg acataattaa accaggtgag 360
ccggcagccg gtcttaagaa cattaaatgt aggaatttag atacaataag ctattattat 420
taaacaattc tctaccatta gctggtaaaa aaacgctcgc catctgagct acctttttaa 480

<210> 215

<211> 471

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (378)..(471)

<223> Area matching Drosophila ESTs AA950084 and
AA978669.

<400> 215

```

agcctgccag taatgccggg gtggattttt gttcttgcct ctttttcaat tcacttcgtt 60
ccattgcatt ttagattgat gttgttggtg ttgctttatt cgtttccttg cgggagaaca 120
tttccaattt tcatcctttt cgtgggtttt tctcaaattc ggggttttct tttcctcttt 180
tcgcgtcacg tacgccgttt gttatatccc tctctctcgc gctcttgccg tcttgccgctc 240
tcgtgctctc tcgccggcat gagcgcgcgc gagcgagacg gcggacgcag agatgagtga 300
aacagctgta agcgtcgatg agtataaaaag gcgggcgcac cggcgagaaa ttcatagtag 360
cttcgaaaaa aacactgaca cagtacacaa gaaaacagac tctcgcagcc agaaaatcaa 420
atgaagcagc agcagcaaaa acgtgcatag ccagactttt tccactgcta a          471

```

<210> 216

<211> 439

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (20)..(236)

<223> Area matching *Drosophila* EST AI062945.

<220>

<221> intron

<222> (237)..(291)

<223> Probable intron in gene represented by EST
AI062945.

<220>

<221> misc_feature

<222> (292)..(439)

<223> Area matching *Drosophila* EST AI062945.

<400> 216

```

gtgcgaacta tacggcttca gcacgcgctg ggcaactact ggagcaccca ggcggacctg 60
ccggttcggg tgccgacggt gggccacgcg gacaacccca aaccaaagcc gacatcgagc 120
agcggagcaa gtgcatcggc atccgctgct gggggccacca agagtgcgga ctcagccgctc 180
gctacctcgt cagcttcggt ggacatcgca ccggcagcga ccaaggccaa gccaaagtaa 240

```


gcgataagag ttgcaagggt cgcgataaat agtaatatat ttcctctcca gattcgcaac 300
gcttagcgac atgtcgaagg agtcgtctag tgacgatgac cagcaggcct tctatgccgg 360
cggctcagat cgctccggtc agcaagtgtt gggcccgcca agcgcaagaa cttccggggag 420
cagctcaccg acatgatgc 439

<210> 217

<211> 312

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(312)

<223> Area matching Drosophila EST AA440345. This EST
forms a 2293bp contig with ESTs AA201536,
AA539993, AA942332, AA979174 and AA202096 and has
sequence similarity to Human cleavage factor gene.

<400> 217

ggccggcaaa ttgttaaact ggctgaaatt gttaataatg ttttaagaaa ttgcgacacc 60
aattaaacca ccgcaatgtt ttcgatgtgc aagcagacgc actccgccac ggcggtggag 120
ttttcgatag catgccgctt ctttaacaat ctggatgaga acctggtggt ggcgggcgcc 180
aatgtactaa aggtgtaccg gatagcgccc caacgtggag gcgagcccag cgtcaaaagc 240
tgaatcccag cgagaatgcc gtctggcgcc caaatggcg actgggaaat gcctagccac 300
atatacgtc ta 312

<210> 218

<211> 501

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (10)..(501)

<223> Area matching Drosophila EST AA696930.

<400> 218

ctgctgactg tcaaagccg gcggccttag atttttcgac tattttcaat aaaattgtga 60
aataccagtg aaaaattaaa gcaataaat aaaatgcagg agcaggagat ggaggtggaa 120
gtgggggacc cggcaaaggc gtcgaatttg ctgcggtca tcaagcagct gctgctggaa 180
aaagcttacg atggcgtgcg gatgttggtt caaagtgcc aggaatcgga aaagaacact 240
cggctgctgc cccacatagc cattgggacg tataccttga acgtgtgctt ggaaaacatt 300
tccgaccgag gtgaactccc aggagccaga actattcgac tgctctgacg agctgctcaa 360
gctgctggcc caagtacgcc cactgcatg agcttatgct ggaactgatg gaacgcttgg 420
aagagagtta gcagattcaa atggtgttcg gcgcctatct gcggccttac aaagttgtgc 480
tgcaacgaca gggacgcaca g 501

<210> 219

<211> 586

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (8)..(437)

<223> Area matching *Drosophila* EST AA440135 (inverted).

<400> 219

ggtgcgaccg gcatgaaagt gacgaccggc tgcaatcatc aagccaatgg cgagatcggc 60
cactgcattt ttcaccaccc cgggagtgtg gcccaatggg attcccctct tctggaactc 120
cggaatatcc acaaaatcga ttccggagga catggtgctc acgcaacgca gctgggatcc 180
agcagcatcc aggattccgg cattcagggg ctggtaatgg gcccaataga tggcatccac 240
gccgggcacc ttctgcagga tctcatccct cgagggcggc acactctggc agatgatggt 300
ctccgctcca cgggatcgga gcagttccag agccggtgct gggacatttg ggtgcgaaat 360
cagcacttta aaagccctgg tcgcacgaga catttcgggg gaaaatatag cacttaatat 420
caactagtag cggcgaattg caaggctgaa ctaaagtggg aaattttcca aatgaccatt 480
caagcttttt ctgtgccccg ctcttaagct taaaagggt ctcttaagct ttacattttt 540
taatttggtc tcattttttg gaaattcaca ttactatttt ctggcg 586

<210> 220

<211> 176

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (75)..(157)

<223> Area matching Drosophila ESTs AI063979 and

AA802032.

<400> 220

gaaggaagta agtagcaggc gtaattttat gtttcataag aatccgattt aagaatatat 60
ctcaaccaa ccagcgcgat ggcattcggt gactatccag ctgagtacaa cccaagggtg 120
cacgggccct acgaccccg cgcgttctac ggcaaagggtg agcagggttac gtaatt 176

<210> 221

<211> 169

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(144)

<223> Area matching Drosophila EST AA699194.

<400> 221

cattaaccag aaccaaccaa tgtttgatct tcttatacgc aatataagcg atacgttttg 60
ttttaacctta cattatttta tgaactgatt attaactgaa atggaaatac attgaacaca 120
tctagcttgt taaacgtata atcgatcctc catgtaaaga taaacgctg 169

<210> 222

<211> 546

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (507)..(546)

<223> Area matching Drosophila ESTs AA441233 and
AA392152.

<400> 222

```
caagctgggc gacttaaagc ccgcataacc gataactgaa gtgggagagg taatggcact 60
tgggtctctct aaaacttgct gcgggtatttg gcaggactag ttgggactcg aaccagggcg 120
tgaatcttttg cttgccaac cggtaaacct aaccggttgc taaagtgggc caacattaat 180
aatatTTTTTg ttgaatgttt cataaaagct attttaatat aaattcgcat cgttaccgat 240
tcaataagggt ttagtaaattc attatatttc tgactccata ttgatttcca acagcaaatt 300
aattaactcc ataacttccc ctctcccttt ggagcaaagg atgtagttaa tatcttaaca 360
tctaaacttg tttcgTTTTt ttattcaaat aggagttata ttaaataagaa atgtaaaaaa 420
caaagcaggt tttaagaaaa tgatgtcagg agatttgaac tcctactcat ggtccactct 480
aatccgcagt ctttgcaatt tactgtgttt ccaacttaac gcccccaagt taatagccgt 540
aatcat
```

546

<210> 223

<211> 474

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(79)

<223> Area matching Drosophila EST AA438352 (inverted).

<400> 223

```
gtaaataaaa cacaaataga ttgcttctga aaattatctg gaaactcaga gctccgaaga 60
gacgatgtga acacgacaag ccaactccggc agactgaccc aaacaaacgc cggcatttgc 120
aataatatta ttgtctaattc ggtatatata tatcatataa gtaaccattg atgtaacata 180
cttttggggtg taaggaatat atagttgaaa agtaattcag aaaacatgca ataactataa 240
tttattaaat attaaagtat cttgctaaga ataattgatgt gcaaattgagc cttttgccag 300
agccatagtt atatcatatg cgttttgtat tctaaaatat caaaccaaat aagatgaagt 360
```

taatatattc gtagtacttt aaatcctgac ttacacgtca cttgtcgtct gcttagttgt 420
aatattctaa atctttttgga ttaatcagtg cagagttctc aggatgacct acat 474

<210> 224

<211> 534

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (480)..(534)

<223> Area matching *Drosophila* EST AI455428.

<400> 224

ttgatgctgg ttgtttaact tccatacttg tctctctcgc tttagctctc tcttaggagc 60
cccaactaac actaacagcc ggggtgttcgt cccctcttta accacttttt ctcttactct 120
ccgtctctca ctgcgaaagt gcagcgtgaa gtgttgataa ggggcacggc gggggataca 180
ctctccggga tattgcgctc tctattgggg ctctcttaca ctctcactac gcgttggact 240
ttcagttcat tccatgtgca aaatcagaat ctgatatctg aaatacaaaa atgacaaaact 300
attgtgttta gttttgaagt acttatecta acattgatta attttgcata gatatgcat 360
tcatatactt acatttttat atgtttgtac gctatattca aattttaaat accgacaatt 420
tcctgatttt actttacgct acgtgttgct tgaaaagaac caataatcga ttgattgtta 480
tagtttgtaa taaattcgct ccgcaagctt ctttatttta gtgaccaatg aaca 534

<210> 225

<211> 507

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (11)..(190)

<223> Area matching *Drosophila* EST AA246916 (inverted).

This EST has sequence similarity to Mitochondrial
import receptor genes.

<400> 225

ggggattctt acgctcacgg actttcttct tgtactcggg atcgctgcgg cgcttcttgt 60
cgaattaaat gcattatcca ataaacagag ttccagctac tcccgcgtgca atgccgattg 120
cagttttgtt catttcaatc atattactac ggaaatcctc tgtattaact tggctttatt 180
ttacattccg catgtgccat cgatttacat aaaacaaaaa tcgatatcgc ctacaactac 240
tggtgtttca tggtttttcac ttgtttcgca ctaatttgaa acggcgggact ggaacactgt 300
tttctttttt aaattttgct aagggatatt tatttaattt taagtaagag attttaaagt 360
atttttttta gtttattcag aaatactgtg ggatcaagtt ataatacgct aagaaataat 420
cgtaagctca cttcttgtat tatatttatt aacttgcatt attcgcttaa aatccccctat 480
cccccaaac taatgttttt aattttc 507

<210> 226

<211> 376

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (233)..(348)

<223> Area matching *Drosophila* EST AA392258.

<400> 226

cgtgagtgtg taaaaaatac aggcagcata caaaataata atattgaaag cgatacaaca 60
acaaaggccg tcccgtcgaa gacgaaacgt ccaaaacgga agaactggag agcctgtcca 120
gttaattacg gagcacaaag tagaatcgaa cagcaaaggt gagagagaga gtgaggaggg 180
ataggggtca acctggctct ctgcgaaaga agacgggggc gaggagcggc caaaatgatg 240
atgatggaca ccatggacac ctgcgaatcg cagccgatgg acgtggctcc ggccgtagca 300
gtggcagcca cttcggggcg agctcttggg ggactttacc gctgccattg gtgaagcatg 360
gcggccaccg cctaag 376

<210> 227

<211> 487

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(41)

<223> Area matching Drosophila EST AI296848 (inverted).

This EST has sequence sinilarity to Mammalian

40KDa V-ATPase subunit genes.

<400> 227

gaattcacac gccaggcaac ttttaagtga aagcagaaat tgatagatgg aacatgcggt 60
gataggtatt tctcggatga actgattctg atataaatac taaggattct agatgctaaa 120
ataatattta ttaagctaca aatatattta tatataatat ttaaatttc ggtggcggta 180
tctaccgatg cacgctagat ggcgctaccg atggtgcaag gctgccattc gtttatcctt 240
tttgacaata tggcagcgct ctaacggttt tttaaatttt aactttaaat ttgaaaagat 300
attatttggt tggtttggtc gttttaaagt gcatccaact agattatttt agttataaga 360
aaatgcacct agttaagct tgctatttga atttcagata gctattttatc ggcccattct 420
aacgcaattt ccgcacatgc gcctggagga tgctgtacgg aaatacctgg tgctctgggc 480
catgatg 487

<210> 228

<211> 354

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (255)..(354)

<223> Area matching Drosophila EST AI388389.

<400> 228

tctactgacc actcacaaat ccggactgaa cactaaaaac tgaaaactga aaactcggac 60
tcgggcgcgt aaggagtcg gtcgtcggga gtcggtcgtc ttttggtgat cttgaaactg 120
aaattccaat tggtgattta tctctcggct gctgcgccgc ggctgcgctg ctgcagcgca 180
gtcccactcg atttgaccag cgaccaagtt tataaaactt tgagccaaaa tgcagcggcg 240
cacagttggt accaaaacgt tgcacgcgct gtggccctca tcaaaacaaa aaaaaaata 300

taagcgaaaa tgaaaacgaa attcgggttaa cgtccacaga agctgacaaa aggc

354

<210> 229

<211> 471

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (335)..(448)

<223> Area matching *Drosophila* ESTs AA441471 and
AA540182 (inverted). These ESTs have sequence
similarity to Mammalian RHO GDP-dissociation
inhibitor genes.

<400> 229

gtacgaacca tgccactttt ttttcttctc tttttttgat aaagaaatgt gcacgaagaa 60
tggtaaaacc ccagacgaat gaatcacaca caccagctca cacacacaca cactcacact 120
gaggccggca catgaatcgt cactgatttt caagtagaat ttttgggagt ggttcttggc 180
ctgcagtcac ccaactacat acatttgcta tcaatgccag cttgtattaa attaataataa 240
taatattata aatatttttt ttatgtaaaa tgcattggaa ggcaccgcac tcacacacac 300
acacagttgc aagttggcaa cgacgcgcac tcacctttta atatgcgaaa ttaatcaaat 360
agtacgatct ctgaaaatta atcactgaaa agttactgta tgtttatatt tttaacaact 420
ttttgaataa ctaacttttt taaaccaagc caataatata aaataagaat t 471

<210> 230

<211> 480

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (22)..(242)

<223> Area matching *Drosophila* ESTs AA439855 and
AA567284.

<400> 230

actacaacca aacaaatatac taaaagtga tgacaagtgt gaccgcgggc gaaccgttaa 60
aatatacgaa gaacggctga cagggctggc gaggatcatg gcacagtttg tgactgaagc 120
cagaaaaaat actaagcgtg actaaaatta gttcagtgtg tacatgttaa aaattactta 180
aatatTTTTg gcaatataag tgaaaacaat acttataccc gcacatcatt tacagtccta 240
ttgacatttt aagttgtaaa tatcgaaact accaaaacga aatatttggg aaattatgaa 300
gccctgacaa ctctgtagtc gataggcaaa agagctcgca ccatgagcct atcgttctca 360
gctgttttga acccaaaaca aaggggaagg actatcaatt ggaaatgttt ctgggtgagga 420
ataataagtt ctgaagaaat gcaaaatatt aaaaagctga acggtccagt tcatccagcc 480

<210> 231

<211> 625

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(141)

<223> Area matching *Drosophila* EST AA941606 (inverted).

<220>

<221> intron

<222> (142)..(396)

<223> Probable intron in gene represented by EST
AA941606.

<220>

<221> misc_feature

<222> (397)..(446)

<223> Area matching *Drosophila* EST AA941606 (inverted)

<400> 231

ccaaaggcat ccgatactcc cgaacttatg cgaaaaattg tgtcaaataa aaatttactg 60
gttcgtttat tgtggcccgt gtgaattgtg ttaataccgt ccgactcatt gaaacctttg 120

gaatattcca agcttaaaac acttgaatag ttcgccgtca acatccaaaa aaagattata 180
 tacttttaggc tcatgttcac aaattagata tcattgtaac aaatggggggg atatgtttgt 240
 gtttatggga aacttgatca catcaaaaa acaacgtaac gagttcaaaa cattotttaa 300
 cacaacaaaa catttgcaca actaatcgt aatactcaac acaacattaa caaggtttct 360
 gtagatacgg cttaagaata aataagagtc tgtaactaat taatgtaaca taaaatatgt 420
 actaagtctg atagtaatgt agcgtacgga tcgcttaccg ctaataccaa atgtgagagt 480
 tagtcgcagt gtggccacgt tacactttct acctgttgac actttcatgg tcaagatgtg 540
 tccgccgtcc acccagtttt ttcactttcg ttataaaaat cctacgaaat tatatttcaa 600
 cctttctaca cgcctttttt ttgaa 625

<210> 232

<211> 435

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (209)..(435)

<223> Area matching *Drosophila* EST AA392324.

<400> 232

aaaatactat cgtgatcatc tcccactcg ctctaccca ctgcctaaa ataatgggtgc 60
 catcaagagc gcagcgcacc tgccgtatat cgttctcttt tgcactcgct cccgctcttg 120
 gagcactcga cagcgacgcc ggcagcgacg tcgagccggt cgagcattta agcttacgac 180
 ttgacgaaaa tcaaatcaaa agatcgacaa cattcgacga gtgcagatca ccagctaaaa 240
 gaaaaccagc tgagacatcg gaaaagtccg cagattttca cgtaacgcct taaagatttt 300
 ccgtgcggtt cccgaacaaa ctaaacatta ttaacaaaca ataaacgaat ttgtagtgtc 360
 agtgactttt gaacgcacga acaaattccc aaacacacca ccaaacgtga ctgtataatc 420
 agccccaaga aaccc 435

<210> 233

<211> 393

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(393)

<223> Area matching Drosophila EST AA264796 (inverted).

<400> 233

```
cgctattaac tgttttgatt atacggcg tgataaaacg accggcattt gttgtgtcg 60
ctgctgctgc tgctactgt aatgtttcgt tctcgncgt tccccggccc gttctgcac 120
ccaccgccc gtgttcggt cccctgccga agcttcggcc actgctgctg ctgctgctac 180
tgctaaatac gctcgtatta ctattaacac tattctcttt tgttttcgcc cgttcgccg 240
acgactgcag cggcagcaat gctttgtcac acttgcgctg ttttcgccga attatggcca 300
ctttttgcgg ttcttcgccg ggcgcccaa ttttggaagt agttgggctt ttttttgtg 360
aatttctgtg atttttccct tgcttttctt gtt                                     393
```

<210> 234

<211> 522

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(152)

<223> Area matching Drosophila EST AA540030. This EST
has sequence similarity to a Rat calcium binding
protein.

<400> 234

```
ccaatccaaa tggaatgcca ttcaatgctc gtctgcgatt gttgaatgtt taaacaaacc 60
gatcggcgca caacacaccg tcaccatggg caataagtcg tcgcttttcc tgcggaacga 120
ggagatcgcg caaatccagg aggagactgg ctgtgagtac gatttctggt cgggatgtgt 180
gataaccttg ggctttttca accggagact ttcaatgcgc cgtactaaat cgaaatacgc 240
acttgगतat aaattaattg ggccacgagc aatgcaaaca acaacatcgc actggagtgc 300
taaaagcatt tcgggtccaa gaccatggga ttgccaaaat ggattcgctt agtttcgatt 360
cgtcatttct ataaaaattc caaatctacg aactatatgt tcgtgttcta aaaaactccg 420
ttcaaattat gcagaactga gtctgagcga tctgtgcccg ccttatatta gcggtatatg 480
```

gacagatggt ttgcagcaaa agcaatttgc atttcaatgc cc

522

<210> 235

<211> 596

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (85)..(596)

<223> Area matching *Drosophila* EST AI109898.

<400> 235

agtttcccca tgctcatcta acggtgagcg catggcccca aaattcaagt acaacacaaa 60
cacaacacaa cgagggggcg aggtaaaaag cagcagaaaa gccagcagca gccgcccgt 120
cataaatcta gcaagaaaaa cctaattaat tcaattaatt actacaaaaa tcataccggc 180
atacgttaaa taaaaaccg ttcggtctaa ttaaaattta caaaaaatca ctgctttcat 240
ttaaagcgat tttaagtga attctattga tttgtataat tacataaaaa gtgttgcgga 300
aattgactct ctctatcttt ctctgcaa tttcacgcgc cgatgaaaat tcgcaaaaaga 360
tctgtattaa atcatcaata aaaatagcga aactaacggt gcaatgaatc cagctgtttg 420
aaatccgcaa cataaaagca aaaaacacaa aactataaaa caacacgcac cgaatcacac 480
ggaaacaaca acaacaatag gcatgctcct tattaatatg tacgaaaaaa cattaaacat 540
aggaactgcg aaagttaata atggcatatg aatggggaaa agtgaaatac acacca 596

<210> 236

<211> 473

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (365)..(473)

<223> Area matching *Drosophila* EST AI259723.

<400> 236

acaccacctc aaaattgatt actcctaaca aaaaccgaaa aaatacttga aaaataccca 60
 atcaacaaca gcacacaaca aataccaaca ttttccttat acaaacctca tctgattagg 120
 ttcttcgtga aactttcagt tacagcgccc tttttagagc agttagatca cagtcagtta 180
 gtcgagagtc ttaggggttat ataaacacac catttacagg tcttcacagc actacaaacc 240
 aaaaactgca agcaatcaca ccaaacaaaa gcgttatact ctaaacatta ctcttccaaa 300
 ccaaacaaaa accccaccaa atcaaaaacc aatccaaatc gacacgaaca cgatcaacga 360
 aaagatgcct ataggatagg ctacgatgtc ggtaagacgg caacttccat cacgaagaac 420
 ccgcgggtccc gaatgggagt tacctacggg tggctatggc ctgatcgaac ccc 473

<210> 237

<211> 141

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(141)

<223> Area matching *Drosophila* EST AI294469.

<400> 237

ctaatgcttg attgtgatta tctggaatat tccactggaa aacgtgccgc ttcccactca 60
 ctgcagtcac agtctacttt cggttgagtg agtatgtgtg agagaaaacc tgcgtcctct 120
 gtcgcgggggt cttgacactg a 141

<210> 238

<211> 355

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (145)..(325)

<223> Area matching *Drosophila* EST AA140945.

<400> 238

ggctatgggt tattgaccgc tcgatgtctg cgtttgggat tgcggtgag acgtaggaga 60
 agtacgcgtt gttgcgctga attgagagtc ggcgttcgtc atgctcgcgc tgacgctggg 120
 cgcgagtgtc attctgactc atagttttat tatttaagat aacaattcac tatgtattta 180
 agcgatcttg catcgcatag agcgtctctt tcgctttcag attttttatt tagtttattt 240
 tatttggcgt tcacttcact caaaacaacc gattttgtgc ggagcacgaa aaaaacgtct 300
 tcacacgtcg gggatcgaat tatttatccc cgatcgaatt atttatcgtg ttctc 355

<210> 239

<211> 626

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(331)

<223> Area matching *Drosophila* EST AI259816. This EST
 has sequence similarity to Human Epsin gene.

<400> 239

caatatcatc gcaatcgcac tcgagagccc tataaaccgc atagagtgcc aggatttttt 60
 gatatccata tcgtgcgcgc agctatacta ttttccccct ttgttgacgt cgcattgtcg 120
 tcacgtcatc cttgtgaccg tgtctattcg agtccgaaaa aagaaagaaa agaaagtcgt 180
 aaaatataga aaagaaaact agttggggag gaggagtgc acacacagac acacacatac 240
 acagccgagc ggagccccca cagcacaca cacacaacca aaggcgaatt gcagtgaagc 300
 aacaaaaaca acaataacag aaacattgca ggtgagcgaa agagtaggtg ggagggggcc 360
 acaaacatat tttctgtccc tctttctctg ttggggcttc tttttcttaa ataataattt 420
 tccgtaatta tagatcccc ttgtctaaac gtaattcccc gctaaccgtt ttttacaact 480
 ttgcttattg atagcgcttc ctttggcctt tgctctttgt tgtttttttt acaattgaaa 540
 actgccgtta gccggtcaag ttgattagtc catttggatc cagggttgcc aggggcttgg 600
 tgaaaactggt ttatttttggg aagggg 626

<210> 240

<211> 433

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (209)..(433)

<223> Area matching Drosophila EST AA141103.

<400> 240

```
ttgggacgtg tctcagatTT ctatcgacta gacatcgccg atattcgaaa atgctcttcg 60
aattatcgaa atgtaggcat actgcaatTT acgcgcgcaa cgcaaaaatt caaataatag 120
aatatttggc tcaacaagac aggagactTT agatggaaaa atagaatcca caaaagcaaa 180
actatggaat aactaaaacc actttttcata aatagtacac acaatcgatt tatttcgTTT 240
ctttttgtat ggcaaaaatt aatacaaaaa attaaatatt aaatgtatgt atgtatgtat 300
aaaaagctta aagcaaaacta tataatgtaa atttaattgg ctgtttgTTT ctctcccgat 360
tgatctgtca gtatgggtaa gttagaaaga aaaggcaatc tcaagaaact catacggaat 420
ataattccac cac 433
```

<210> 241

<211> 401

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(98)

<223> Area matching Drosophila ESTs AA246767 and
AA141059 (inverted).

<400> 241

```
ttcgtgatta tcagcgtaa ttgtacaata ttatgattta ttcgagctgt aaatcttcac 60
agcaagcaca aactgtaatt ataccactta gaattccatt ttaatggctt tatttatggg 120
gcgtgcattgg gcagcattTT ctcgctTTTT attttttttt tcttgatttt tgtatattta 180
tgagagtgcc gtctccggcc acaaaaagtt aatcccacta aatgccgttg atagtttata 240
ttacgatttg ttgtgctggc taaaatgaaa gatattgggg cattttaatt ttagaattgt 300
gacaaatgcg caactTTTT ttaacggctg catatgcgac gaatgatcca agttctagtt 360
ttatgattga atttcattgt ttttcatttg gcttaatgag a 401
```

<210> 242

<211> 368

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (118)..(239)

<223> Area matching *Drosophila* ESTs AA441468 and
AA142226 (inverted). Sequence similarity to *C.*
elegans protein Z66496.

<400> 242

```
ggtggtacac aaaaatcgat gcaacatatt tttgggccgc ccaatgtcac ggatgttttt 60
cccaactttt taatgtgtta agctagtaga taatttatta tatatcctac aacttacaga 120
aggcggccac aatgcccagc aatcgacttc catatttgag ataccacggc tgctccggtc 180
caattggatc ttgttgattc ggccgtgccg gcagaccgct tatcttttcc gcaaacgact 240
gatccgggaa atagacggaa atagggagaa atctaaatgc aattaggaaa aatcgaagca 300
caattttgta ttgtgacgcg gcggggcgctt tttttaacac gcacacattg ccacgacaaa 360
aaacacac                                     368
```

<210> 243

<211> 321

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(82)

<223> Area matching *Drosophila* EST AA247070 (inverted).
This EST forms a 1366bp contig with ESTs AA567381,
AA568013 and AA540724 and has sequence similarity
to a *C. elegans* protein.

<400> 243

aaccagatcc gcagctgcag ccattgtctt ccaatctcac acgcacacac acacaggaac 60
aagcacgtcg gtggtgttgt tgcgttgttt tttgtgtcgc tgcgtctga tgtacaatca 120
gtgttggtca acaatttcgt gottgaattg gtcacacacg gttgccgtgt acgcggtgta 180
tcgataaccg atagtaaaca tgcattgggca ttggcgccac aacgacacgt ttaaacaatca 240
accaaaccac accgaacgta tttagaactc caacaaaata tctgctccac gttgaattta 300
aaaacatttt aattactaaa a 321

<210> 244

<211> 469

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (433)..(469)

<223> Area matching *Drosophila* EST AA802401. This EST
has sequence similarity to glycosyltransferase
genes.

<400> 244

ggccgagtaa caaggtcgat ttgggggctaa aaaacgccaa aagcgggcgc tgtcaacatg 60
tggtctaggg ttaccgcagc gcgcgcattt cgtgtgctaa aaagtgaatt ttagatttaa 120
attgagatcg agttttttaa ataattggctt agattaccgt agtctttata tatatatata 180
gcaacatagg tgaaatagaa aaagtaacaa ataaatattg aacgtaataa aagagggttac 240
agaacatata ataaataatt aagttaatat aataataata aaccgaagat gttgaatact 300
ttagacttaa atagcaatac ctccagcgaa agcctccctt tataatttat caaaaaaaat 360
taacctatct atttgggata ttcttttagaa ccgcttttaga acattcatcc taccacgggc 420
acactttcgc ccaatcagct gagaaaatat tttaaagttt taaataata 469

<210> 245

<211> 383

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(96)

<223> Area matching Drosophila EST AI135263 (inverted).

<400> 245

ggtggcacat gtgctcaaaa aggccgaaga cgggtgggaga gggagagcga ctacggcggtt 60
gccagatctt tggtcgatga cattcaatag ttacttttaa caaaaatagc tagatcataa 120
aatataatga attgcaggat acaaattcag ctgaactact ggtcagaaga atgcttgtat 180
taatattaca catagatata tagttattga cttagaatta aattttgtat attgaattgt 240
taggaaataa ctattctttt gtatcttaaa gaaaagaaaa ttattcatat taaacggatg 300
ttgtcttgag actgctaacg attttaatag acctgttaag ttgttagcac ataaaataaa 360
attattttga atccagcatt ttc 383

<210> 246

<211> 489

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (243)..(489)

<223> Area matching Drosophila EST AA695904.

<400> 246

aaccagaacg aaactccaat gcagtttcat tttgtcagtt taatcattaa acaaagaatg 60
cgcaaccgat cgcaactagc tcgtggactc ttgtttctccc aataattggg atgttttcca 120
ttttgcgtta acatggaaaa tgtgtgaaaa gctttttccc cctccaaaag aagcgtactg 180
aactaagctt tcggtgggta gtaatagtag tcgttatatc ttatttttct tatttacgtg 240
cagctgcaat cattggctgc gtcactttgg cgtcagctat aaactgggtg atcaactcgg 300
cggcctccaa aagctgcgca tctgctccag acacttttagc caacgccagg agatggccaa 360
aaccgcacac aagatgacgc cgctgcgcaa gtctctgtcc tccaagggca ttgtgctacc 420
cattaatgcc gctggaaggt tcggtcattg caggcgcctt agcaggaaga agaagttcag 480
gaatgggaa 489

<210> 247

<211> 417

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(317)

<223> Area matching *Drosophila* ESTs AA246386 and
AA541060.

<400> 247

```
gccgtatgcg aaacggcgaa tgcgtcaac gcagcgctgc gcgaatccct tggcggcaac 60
tcctccgccg gtcgctcgac tgaccaggcc aagagcggcg aggacaccaa cggcagcctg 120
caaaatcaca tcgtggccaa tgccaaacgc atcctgatgg ccaaaatcga atacgaggag 180
gtgcccact accacgaatc ggtgctggag aacctcaagt ccaaatatat tgtcatcaag 240
ccgggaaatc caggcgccat caatggcttt agtggcaaaa acaacacagg caaacttggt 300
gggcgcgaaat ggacatggtg agttacactg tgttaaagat acaacaaaat gttaaaatcc 360
aaaagttgct tgcaaagtgg cttttccctc gtccgtgttc ctcctttgtg ttgcaat 417
```

<210> 248

<211> 427

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (311)..(427)

<223> Area matching *Drosophila* EST AA264961. This EST
has sequence similarity to mouse Thioredoxin gene.

<400> 248

```
accctggcca aatgggcggt aagcttaaga tgagcgtgaa agcatagatt gctagtcgta 60
aacgctgaat gaattttaaa tgaatgaata tgtcaaatga gaatatttca tagttttaca 120
tattgtaatc cactaatata tcaataaaag tttaaattatt aagtttcggt ttttttctat 180
```

tacacattaa tgggccctct aaaaatagga agtcaaagag ctcgaaatat cgataccatc 240
acagtgtgac cgctttggaa ataccgcatt cgggtattttt cttagcacga atttggacta 300
aatgcatatt acaagtcatt tttaacaaaa aaaatttgca ttgaacgtta ataataacag 360
ttacttgctt aaatccaatt cggctgccga aacaaaagct caattaatag aaacctaata 420
ctatcac 427

<210> 249

<211> 459

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (136)..(293)

<223> Area matching *Drosophila* EST AA202880 (inverted).

This EST has sequence similarity to Calcium ATPase genes.

<400> 249

cggcagcaga atagggaaaa caggcgacaa tcacgttaca acaacaacag cggcacaaac 60
agttcccgag agtgcgggag agggacgcaa cactactaac agtgggcgca tgcagcaccg 120
tttcttttga ctacgcgcac agcttgcagg ggggcgcgga aggcttaatt aaatgtgtca 180
catggagcac agactgtttt gattcacaaa aaaagatatc gccttatttc acttatatgc 240
tccccgtttt cttgtcggtg gacacgcgca acgcagcaaa aatgacgaat gcgatcgagc 300
gacgtgtaca gactgagaag cgtgcgaatg cgagagcggg agggcgccac taacagcact 360
gtgtgtgctg ttgcgacgca agcccaaagt cgcgagagca gcctcgatgc agctgatctc 420
caattagaat ccattccctg ttattgttat tgctggatt 459

<210> 250

<211> 438

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (74)..(276)

<223> Area matching Drosophila EST AA263803.

<220>

<221> intron

<222> (277)..(343)

<223> Probable intron in gene represented by EST
AA263803.

<220>

<221> misc_feature

<222> (344)..(438)

<223> Area matching Drosophila EST AA263803.

<400> 250

```
gcccggagca ctggatttca cgagctccgc cctcgaagat ttgtgctttg cttgactaat 60
tggaatttat tgcaggtggt ctatatatat gagctgttgt gccggggcga ggatoccagc 120
agcgagagtc ccgaattttg gaacgagttc ttcctgctgc agccgaactt cgaggcgctg 180
gagaatgaga ttggcaaact caacaacgag cagctgcagc tggtgaaacc gaacctgaac 240
accctcttcc agaggtgcat cgaaatgctt gacacgggtt agaccagttt gacctattaa 300
tatatacctc cagccaccta taatccgtga tttccccag aaagatcatc ctaagcggct 360
gtgcaacagc ctacacagc tgtgctccct gttctacggg atctttaaaa atccaaccaa 420
aaccacatt aaacatcc                                     438
```

<210> 251

<211> 387

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (3)..(166)

<223> Area matching Drosophila ESTs AA202200 and
AA202128 (inverted)

<400> 251

gtccactac tctacgctaa atggctatgc ttgttagaat tgcacatata ttttatgtat 60
tttatttagc taaacacgga gacatatcct tacacgatat ctacgagcga cgcgaccagt 120
gtgactgcgc ctacacaatt gaaacatgtc acatgcagtg tgaccgttct tggtcfaatg 180
gaaaagctct cactcatata aaattcaata ataggttaat aaaaaaaaaa tactgactta 240
ttttttaaat acaaacgtat ttactctaac aatataagta aaaagctaaa attatttttaa 300
tgtttattta ggaaacctat cgatatatcg atacacatgt ttttttggcc accctagaaa 360
ttgctaacgt atttttagca acaaatt 387

<210> 252

<211> 135

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(48)

<223> Area matching *Drosophila* EST AA439530 (inverted)

<400> 252

gtccgatcca tatttttagca cagaaattaa gtaaaatatg gcggtttagt ttgaagttct 60
ttgtttttgt tgctgccag tgttaccaag tgggtgaatt ccgcgtataa ttaggagact 120
ggagagtggg tcaca 135

<210> 253

<211> 207

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (28)..(207)

<223> Area matching *Drosophila* EST AI109459. This EST
has sequence similarity to GPI- anchored protein
genes.

<400> 253

cccgagagga gcagacaagc gaactggact gggaaacagc agcagcagca gcagtcgttt 60
gaattgaata tcattcccca tttcgagcta aacgtcgttg agagccaacc aggaagaatc 120
caacggcgca ccatgccttc ggctgcaaat accgctactg ttaccgctgc aattgccacc 180
accgtcgccg ccacagccag caacacc 207

<210> 254

<211> 574

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (471)..(506)

<223> Area matching *Drosophila* EST AI109779.

<400> 254

taccagacag ctgggcaccc gaaggagtaa gagagacgga tgtgaagaga gagtccctgcg 60
agagcgaaca aatcggagaa ggagcgagcg tgatatgaat atatctaatt actttcacct 120
ccttaagcat aaacttggtt caatttatga aatcttttaa gttactttct gcttgatagt 180
tattcataat tggtatatta taatgaatct tcgcacatgc ggcattttctg cgcaagtgc 240
tgaagagagt gaacaaggga gagagcggca agaacaagag aaatggcaaa caaacaaaag 300
ccacagacac agctgtctta tcacagggcg gttttctgcc accccctttt gacttgatag 360
caaagacaac cgttacttgt gggtttgtgt ctcccgataa gtatgtttat aaaaattcaa 420
ttcttatatt ttatacata ttaagcattt ataacaagaa gagaatgcta tagtcgagtt 480
ccccgaatta tcagaatacc cgttgctccc gttacctaaa ttaatatatt atataccttt 540
aaaaccgcaa ctgtagaaa cttgttgga aaag 574

<210> 255

<211> 247

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (147)..(247)

<223> Area matching Drosophila EST AA141054.

<400> 255

ccccgcgcg aaacgaattt tctttttccg gtgaactagg ggtgtgggtg gaaagagaga 60
gtgagaaaga gtgtggagtt ccgcttgccg gcgcttttct acaactattt tgcattgcg 120
cctctctgcg ctcttcccg attccgcctc gttcattcat tcattagccg cgctctttct 180
tactctctgt gcgcatgcct tgtgcggcgc tgcttctgcc ggcgtcgccg tcagcgctgc 240
gttgttt 247

<210> 256

<211> 127

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (65)..(118)

<223> Area matching Drosophila EST AA141365(inverted).

<400> 256

gtatgcttct tcgtatgctt cctcgatgc ttcgtgggcc ttatgagtgt tcctcctacc 60
acaactcggc catcctgact agctgatccc ctgatcatgg tttacattga ttgcttagtt 120
gtatgat 127

<210> 257

<211> 1022

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (144)..(549)

<223> Area matching Drosophila EST AI063643.

<400> 257

acaacccaaa ataaaggtaa ggggaatttt taattaaaaa attagggaaa ataacaagtt 60
taagttgccg gacccagcca aaaaacaaac aaagcaacgc ttgtaaaaac tgaaaacaac 120
atttcagttt atttcgcttc gtgccatgtg agcaacttca aattgatatt gaatcggaat 180
cagtgtgcgg gtggtgctaa ttagcggaag acggcaattt attgaacgcg aaaaaagccc 240
cacaatccaa cttccatttg gacacgaaac caaccacccg ccaaatcaaa tcgccgtcga 300
gttgtgcatc aaatgaatgt gcgaaaagtg cagtaaataca atgtttttgt gagtgtttga 360
aagaagaaga cggaaggagc gccacaaca aaagcaaaga gagcaagacc taacgggaca 420
cccgaaacca aaaacctatc ggcacaacga cactttctca atagctatag ttttagttca 480
tatgttcata tctcggaaaa tggacgaggt ctttagccta cacatggaga aattggacgt 540
ttacgacggt tagtatctaa tttgccggaa gttctactta aacgtagaac atatgtatat 600
gatggaatct gggttgtatt tctgattaat gagttcatca actttcaagg aaataataat 660
agtagtagta gttgtaaaca gctgaagtat tgggtataaa ataacactga tatgggtaaa 720
atcataatag acactttatt tgattcaaga ctgcgatgat tttagctgta tgaatcatgt 780
cgaaaataat agaaatcact attactaaat atagataatt ttaaaattta gattcagtgc 840
aacatggata cagtgattaa gtgttacaat ataaacaaaa gtaaaagaaa agtacaacaa 900
gaaacaagta tttggtgaga aatgataaaa actcaccaat aatgaaaacc atttatgtag 960
gattttaaca aacactgttc tcgtctgcat tagtgcttgt ctttgtaata gaattcgaac
1020

tt
1022

<210> 258

<211> 497

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(148)

<223> Area matching *Drosophila* ESTs AI107445 and
AA390813.

<400> 258

acataaacia acggagctcc gatattctaaa taaatattat ggaaatcgca ccactgatca 60

ataacgccgt cgtgtcgtc acagcctctg cctctgccg cgtctctgcc tctgctagcg 120
 tcggcagtag cagcaaggat gataacggta ggcgggtctc tagatgataa gcggtacact 180
 tccagtgggt tcataataaa ctataaaaat aataaaatat atgtaaatac aaagcataaa 240
 gtgtagtacg tgctcgaaag agtcacactt tctcgtaaa gaacttcacg ttctatccat 300
 attatatgat tattatgttt caaaatcctt tataatcaaa agcgaattag acaatcagaa 360
 tatctccac ccagcaattc ataatctata taaaatatag tcagaatatt gcaatcatac 420
 caaaattaat accaacccca ggacttaagt ttttggttt aatccaaata tatccatttg 480
 tttctttgcc ttaattt 497

<210> 259

<211> 411

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(75)

<223> Area matching *Drosophila* EST AI297362.

<400> 259

tgtgttggtg tggtgttagt gcttgtgcaa cttaaaaatt caattgttta ttgctgggca 60
 aaactggtac cgtgtaccgc gtacctggaa aacaacattt aaagcgaacg ccaggcgaat 120
 cgagagttcc gagcaagtgg gcaacaataa tgtgtcgtc cggcgcctgc tcatttccac 180
 cgtgataata atcggcatag ggttccgacg cgaaagccac aagtgaaggt ggaatgctct 240
 gcctatccgc gtagttggc atagtcttca acaccagcg aattacatct ctccgactgg 300
 atatgaagat atcgtgagta tttccctctg gaatcaatga aatgaaatgg tgtgcctagt 360
 ctgtgatgat aaggcagcta ccaccaccac gtccatatcc ggatgcgagc c 411

<210> 260

<211> 230

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (96)..(230)

<223> Area matching Drosophila EST AA392916 (inverted).

<400> 260

```
tgtgggatat tatattaatg gaaagccaca accaaattat aactgtttgt aaactacatt 60
taaagacgta gttgaaatag aaagaggtaa acttacagat ttgaaatgaa tcagtaatcc 120
aataatgtgt tttgtttgga atattttcaa aatgtcttca acggaagagg caagaacaca 180
aacagaaaacg gcacaaacac aaagagataa tttggcagca taaaagagcg          230
```

<210> 261

<211> 331

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(47)

<223> Area matching Drosophila EST AA201223 (inverted).

This EST forms a 2631bp contig with ESTs AA538867,
AA439491, AA390780, AA390983, AA201661, AA391700
and AA202007. Seq. sim. to Human nucleopore gene.

<400> 261

```
ctgcagcgtg tccagcgccc taagcggctt tcccacttca atgaactctg tgacgaagag 60
agcggcgctc agttaagaga gcacacgatt cgcggaagacg aaagtttctc ttcagacacc 120
gcatggaaaa ttttcagcac tcaccattag cccttttttag ggcgttttcc ggacggttgcg 180
tatagcgggc catttccgat cgcttttactt acttgcgggc gcacttcaag ttgatttcga 240
tagcaggtct ggagcgtttt gagacctggg gctgctgaaa attgtataaa tcttcggctc 300
gcctacgtgt ggctgcaata ttaatgcaaa a          331
```

<210> 262

<211> 687

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (537)..(687)

<223> Area matching Drosophila EST AI454966.

<400> 262

```
gagaggggata atgggagatg gcgaatagtg ggaaagagggc acctgaaata gataagcaat 60
gagcaccact caatttaata tggacaactg ggccatttta agaagcaaata atgaatttc 120
aatttagttg tatattcttg agattaaatt atttagggta gcacaatgac acacatgcag 180
ggatgatgggc taagacaaag cctttaagag agagggagag tttgttgacc tcattctcgg 240
gggggttgagt gacctgtttt cgagtagttt tgagtgattt gttcccagtg tccaggtagc 300
ttgatattaaa ttagactggtt tattataact gcattgtggc ttttatatgt tttacacaaa 360
ccattcctaa gcgcctacc tatatcaata ttggtttgag agcagttgtg ctctcttaca 420
ctcaagtagc tcttttaatc tcttccactc attcgctact cagtcgccat tttcgccga 480
gcgctgactt tctgcggtg ctgcttctgt tcattcgtgt gttggatttt gagatgcgtg 540
cacagctgaa aagtaaaata atgcaaacgg ctgtattttt tatatcttcg ggtccactgg 600
gtacatacaa atgaaaagggt gcttgctgtt atatacttcg aaattatcac gtttgcgta 660
gaccgaaatt gaagaaatcg attactc                                     687
```

<210> 263

<211> 441

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (10)..(441)

<223> Area matching Drosophila EST AA202767. This EST
forms a 715bp contig with ESTs AA201231 and
AA392823. Sequence similarity to Rat NUP84 gene.

<400> 263

```
agccggggcaa cgaattgaag cataaacaaa cgatgtcgtc caccgatgtc ttggaattga 60
acaaaacgga gttgttcgag aagattcgca atgggttgcc cgtgggtgcaa aggactcaga 120
acctgctgga ctgcaaggac gatctgctct ttgcctggca cgcaaggac agctgtctgt 180
```

tggttcgcaa ctggcgctca tcgctggcgg caaagggtgaa tatccagttc cagacactga 240
 ttccatcgag cttggtgagc ctggaggtgg accgcgtgct ggcctccaac gagggctccc 300
 tcgtggcact aagttggacc gcgcggcggt gtcataatgg agctgccccg ccgctggggc 360
 cccgatggat actacaagga tggcaagcca gttgatcacc tgccgcacgt tcgggctgga 420
 cactcagctt ttcctaaaaa a 441

<210> 264

<211> 40

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (3)..(40)

<223> Area matching *Drosophila* EST AA201212 (inverted).

<400> 264

cccagtcgcg gcgatatac ttcggtacta cggattgtgg

40

<210> 265

<211> 564

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(33)

<223> Area matching *Drosophila* ESTs AI404994 and
 AI260898. ESTs show evidence of alternative
 splicing.

<400> 265

atctcaacga ctctacttgt tattttacat aacctgcacg gcgctaaaat gagcatgtta 60
 tcgataaaat atcgatgcaa ggcgtgcagt taagaaattt atttaaaaag gtataggtga 120
 atacctacaa atgtaattca tttaagttac tattaaattt tttctgacta tataaaatta 180

aattaaatcc tcagaactcg atatgtcgat atgtaacagt gcataactac gcttattggt 240
acaggggtgg ataggctaaa gagaattgcc cgcataatth atttttaaaa ccattttctg 300
ctaaacgtgg tgttaaatat ttatttattt aatttaattt atgatttatg atttatttta 360
ttaaaagctg taagaattat attactgatt tctatgataa tcacgaagcc tatacttttag 420
cggttattca ctgtgctgcc tatcggtatc gaaagctttg ccggtttatt tacattttgg 480
cgcattaaac caagcaaattg ttttaaaaaa cctcaatttc cgtgtttttg cgccacagca 540
gcagcacaaa agaattcccga atcc 564

<210> 266

<211> 404

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(292)

<223> Area matching *Drosophila* ESTs AA539914 and
AA201959 (1042bp contig).

<400> 266

gtctcgtgtg acgtgcgagc gcagaaagtg tcgtcttttag attttgtttg tgcacttttc 60
gccatttccc tttgtattcc gtcgagttag gaacagcggg agccagggag cgcaagagtt 120
gccgagaagc acctgcaaaa tagcggcacg agatcgccag aaaaccagaa aatcgcaaga 180
agcaaaagcg accgggtcaa cacttccaca cgcaaatacc cagagcccc catcacacac 240
acacacacac aaacatccaa cacttggtgc agtggtcgat gagaaggggc accacagcga 300
taagaggaga agggacgaag gagcaggaag aagaactagt tgcctaagaa agacaccacg 360
cgcatcttgc tatcagcgaa ataccactg caaacgttta gaac 404

<210> 267

<211> 454

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (36)..(454)

<223> Area matching Drosophila EST AA440953.

<400> 267

```
ctctagaaag acaacaaatt ttttggcgag cggacgtgtc ggcggacaaa aagcttgcaa 60
acagaacaga acggaagaac acagaagaga acgacacgac acggacagcg gggaaagggtg 120
gcaattgaaa gaaagtgcc a tacttagtgt gcgagcgaaa gagagagaga gcaaactggg 180
tattgcttgt gtgtgtgtag tagtttagtg gtcgtgtgtg tgggagtttg tgtacgaagc 240
gagtggcaaa ggaaaacaca acaaacatta ttccaaggaa atttccaatc atgtcgggtgg 300
aatcctccag ttcggcggtc caacagccgc cgtcgtcctc gaacctaccg ctcttgggcg 360
acaaccaggt tggttggcca cgaaccagct ccgcctcctc gggctcttcc tcttccacat 420
cgtcgtcctc ctctccggt ggcggcgca tttg 454
```

<210> 268

<211> 253

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (145)..(253)

<223> Area matching Drosophila EST AA264591.

<400> 268

```
gttcggcgct cagttgcgaa tctgcgacca aaacgtttgg agtttctcag gtaagcactg 60
gactctggga actggttttc gctgttatca gtgcgaccag ttgcactttg cactttgacc 120
tgcattcttc acaccagtca cattccaggc acatctctgc accaccggca acatgattct 180
ctccaagccc ctgtactcgc tcttcggcac ttatctggag cagctcttca accaccgggt 240
ccgcaccaaa tcc 253
```

<210> 269

<211> 380

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (47)..(380)

<223> Area matching Drosophila EST AA539491.

<400> 269

```
gtttcggtcg tggacatgaa cggcattacg tttttcaact cggccgcgcg aataactcga 60
aaaaggcagc tccgcagcca aggcattttg aaaaacacaa gtccccgact cgaaacgcga 120
ccaaatattc ggtgtgtgac gcgaactgcc aatgcaatag ttcacttaag aattgcagat 180
taccgcgact ctgggcagtt ctcatcgat atttgaatgt accaaaagaa aagtgccaga 240
accagaaaac aaaataaaaag atcttctaac agaataacaa gaagtgtttc ctccgaaaga 300
ttaaaaaatc gcgaatgatt aagaatcgcg gcaccgtag ttccctctct cgcttttccc 360
ttttgcgctt ttctgcgttg                                     380
```

<210> 270

<211> 398

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (202)..(381)

<223> Area matching Drosophila EST AI403737 (inverted).

<400> 270

```
ctctgttcgc caaccaaca acaaatcaaa atatcagtgg tggggcgaaa aaatgcgatg 60
agccatcgat agttcgataa catcccgaga acaatctagc ggatgcaatc gaatttaagc 120
taagtgttaa atggttgtaa atattacaaa tgtaatctta tcatgttcag ccacacatcc 180
ccaatcaacc tgatacagta ctttaaatat gacgtaattt tttaattatg cagtgaaaaa 240
gttacatcgt tgtgcactaa caaaagaaat accactcaaa gtggttaagat cacgaataaa 300
gctgcgtata aatattaaat aatttacgtt gtatttttgg taatgattga agaaacattc 360
gttggttaaac gaataaggcc tcacaaggct tggcgatc                                     398
```

<210> 271

<211> 496

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (270)..(443)

<223> Area matching *Drosophila* EST AA567141 (inverted).

<400> 271

```
gctaaagccg tttttttctc ctgctttttg tttttcgtct gctttcgtgg ttctcatcta 60
caacatggca catcagtttt ttttttttta caatgtcaat taattctata cttccatttc 120
gaatgttttt tgaatacata acatacatgc tattttcaga caaacccaat ttattctgtg 180
tttctgccat gtgcttcaag tgttgccctc ttttcgcttc ccttgcttta aatccggcga 240
ctgtacagta gttcagaatt tatgcttact taattgctcc ttctttctct gaagtgtgta 300
cgaattggtg aatgccgcgc aaatcaaaca ctctcccg tcaatcgctt ttaggcgaa 360
taaaagtgtg aataatgcca acagtttggg cagttaaaaa atcggagata tctccccgcg 420
acacaaaaag ccgtgcggac tgcgcgaaac accaaacagc aactaaaatg agaaacacag 480
tccoctgctt aaatat                                     496
```

<210> 272

<211> 546

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(478)

<223> Area matching *Drosophila* EST AI134670.

<400> 272

```
cccgctgctg tggagctagt aaatttcgtg ctggcgctc atttttattt tagttaacga 60
aacgaacgaa ccagcggcgc gctaagaaat ccaagaaata ctatagcaaa aacactcagc 120
cgaggcggaa ataattttgc tgtagttctt ttttctagc gtgtgtgccg tcgaaaaaaaa 180
aagatataat acaaatcaaa tttataataa ttttctcta tgcgagtacc gaaacgaaat 240
caatgagcaa agaatcgtgg gttttttttt tgccattaa cgaacaatta aacgaactct 300
```

ctttgttatac agtattgcac aaataaataa aaccaatca cacaacgaac aacgaaagtt 360
 agtaaagaga ataccaacga aaaagttgaa aaagtcagtg agttgaaaaa agttaaagtc 420
 ctgcaagttt gaaaattgcg gaaggcagaa agtaaagtct atatgaaaat atacttgtac 480
 atattttcta cagcctgtgt gtgtgtctgt gttccgaaaa gcctctcatc ccaatctgaa 540
 tcttca 546

<210> 273

<211> 534

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (413)..(534)

<223> Area matching *Drosophila* EST AA263763 (inverted).

<400> 273

ctacgtacta tttttctcca cataatatat atgtattaat actagttaga atatgaaaga 60
 actgtttact caccagagcc tcgtgacccc aactgttgct cttttggtga tccttgagca 120
 gctgcagcga tcggagaacc acttcgcccc gttccgtcgc gtagatgttt gtgtactccc 180
 ttaaattttg ctccaaccag tgcgatatgg tgtacagctc ctgcgcgctc gtttgcgaaa 240
 gctgccggaa tgaggtgtat tcacgctgg aatcgctcctc tatgtagata agatccagca 300
 actccaaccgg cttcagcggg gcactgtgct tcttgaggag catactatag tgctgactca 360
 ggccttcgca gccgggtgtta aacaaactgg tgacattctc cagctccacg ctctgggaaa 420
 ttgttgtgcc ggaagtaatc gttggcatcg cgcagtttgg ctagtgcgctc gaggaacacc 480
 gagatgtttc cctccaccgg gcattgatga atcaactggc agacctcttg gaga 534

<210> 274

<211> 535

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(99)

<223> Area matching Drosophila EST AA568011.

<400> 274

```
atcttgacaa aaatttttgc aagcgcataa aattaaacaa attgtagagt tgtggacaac 60
aatcgccac tagaataact ggaaaaaagc gaaaatggtt agtactagac aaacgcgact 120
cacttgctcc gcagcagaga ctttttaact cgcaccaaac cgaagattgc gtctttcggt 180
ttcccgtaga atttgcgcat tttttcggaa ctttcacagt ggcgttgtag cgaccgctct 240
tgggcggcat aagggttaag gggcatgtgg gtggctacgg gtggagggtt ccgaggagca 300
ccccgtcgtg accttgccctc catttgggac tacgacgtca cagctgccag ctccggcgagg 360
tagatacaca tccgaattaa caccacgcgc tccgcacct ccgattcgcc gctctccatg 420
gaagtggaaa tggaattaca gccctttggt ccacatgag gattttacct ggggggtggaa 480
aggaaagggt ctgacatat agcatatgat catcggtatt ataggatagt ttctg 535
```

<210> 275

<211> 449

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (64)..(449)

<223> Area matching Drosophila EST AI107456.

<400> 275

```
gggtggacca cccttataag cgggctctcg ggccgcaaga ctctcataag cattcaagag 60
ttgcttaogt tcggttcggt cgcatttctt ctctatctta tataatatta tattttctcc 120
taaatacaatt ttttctact caacaacaac aacaataata acaactcaac tattctcaac 180
tcggttcaac cttaacttaa ctttctcaaa aacaacaaac tacaactcta ccactacaaa 240
tctgtcaact ttccgttttt aaactgaaac tgcaaaccaa aacatttatt ttctgtctga 300
cgccattga caaagttttg ttttcaaaa acccgaggaa gaaaaattgc cagcccaaaa 360
agatttgaaa ggatacccca aaagattccg ttcaaaaatc gtcccccccg ttatgttttg 420
agtttcaatt cccgtgtttg aaaaacaaa 449
```

<210> 276

<211> 479

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (212)..(414)

<223> Area matching *Drosophila* gene Karyophilin alpha 1.

Acession no. AF074957

<400> 276

gttcaattca actagttcgc attccacgac gacctctacc tatatTTTct agattatttg 60
cactttcgtt tagcatttga tcacagtagc ggcgaaaatc aagtcgcact cactttttat 120
ctgaaacctg tctttacgac ttaaattatt ctgttctcaa agaaatattt tttttaacta 180
tttcaagctt ttgaattgcc aagacgacga aatgtctgcc agccacaaac agcggtataa 240
aaatgccgcc ttggactcca cagagatgcg tcgtcgtcgc gaggaggtgg gcatccagtt 300
gcgaaaaaac aaacgcgaac agcagctott taagcgacgc aatgtgggtc ttgagccggc 360
tacatcctca acatcagccg gagtggagag caacacccga taacgaacag caggtttatt 420
ttgatcaagt ttgggctgat agcatagtct taactatctc tccattccca atgcaggct 479

<210> 277

<211> 533

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(146)

<223> Area matching *Drosophila* ESTs A!295205 and
AA141054. These ESTs show evidence of alternative
splicing.

<400> 277

ctcccgctcg tttgagatcc gctgctctcg caacaacaac aactataact gtagttaccg 60
tctcttttgc atcgttcggt tttcgtttgt gtcgccaagt gattgtgtgt gtgcgtaagc 120
ttaaagctga ctaacaaaac gaaacaagaa aaaatataaa ttataggaaa attgttaaatt 180

tataaccaga aagagagcgg cacttacgtg tgttattgtg tgcgtgtgct ttaaaaagat 240
 ataaaaatag caatagaaag ttattaaagc gttggcaaaa aagtccaacg aacagcgaga 300
 ggaaagcggg gaacgaaata gttaaagcca aagtcgctgc cgacgtcgca cttgaaaacg 360
 tcgcaaaagt ttgtaaacac accagtgtgt gttcgtgtgt gtttttgccg gcggtgccagt 420
 gtgcgtgctg ctagaaaaga gtcaagaagc cgaagaaaag gaagaagccc gaagaagcag 480
 caaaagaagc cgacagcaaa aagtaaataa aatccaatgc ccctggcag aat 533

<210> 278

<211> 506

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (8)..(382)

<223> Area matching *Drosophila* EST AA567704.

<400> 278

gtgccgccga agtggacaca tcgccgcata cggatacggg aacgcatagg gacagagatt 60
 cgaatccggg taatatagcc ttagccaccg atttggaact gcccaagggg ctgccgttat 120
 cgttatcctc gcgacaccac tggaaccagc tgcagagcag tttgcacgcc cttcaccacc 180
 agcaacagca acaacaacag caactacgtt catacagctc cactatcgaa acaaatttgg 240
 aagacaagat gagcaaacc gattcgaaac tagataaata cgcgagcgc gatcgcttgg 300
 gcctttgggg cactggtgac aatgaggtgg tcggcagcct ctccggattc acccgactct 360
 tggacaagcg ctactcaaag gtgagttcca caagtttagga atatgcgaat acgcttttaa 420
 gttgccccag ttccgttgaa cttagtggaa aaatgccagg caaagggttt taagggtggg 480
 ttcgcattcc gttttttttt tccgct 506

<210> 279

<211> 362

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (74)..(224)

<223> Area matching Drosophila EST AA539252.

<220>

<221> intron

<222> (225)..(296)

<223> Probable intron in gene represented by EST
AA539252.

<220>

<221> misc_feature

<222> (297)..(344)

<223> Area matching Drosophila EST AA539252.

<400> 279

gctccagcaa tcaagcaacc gagtatcggc gtcgcttcgt ttcgaatttc agttcgaatt 60
tggatttggt cggcgacgct ctaatttggt taatttttgt tcgttaattg tgtaattga 120
ttagttagtc gctgtgttaa tggaccacta agttagctgc gagcccggtt ctgttttagtt 180
caagttatct ctgttttggc catcccctgc aatgagcgcc ttgaggtta gttgagtcct 240
cttttcggaa ctccggcaat aattttccga gaaataacta gattaccggt acttacagat 300
cacagtgcgc ccatcgcgcc taaagcaaaa gaagcgcgcc gaaggaccga gcccgcgcgt 360
cc
362

<210> 280

<211> 548

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(347)

<223> Area matching Drosophila EST AI260759 (inverted).

<400> 280

gccaaagacga tggcaatcaa cttttcggtt ttgtttttgc agctcgtcgc ttgttgctgc 60

tacacaggtg gctggctggt ggtgctgtgg cctctatttc ttgctatttc tctctatttc 120
tctgtattga tatcgaaatg gatgtcaa at aagccgctcg acgggttttc ttcaggagaa 180
agtgcacgga aatgtgtctc cgtctccgtc tgcgccagct gttcgctatt cttctcgctc 240
cgggtactta cagctccggt tatcgatggg tcattaggtg gtgcacactc atttattgca 300
atgccattta tggcctaatt gatttgcaag ttgcggccaa gaacaagtaa ttttgtagt 360
aaatagaggg cagaatggcc actttgttct tggcgcagca tctggcaacg ctgcgggttt 420
tgtttacttc gataaggccc cttttacact agtttcgaat tatcgcaatt gggaatatat 480
ttcgactata tcttttttat ggcctaatat gcaaagcctg aataaataat tgatttaagg 540
aacatact 548

<210> 281

<211> 199

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(77)

<223> Area matching *Drosophila* EST AI260646 (inverted).

<400> 281

ggtcagacgg aacagcgcag acatcgcggt ggggaagaaa tttcagtcgc aaatttcgta 60
aataatcgag ttttcccttg atcgctggac ttctgacagc tgcgcagtgt gaacgtttgc 120
tgcaatttgt cagctggccg agagggtagc cactcgatgc ggtatttttt cgggtatttta 180
cctagaaccg ttttaattt 199

<210> 282

<211> 310

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (160)..(306)

<223> Area matching *Drosophila* ESTs AA202424 and

AA264609. These ESTs have sequence similarity to
Rat hydroxymethylbilane synthase gene.

<400> 282

```
gtcccgacat tgcggctgca atatccggga tagcggggccg cacagggggcc ggcaaagtcc 60
caacgcacac ttttcactcg gcaaataagg gggcatcgaa ggccaccggg ggcagaaaaa 120
gtaggaatgt ctaatttact tgcttcaatt gtttctccag gacgaagatg gtggcgatgg 180
acgcatcgtc taggcggaat actatgccct caatgacgaa acctttggat ccgctataaa 240
tggcgactgg gaggaagccc atgagactat ggtacgcctg ggcgggaatg gcgaaagggt 300
gcggaagcga
```

310

<210> 283

<211> 429

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (300)..(379)

<223> Area matching *Drosophila* EST AA802555.

<400> 283

```
cactggacgt ccacacaaaa attgtactcg cgacgtgtga gcgtgacgca tgctgtacac 60
tcttaaccac acttaaata gggcaaagca ctctcgcccg cagccgtgcg agtgagcgag 120
atgactatac aagcagcatc tgggcatagc gaggcagggt tgctaattgcc agtggtgtac 180
aaccatcggc ggtcatcgtg agtgggcccg ttatcgctat cgtcgctcag ctgttacgta 240
gcgtgtttgt tacgtcgtaa attttgtgog gaaaaaccgc agagttttca ttgccgccgt 300
gaaaaaaaca taaataatgt ctgtgccttt cagtggcgca ttgcggcggt ccggcggcgt 360
tgtgtccgcc attggcaagc agctgaagag cgtgaatttg aagggcgta agcgggataac 420
cgtgcagtt
```

429

<210> 284

<211> 573

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (322)..(573)

<223> Area matching Drosophila ESTs AA802438 and
AI063681 (1030bp contig).

<400> 284

```
ttgagaagca atggccgctcg accaattgcc aggggttgcca gacatgccaa tagaaatggg 60
gaaggaagag cgcttttggg tgggtgttggg gtttttcaaa ttttttttc atttctttt 120
ggaggtgcaa ggatgggcaa tcttcaacac aagtattgtt ggggcaccca gcaagtactc 180
ataagttttg ttgttgcaag gaaggggtga aacagatagg gagagagacg gagacagtcg 240
agagcgtaaa aataaaatgt gtactaggca cgattaatag ttgtagttgc acttccaag 300
actcaaacac acaattatta ttaaatatat atatatttat atatatatat gtgcacatat 360
ataagtgggg aaacaaatat aactttgaat gtcaaggggc gaggttaatt tgtgggttat 420
attttcagag ggggggtttt aatgggtcctt atttcgccaa tttaccgcca gaagctgcaa 480
gaacttggtc aatttgccc tgctgcgata taggttcgcc aacatcaagt tcaactgctga 540
taaaagctag ttctttgcgt aaaatgcgaa ttc 573
```

<210> 285

<211> 470

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (34)..(470)

<223> Area matching Drosophila EST AA438500 (inverted).

<400> 285

```
cacatgcaca agcacgcaca ctgcctcgtt cggcctgcgc tttgtgtatg tgtgcgagac 60
tcttcttctc tctaactgta gctgtagttt ctttcgcttt acgaaaacgc agaagatttt 120
cactttttat tggccccact cgctttgcta attattaatt tagctacctt aatttattca 180
gcaatcacca gttttcaatt gctcaacaca caaaggcgga cgcgacacg aacacgcaca 240
catctcgaag tcggacacaa aaggagtggc cgtcgcagtc ttgttcttcc agtgtctgtt 300
```

gttggtgctg ttcttacgcg ggccgaaaac tcccttcccg tatagttttt tgttagecct 360
tccaggttc cataactata cggaagttat attggtgatt tgggttttat ctaagccgct 420
ttcagagcaa cactccgaaa attaatactc ttgggttttc ccttcgcttt 470

<210> 286

<211> 444

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (14)..(153)

<223> Area matching Drosophila EST AI456286

<220>

<221> misc_feature

<222> (216)..(348)

<223> Area matching Drosophila EST AI456286

<220>

<221> misc_feature

<222> (419)..(444)

<223> Area matching Drosophila EST AI456286

<220>

<221> intron

<222> (154)..(215)

<223> Probable intron in gene represented by EST
AI456286

<220>

<221> intron

<222> (349)..(418)

<223> Probable intron in gene represented by EST
AI456286

<400> 286

gtgctgtgta taaattgttt ttaggacctt ggctaggaat tactgggtgc acacactcag 60
cgccacagct ccaccgacca cgcaccttgc aaggacccac catgaactcc aaggacaagt 120
ccaagttaa gttgttcctc aaatcgctgc cggcaggtaa caaagtgggt gcaccattgt 180
gggcaagata actcaattgg gattccgggg attcacaggt tacgtgggag agcggaccct 240
gcggccggag ttgagaggg aactgcgtcc ggagcagccg gtggcccagc gctgccggat 300
gctgaaagag ctgggagaca cgcagctgca caacttcaat ctggacgaag tgcgttccat 360
cgaattgccg ccatgccatg aacatgtttt tatttctcgt taattcgtcc ccacagaacg 420
ccatcaccat tctgttcaat ctca 444

<210> 287

<211> 512

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (41)..(56)

<223> Area matching *Drosophila* EST AI062265. This EST
forms a 1475bp contig with ESTs AA694862 and
AI064128 and has sequence similarity to *C. elegans*
UNC51 gene.

<220>

<221> intron

<222> (57)..(222)

<223> Probable intron in gene represented by EST
AI062265.

<220>

<221> misc_feature

<222> (223)..(353)

<223> Area matching *Drosophila* EST AI062265.

<400> 287

```
atctgagtgt caaggggacg ctcagcgagg ataccgtag actcttctc gtgcaactag 60
gtgagattcg aaaatcctat ataaggggta gccctaacta ataattgtaa aagatcaata 120
taaaatgtaa cattaatatt actttagaac aacgaaatgt attataatta actatcagaa 180
gatcggaagt tatagtatac cattatttcc atttcgtaa ttctagctgg tgctatgaaa 240
gcactttata ccaaaggaat tgtgcatcgt gatctcaagc cacaaaacat tctgctatcg 300
cacaattatg gcaaaacatt gccagctcca tcgaaaataa ccctgaaaat tggtaagtct 360
tgtaatcttg taaaatctaa gaaacaaaat ctgttacctc ttttgaaagt tgttacttaa 420
aaaactggtt attactacga aatcttcatg ttaatcaaat acttccactg ctacttgta 480
cttatactgc ctgcaacttt tctttattac ag 512
```

<210> 288

<211> 465

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(429)

<223> Area matching *Drosophila* EST AA247020 (inverted).

<400> 288

```
gcgtgggtgca cctgcggccg cttaaagatg aagaggaagt ggagtggag gaggaatgga 60
acaggaggac caggagccag gaggtctctt tctcttcttt ttctcgttca atgacacaga 120
aatctttcct ctctgtcttc gctttgtgcg ctcttcttc caatatacaa gcgagctttt 180
tatatgtgcg agtgcgactg cgaggccatc gctgcgttta tctccctctg tctgtgtgtg 240
tgtgcgtttg tgtgtgttgg agtgcgtgtg gctacacaca aagtaatatt ttcaagcacg 300
tttttcatgc acttcgagcc gttttttgtc tattgccgca tagaaaacga ataaacgcca 360
ctttcatcta caatttggtg ttacaattcg tgcattttg tgcacttttc actatcaaaa 420
accgtttaa tctgtttcac cttgcgacaa gaaaaattac acacc 465
```

<210> 289

<211> 285

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(143)

<223> Area matching Drosophila EST AA264635.

<400> 289

```
gccagtagca gcaacaattc cagttccacg gacaacaatc acggaggcca caatccgctg 60
aaccgactgt cctgaagtc cgccggaaag cgtaatcagg agagcatgtc gcattcccag 120
ccgaacggcg gctggataaa cggttaaggcg gaaaaccggg aggaaaatca tctaaggagc 180
cgactgtttt atggttggtc gagagggggg ggagggcacg gcaggtgcac tgcgtctgtg 240
agttattgat ttttcacaca acttaagcag tgtcccaggg gagcg                      285
```

<210> 290

<211> 575

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (58)..(491)

<223> Area matching Drosophila EST AA201749. This EST
forms a 877bp conmtig with EST AA803278.

<400> 290

```
tcgtggccct tatgtttcct gcaatcgatg tttctacett cactttcggt tccggcggtg 60
tgcgtaagtt gctccgcgtt ttcgcaattt taagcgatta tcactttggt tgaactctag 120
gccggccatg tgcctataag ttaacagcaa agcatatcgt cgccattggg accaaagtaa 180
ctctcaaadc tggttcaatt ttaatccgta gaaattttac atcatggaca attctggaaa 240
taaccgctac gagctgttgt tcatggacga cgatgactcc tctgggctcg cacagcccac 300
agattgccgc tgtagtcgcg gcgccaaga agccggaacc ggcaaaggcg ccaaaggcac 360
caaagagcaa gtcggagaag gagaacaagc cggttggtgg tgcccgaag gccaacgctc 420
cgggtggctaa aaacgctagt ccagtgaag gcggcaaggg tcccgtggc ggggatgtgg 480
gtcgtcccaa gaacccaaca gcaaacggtg ccaacaacca gggcagggtc aacaacaacc 540
aacgctacgg aaataaggag tcgaacggag aattc                      575
```

<210> 291

<211> 460

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(162)

<223> Area matching *Drosophila* EST AA392551.

<400> 291

```
cactggcccc aagacgttgg aattttgtga attgttggtg ctgcagccca gcaataacgg 60
tacagaggac aacagtatca gcaacaaata caacaaaaag gaatgacaaa gtgaaaccga 120
ctgcgctgcc ccacaaacta cgacaacatt aataacaata ataacaaaac gaaataggaa 180
gagcaaaact gtgatctctg cttaactttt tttatTTTTT gggcaattgt tcaatttggc 240
tgtgctcaaa agtaaattaa gtcaactcgt tacgcgtatt tgcggtgttt ggcaacgctt 300
tttccaaccg acgactggaa aatcaattct tcggattgcc aaaggggaac aacaactagc 360
agttgttgaa gttttccttt atattttttg cggcccaccc caaaacaaaa agcctagttt 420
ttagaagaaa gaagaatgga agaagaaaga aagaaccgcg                                460
```

<210> 292

<211> 473

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(379)

<223> Area matching *Drosophila* EST AA438539. This EST
forms a 1200bp contig with ESTs AA201773, AA263752
and AA439563. This contig has sequence similarity
to Human ERF 1 gen.

<400> 292

ggtagagtg taataatgaa ataaccagtt ttogaatttc gttcacaaca aaagtgcggg 60
 cctttcatgc caaaatactt tggtttcgaa ttgtttttca aattcgaatc gaggttttcc 120
 agctttccag tttgacagcg agagaacgaa agagagcgag ggcgaattac ggtgttcgcg 180
 ctctgcttgt gctttccact ccactcccct tcttaacttc cccccacca gcctatatac 240
 tctgtgtgca tgtgtaaatg aatactttta aacgttttta atcgttgagc tgtattcatc 300
 gccagccacg ttaaaaggaa gaacgtgtta tgttgaatac gaccatcaga agatcttagc 360
 gaaaggattc caggagccca aattcttaat ccccatccca cacacacaca tatactcgca 420
 cgtaggcac gctctcttgt tgagaagaaa gggtttaaat taaagaagcc acc 473

<210> 293

<211> 446

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (297)..(446)

<223> Area matching *Drosophila* EST AA141715.

<400> 293

gccttaccgc tttttattta tttttcttcc tgtttgttta agttccctct tttctttgct 60
 gattgtttcg ctttctgctt gccagtgtga gtgcaggagt aactgtgtgt gggcaatgag 120
 ctctcttttc gtttgtcttt cgctgtcgtc tgtttatgta tatttaatgg cctgacttcg 180
 aaattaaagc caccgacatc ggatgacgca ctggtgactg ggcctacaat agtggtagtt 240
 gcgctgctca cattcttgtc catggcgaaa tatttctttt tgtagagtta ctttgagtta 300
 cgatcacagg gtgcctagtt tcatgcgaat agttgccaat tgtgggcaac attaaaaata 360
 aattaaccga attggtctta tttgcctcta atttgcaa atcagagttg aagaatgtgt 420
 agcgaaatag gtatctcaaa aaccgc 446

<210> 294

<211> 161

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (80)..(161)

<223> Area matching Drosophila EST AA695862.

<400> 294

atttaactta accacttata attgcctcct cgcagtccca tgtaactca gtttactgcg 60
aggcgtcgag gcgttcgtac ccttagtat cagtttcacg gtcgttggtc gttaagaacg 120
catttcacaa ctggcaacaa ttaagccaaa ttaattgtat t 161

<210> 295

<211> 132

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (2)..(132)

<223> Area matching Drosophila EST AA201517.

<400> 295

ctcgagaaaa cgtgggggttg aaaaaccttt gagcaacgtt gtgccaattc cacaattaaa 60
ccgcagagtt tgcacaattg gcggttacac ctcatgtct gcccttattt accaaaccca 120
ttaaccgaat tc 132

<210> 296

<211> 238

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (176)..(238)

<223> Area matching Drosophila EST AA202297. This EST
has sequence similarity to vacuolar ATPase genes.

<400> 296

ggctagattg accagcaaag cagcgaagag gaggagagaa gaaagcggga gagaaaagag 60
aaggcgaaga gaggacggca cttagttggt gttttgaagt cgaactgggt tacagttagc 120
agtttagcagt tgcctctcag ctggctcagt gtttttttag tgttcgagct gtgcgtgtga 180
actgtgatat tgcgatattg ggctatcgca attggaaact ggacttttgg ttgaattc 238

<210> 297

<211> 51

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(33)

<223> Area matching *Drosophila* EST AA567483 (inverted).

<400> 297

ctctgggggt tgcgccgct ttctgagcgt cacgggtgtcg ttccggaatt c 51

<210> 298

<211> 468

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(209)

<223> Area matching *Drosophila* EST AA817479.

<220>

<221> intron

<222> (210)..(270)

<223> Probable intron in gene represented by EST
AA817479.

<220>

<221> misc_feature

<222> (271)..(468)

<223> Area matching Drosophila EST AA817479.

<400> 298

```
gttcacagca cttaaaagaa cacttgggaa aaacaataaa aatatttcgc aaattatggc 60
gaagcgataa gtcagccaaa aattgaatcc atcggagcga ctgccttgga gccacagccc 120
acccatgatg acgaccgact tcgcgggcag ccagttcgtg tccagcaatc ccaacaccag 180
ctgtagtgca tcccgtctggc taacggagga ggtatttgca tggatatgca atttgaaaat 240
gatttgattc acatatttct gttgttctgt aggtctttaa actaatcgaa attgtgcagc 300
gcgacgaagc catctacaat ccgaagcaca aatactactt ttgccgcccc gtacgttgga 360
aaacttttgg cagaggttga tttgaaactt ggaaaagaat ccgggcgccc agtctggcca 420
attggaacaa tttgcgcac tcgttccgac aaaaattcac cactatct 468
```

<210> 299

<211> 365

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (17)..(139)

<223> Area matching Drosophila EST AA441327. This EST
has sequence similarity to Rat sodium dependant
dicarboxylate transporter, AB001321.

<400> 299

```
gtcgcgcatt tcaccgtttc cgaatcggac gaaccgggcg tgattgctct cctgctgctt 60
tcgagatcga gtcccagataa ggatataact acaacctaaa gaggaatcca agcctcctcc 120
tgccgctagt ttcgaaaagt aatagagta cttgttatca actgggaagc ggagatacat 180
agctccgata ttctgtgaa agccagacaa acggatacca acgaacaatc gccatgtgcy 240
tcgtcgtccc ttctcgtttc acacatcgtg cgataaaaat accgctttgc tttttgtgtt 300
tatttaaaaa ttttggttag gaagttgaac tccaactcct tgacgtttgc attttcccca 360
ccacc 365
```

<210> 300

<211> 432

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(391)

<223> Area matching *Drosophila* EST AA698011.

<400> 300

```
ccgtcgcttt cttcgcttat cgggtgtgtgc gtgcgcctgc ctacgtgtgt gctgtgcatg 60
cgatttgtgt taacaaaatg tgattagcaa aaatacaaag aaatcaggca tagtggaaca 120
aggcattgtg gctgaaacaa cagtcggcgg cagtaacagt cgacactaaa aaacaacaaa 180
atatacacat atacatatat taataatagt acatacgaaa catatctttt gagatataca 240
cgaaatgcga aaatttgcac aaaaagcaat gcgctggcgc ggcaacaaag cgcggccgta 300
aaaaaataag ttacgccaac gacaattctg aattttgtgc tttatccgca gcagccagca 360
caattaaatt aatatttgaa ctacccccaa agttaacaaa agttagccag cccattaaaa 420
aaaaatacac ac                                     432
```

<210> 301

<211> 207

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (67)..(207)

<223> Area matching *Drosophila* EST AA951986. This EST
has sequence similarity to Human nucleolar protein
p40 gene.

<400> 301

```
gtgtatctca ataatcctcc cagtaagccg cgtgaaggtc aactgcaac atcgatagcc 60
```

gatgactagg ccagcaacaa tcgataattc ttacccccgc acgtgttgaa attgttttct 120
tttatttgga tcagatttaa tttagctaata ccagacatgt cggactttga aatggaggac 180
agtgcctcgg gctacgactc aggggat 207

<210> 302

<211> 186

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(186)

<223> Area matching Drosophila EST AI295731. This EST
forms a 2018bp contig with ESTs AI258429,
AA696170, AI109519 and AA391348, and has sequence
similarity to Mouse APG-1 gene.

<400> 302

ggccggacgc tagaaatttc cattcgcagg cgaaaagcga atccataatt gatgtgaatg 60
tgagaagcat atatcgaatc gaatgttctg gacttgtttg tcaaacgaaa agaacagatt 120
gcaagccgac acgtgcgtgg ctgtgtgttc agtatacatt atatctaatt cccgtctccc 180
ctctct 186

<210> 303

<211> 82

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(82)

<223> Area matching Drosophila EST AA201430.

<400> 303

agaccgacca actggaggcc agatacagat accatcattg tcatttccca attgaccaga 60

gaaagaaacc tgctgcgaat tc

82

<210> 304

<211> 54

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (15)..(54)

<223> Area matching Drosophila EST AA263209. This EST
has matches Drosophila ARP gene Accession number
AF132912.

<400> 304

ggccacctaa cgccaacaat tcggggacaa aatcaaatcg catgcaaaga attc 54

<210> 305

<211> 1004

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(140)

<223> Area matching Drosophila EST AA541045.

<400> 305

ccccaccgc agccactcac acacgcaaac atgaggctgt ttgcggcagc aacagttgcg 60
cttgtattgc ttctgggcca agcagctggc gaggagcttg cggaggagcg agcgggacag 120
gcacagggcg atgcggaggt gagtgtgcgt gtgttgtttt gttatgattc agcagcgcg 180
ctatttccac atcaaaaagc tttcggggag caaaaagtaa cgtaatcccc ttcaaagtga 240
ctaaggcttg tgggcaggga ttacggttcg acattaagcg ggaaatatgc aattttacag 300
ttaactctca ctgcgtctca cccgcttacc caaaaacaca tacacaggag ctcacctaaa 360
ccgaacacac ctatactcac acacattcgc catattggct gacgtccctt gttttttcct 420

ctttgaagta cactgacaag aaaggatgtc aactgtccag cctcagtggc tgaagtgcaa 480
 tttcaacaat gattttcatc ttcaatgaaa tctgcatat tccaaacaaa aaatgtttaa 540
 ttgcgagttt taaaaaatag cccattcttg ctcttttcgc ttttctacgc ctgttttggc 600
 ctttgtttat tctgcgacgt gtcagctggt tgcttatttt gaccgataga accccattga 660
 tccccagact gccgttgttt ttgcaactgc ttcttatcgg ggtattttta taggccccac 720
 tagtccgttt aaaattgctt tgtgcccga attgcgtttt aatttctgcg ttaagtgtg 780
 cttccccaca agcggaaggg gaatttaa attgcaaggct tttttttacg tccgttcaaa 840
 cgcagccact gttttttctt ttgcggaag cctgcaatcg aatgatgcta gcaagtactc 900
 atagggtagt tatgaagctt acgaaagaat ggggatcatc ttcacagcc cactctatat 960
 taagtttgcc accatccgtt ggacattaac ggtcacttag tatt
 1004

<210> 306

<211> 566

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (392)..(501)

<223> Area matching *Drosophila* EST AA390337.

<400> 306

gaccagggtca ttgaccccaa aggattactt tccgatagtt ttgtcgtgca gtattggtga 60
 acttggaat tctttcgaca cttaacctat aaacttgga aggaacgcaa ttagcaaaa 120
 ctactgttct tggtagacagg gggtttaagg tagactaaca aggacaattt tatgacactg 180
 aagccctatg gagtaagaat caaagaactg ctgtattttg gtttgtataa atgaataaaa 240
 cgttctacgc taattgaaga gcattcgaag aggtttgaat acagcgccat agggtagacca 300
 gcttggtggag cattgaaggt atttcttggt ttaagaatga tcacgggatg gtcacactag 360
 aaatacagcc aaacaaaaca actaaaagca tttcgagcgc taacaaatat atatctttcg 420
 acttgactca ttcgcattcc ggttgaccgt gtcgcgcctg cagcatgtct gaaaagccga 480
 ctgttctgat tttgggtggc taagttggtc ccgcctgcac ctctcatcg tcacctgccc 540
 ccgtcccat ccacacttcc gctta 566

<210> 307

<211> 440

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(202)

<223> Area matching *Drosophila* EST AA141555 (inverted)

<220>

<221> intron

<222> (203)..(272)

<223> Probable intron in gene represented by EST
AA141555.

<220>

<221> misc_feature

<222> (273)..(440)

<223> Area matching *Drosophila* EST AA141555 (inverted).

<400> 307

```
tgtagaactt tattttcgat ttagttttgt ttactaataa acttcgttag ctatgacaaa 60
tctacaacgc tggctathtt acgcatcgct ctttgcgatt ccctatctct ccggtgtttt 120
gggaacagtg caaacgccac taactaccaa gtatttcctg cacattcagc ttttaccact 180
tttgctcctc gtgatttttg gtgtgagttt ttggatatga atcaatgcag ataacagctc 240
ttattgacta ctattatata ttaccctcag atatattccg tttggactgt tctatataga 300
actctgactt ttaacgattg tcccagggcc cgccaaggag ctgcaggatg aaattcagga 360
ggctcgcaag ggatttgata tccaagggga tttcggttgc gagattagga gacttccaga 420
acttgtgcat ggtaaattctg                                         440
```

<210> 308

<211> 402

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (158)..(252)

<223> Area matching Drosophila EST AA263730.

<400> 308

```
ggctacacct ggctgcgtta tcgatagttc gggccgatag ttgccgatgg tcagctaate 60
gcagtgaac tccgctagct cacagcaata acacgaggag taatgaagtc gctctagaat 120
ataaataaac aattcattaa ttaaaatagc gacatgggtca actggaggaa gtttatcttg 180
tggttcgccc aggagcatgt cgactttcgc gtgcaggagt ttgattcgct ggtcaaaatg 240
tttggaacttc aggtccggcg gcttacagaa cacaccaggg taaagtgttt tagtaccaga 300
atthttgaaaa cgcaagatta acaaattcca ccttccttat aacttttaaa acctgggggg 360
ttaatgatat atcccaactt gggaatttta attaatatgg tt 402
```

<210> 309

<211> 573

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (324)..(370)

<223> Area matching Drosophila EST AI259832. This EST overlaps EST AA990765 and has sequence similarity to Human ubiquitin conjugating enzyme 12 gene.

<220>

<221> intron

<222> (371)..(447)

<223> Probable intron in gene represented by EST AI259832.

<220>

<221> misc_feature

<222> (448)..(545)

<223> Area matching Drosophila EST AI259832.

<400> 309

gagcagactg ttatcgggtg caaccatoga ttaattacac atategctgg gcagaaacaa 60
ggaaaggata gaaagcactc gaagtgattt ttacatcag ttctattgtt aacggtaggc 120
caaagattca gtgaaacaat tgcccttaaa cactgacat ttcaaacaat gcaacctgtc 180
cctcaagcag caaaagcccc ccagagagcc agaaactttc gagcacagcc aaacgcggaa 240
gacgaaaacgc cagcgagacg aggacgcca gatgattaaa ctattcacgc ttaagcagca 300
gaagaaagac ggcgagcaaa agggcagtca gcagaagaaa gcgtccgccg gccagctgc 360
gcatacagaa aggtagtctt caatccagca cctggtatga tcaactcttg cttattactt 420
atccatcttg ggctggtttc ttccccaga tattaacgaa ctgaacctgc caaacacttg 480
cgccacagac tttcccgatc ccaaggactt gcttaacttc agcttatcat ctgcgccgac 540
gaggctttta cgaaacggcg ctttcgtgtt caa 573

<210> 310

<211> 483

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (75)..(483)

<223> Area matching *Drosophila* EST AI514268.

<400> 310

gctgagctat gggcagcagc cgacgagtgc tctgctcggc acggtcggca gtcattctaa 60
tcgacgcctg ctgatgcgga cgcgctcttc ggatcgaatc gaatcgcctt cgaatggctg 120
gtcgttgggt gatcaagtgt cgcgtgcgct aatcattaat taagtgtctt aggaaaaagt 180
cccaattggc tatcgaaacg ggtttccatc taccagtgc tttgcgagct gccttgccctt 240
tgccggcaggc tcatattgtga aaaagaaata tcgttgccgc cagttagatt tcacctgaat 300
acctgcaatc gaacgcaatt atcataccgg caaatggaa accacaacac ctgtgctcga 360
cctgtgatgc cgcacaactc aactactgtg gcgcctcgaa agcgctctat gcaaatcgaa 420
atcgctgat atgggtgtata tcatggttct ggcgttttgg caattcgctg gcctttcatt 480
tgg 483

<210> 311

<211> 435

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(435)

<223> Area matching *Drosophila* Genomic sequence

AC006562. This EST matches the genomic sequence

20bp 3' to NPS0411. This EST has sequence

similarity to Human molybdenum cofactor

biosynthesis protein gene.

<400> 311

atcatatgga cgagctgcca ggcagcttt cgccaaagct tttgttctag tgccagtgtt 60
aggcagcatt tgaaatTTTT tgccggttga ttgattgtat gggggggggg gggggagcca 120
ccaggggggtt gacgcttcag agctttgacc tgcaaaaaac ctagcagaaa tgaagatgca 180
gtgacagcag tttacttata agtgaatgga gtttaatttc atttatttta gtacagtata 240
caataaatga ttaatatTTG ctatacagat gtaatgcctt gcaaagagtt acaagtgtta 300
taaacattca agcatctaaa ttttgacatt cttagtttgc ttttaaattt tttttttaa 360
ttttacccaa acttaaacad aaaaatgatc aaatacgaga tataaagacc catattaaat 420
accaggccct tctta 435

<210> 312

<211> 442

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(71)

<223> Area matching *Drosophila* EST AA201987. This EST

has sequence similarity to aspariginase genes.

<220>

<221> intron

<222> (72)..(147)

<223> Probable intron in gene represented by EST
AA201987.

<220>

<221> misc_feature

<222> (148)..(435)

<223> Area matching Drosophila EST AA201987.

<400> 312

```
agttgggcca acaacaaggc gcgagcataa acagcgatac caacatggcc ggcttcgtcg 60
cgggtgcacac gggtaactat cttggccatg gcggttccga tccgccgggc agacagccag 120
atgattgatg accgctactt gctctcaggg gctgggaact gcatcgacga aacgaagtac 180
cagcgggtga ttaaggaggc ctgcctgcgc gccacggaga tccttcgcaa cggcgggatcc 240
gccgtcgatg cctgcgaggc ggccattgtg cggctggaga actgcggcta cacaaacgcc 300
ggctatggct ccaatctctg catggacggc tctgtgcagt gcgatgcggc tataatggga 360
tggctcaacg cttaactttg gcgcctgcac cgaacgtagg tcggggtgaa agaaccccat 420
acagttggcg agaccatatt cc                                         442
```

<210> 313

<211> 408

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (12)..(408)

<223> Area matching Drosophila EST AA540020.

<400> 313

```
gttttagtggc gagtttgtcg gcgcgaaacg ctcgttggtc cttttgtttc gaaagagatc 60
ctattcgaag atccccgata cttgcgagga tcgtctagtg caatatatag actagttaat 120
ttacttttgg aaaaataagg acaccagcag ggccgccgat ttgtgcccct ttcttgaaag 180
tcgcaaaaca aaaacaacga cgacaacaac aaagcggaga caaagaatcg acaagtagcg 240
```

ataaacgaaa tcattcccgg ggaaaacctt ggagacgggt gattcactgc caataccact 300
gccaattgga gactgatcac ggcagccatc cttggcgctc ccaataagcg gagtcaccgg 360
aacgcgtggg aagccatatc cggaatgcag cccgccggag cttcgaga 408

<210> 314

<211> 467

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(38)

<223> Area matching *Drosophila* EST AA201670.

<400> 314

ctgtggacgg tcgtcaatgc gtgaatatc ttctatgtgt aagtgggtgtg cgtgtatgta 60
gatttctggt taagaaaagc cccaaaaacc aaagcgcccc gcaaaatata tattgagtct 120
tcttggccca acaacaaatc tgccgccgga ctttcgccgg agggcgagtg aaaaattcag 180
tttctctcct ctcgacgatg cactttggag gctgtgtgag tgtgtgtgcg agtgagtgcg 240
tgtgtgtata catatgcaaa tgattggatg tcgaatcctt gcatcatcat catcttcata 300
aacacttggc gaaaaaccgc aggaaaacgc aagcagccga acaaaaaaag agagcctctc 360
aagacaacgg cagcggccaa aagtgaacgc gcaacaaacg ccggccaagc aggcgcggca 420
attatttata aatctaaagc cgtagcccc cctctctctc cactcac 467

<210> 315

<211> 464

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (15)..(404)

<223> Area matching *Drosophila* EST AA201957.

<400> 315

gcggtggcct ttgtttagt caaattagc gaaaacgaaa caaacaaaaa tcagaaatat 60
 agatcgaatg ctatggcgca cgtaaagcgg tatcggaggt cgtctaagtc ctcggaggaa 120
 ggcgacctgg acaacgagga ctacgtgcca tacgtaccgg tgaaggagcg gaagaagcag 180
 cacatgataa agctgggcag gatcgtgcaa ctggtttcgg aaacggccca gccaagtcg 240
 tcaagcgaga atgagaatga agacgactcg cagggtgccg acgatgtcga gacctgggga 300
 cgcaagtaca acattagtct gctggaccag cacacagaac tgaagaaaat tgccgaggcc 360
 aaaaagttga gtgcccgtcg aaaagcagct gcgagaggag gaaaaggatt atggagaagc 420
 atttggtcca acagaaggcc cttatggggg tgtggcaaaa gttg 464

<210> 316

<211> 477

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(353)

<223> Area matching *Drosophila* EST AA695344.

<400> 316

gcttagacaa tacaattcaa aatgaatgta ggcaagataa gcgttggtcac cagacttcct 60
 gccctcogct cgtgcgcca gtactcgagc gctgcgaaag cggaactgcc ggcttccttg 120
 gtcggcgacg tggatgtgga accaacatat cccagacgg tggacagatc cggcctgcaa 180
 ccacaacaca aaaatgtgct ccttaacaaa ttgccatacc aggaacctca ctctggatt 240
 catttgaccg agaagtacca gagacaggca ttcggccggg atggggccca gagcaatgtg 300
 aatcccaaga tttgcttcga ttcccacgga gagaaagaca gcaggcagggt tatgcaacta 360
 gaaacctcct gaaaatgctg gagaagaacc gcgcgcagaa ggcagaggag ctggcaagga 420
 taaatgcccg tgaagaggac attgcgaaga agatggagaa gttgaccaca gtggaag 477

<210> 317

<211> 451

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(450)

<223> Area matching Drosophila EST AA441018.

<400> 317

```
ggcgggagct gtacatgaat ttcatttggt aaacaaattt attcttaaaa tggtaagaac 60
acggccggtg ccggtgtgttc cgtcgccaga tgtgaacacc gcaacgagac gcaatcccg 120
gcgtcccaag aaacagtcca tcggagctga ctttaagcaca acgataagca aaccggggcg 180
tcccaagaag ctgtccatcg gagctgattt gaccacaata cgtaaaccgg ggcgccccaa 240
gaaactcgga gctgatttga ccacgataat acgaaaaccc gggcgccccg cgaaactatc 300
aaacaaacaa tctttgacag ccctaaacga gccagaagtg tcgcataaga aaatgcgtgg 360
taaaaataag gcgcattaag gtaaaaaacg gtgtcgtatt ccgaaatttc tcgaatgatg 420
cgctggatg tgggatgcca gcacttttga a 451
```

<210> 318

<211> 334

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (301)..(334)

<223> Area matching Drosophila EST AA202301 (inverted).

<400> 318

```
gtatatacta tacgcgagag ggagcaggca cacacaaacg aaaagcctgc ctccaattga 60
ttagtattag tacttcgaat agtattacta tggttattgt tttcatctag ctgaacttca 120
attgtttggt gctgatattt agctagattc ccaggtgcg attactcatt tggcttttgt 180
ttcgagacca ctgtgccaga tttctgggtg agagcgtggt gagtttcgtt tcaactcacc 240
acagaaactg ttgttgcgcg tcgcgtcttc tatttaggcg gctctctccc acacacggtc 300
aactacagt ccaaaaatga acgaatatac caca 334
```

<210> 319

<211> 393

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (245)..(393)

<223> Area matching *Drosophila* EST AA735819.

<400> 319

```
cctaaattgc aacaaagaaa attgtatgaa atatacgaag cgaagagcag agcgaaagcg 60
acgatgaaaa agaggctgct gcttgaaaaa taagaagagg tggaggagca agaagaagag 120
cagcagcagc cgtcgcgagt tttttacacg cgtgtgttag tgtgcataca attgtgtatg 180
aaaaagaata aaagctaata taaagtgtca aacgtaatct tgtatatctc cgtgtttctt 240
gcagcgcttg acaacgaaat ttatattaca tagtaaagtc gaaatacaac aaagggttaat 300
catattgctt aatcagagta ctgcggtttc aaacgtcttc gtcttcccca tcttctaaac 360
tggaatgcac ccaacaccaa acaaccaaaa ccc 393
```

<210> 320

<211> 147

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(147)

<223> Area matching *Drosophila* EST AA440886. This EST overlaps EST AA95395 and has sequence similarity to *C.elegans* UMP kinase.

<400> 320

```
cgctgacgca gcaccaattg cgacattcca aggccagcaa taggttcac accaccacct 60
ccacagcccc accacacaat atcggaatca tgagcgtaga gaagccaaag attgtctttg 120
ttttgggcgg tcccggggcc ggcaagg 147
```

<210> 321

<211> 602

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (76)..(217)

<223> Area matching Drosophila EST AA8033640. This EST
forms a 859bp contig with ESTs AA803683 and
AA803676 and has sequence similarity to Human
Ribosomal L28 protein.

<400> 321

```
accagtgttt cggcaagcgc agccaacttc gcgctatgtc ggctgccata ttctttcttc 60
ttgatttcaa cgagaaaggt ggcatttgcg ttgttctcga tttgggtaag ttctagcggt 120
ctctcagcgt cccaagcgct ccgcaagtgt agaggataaa tgccctgcacc acgtgttgcc 180
gtctatttgg ctgccggccc gctaaacctc ggaggtaaata tgagtttacc cacacgtgca 240
acgcagcggg caaatagtga ataaaatttg aattaattgt agcgaacca taatggactt 300
aatcaaatag tctatattac taagcgaacc tgcgttgatc aataccaaat ttaatatcgt 360
ttctctttct ttgcatgctg cttttcctac tgctgattta catggatctt tcaataaagg 420
taagaacacg tgtggtctta aaatgcgtga ttaattctgt gatgaatgat tgagcagaag 480
agttcttgaa gactatattc atcaccacga ctgatataca gaaatctcgt gctttattca 540
agaaacataa tctaactgcc gactttcttt tagttccatg ttcacctttg gctgctaatt 600
ca 602
```

<210> 322

<211> 1073

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (472)..(786)

<223> Area matching Drosophila EST AI257267. This EST
has sequence similarity to Chick glycine cleavage
system h protein.

<220>

<221> intron

<222> (787)..(841)

<223> Probable intron in gene represented by EST
AI257267.

<220>

<221> misc_feature

<222> (842)..(1073)

<223> Area matching Drosophila EST AI257267.

<400> 322

```
ttttttttgt agagctgata aggggaataaa tcgggccccca gcaacgattt tattgggagt 60
agataagaat accggaggag catcgacgtg gttgtcggaa attaagatga ctgctttaat 120
ctttagtctg atctccaaca tttagaagag ataaaagtca agcacctggt ataaaaaaat 180
acatttttga tgtttgattt ctttacattt tttagtattt caaatagaag caaccatttt 240
gacaacttat gtaattgaag tattttttgtg gtgtactatt ttctaattaa atcgaaagtg 300
cgaaagctca aattttaatta taagaaatac agtcctccaa taaactaaat aaatcttgaa 360
gttttcaatc tgcccgcgga aatgttgggc agtgcgataa ccggtaatct attatcgcta 420
tcgatatgca tgccttacgc catttttagg cacattttga agaagccgct gtttactcgg 480
gtcaacaaaa gttcacgaat tatattctgg attgtgataa gccgggcaat attcgacttt 540
catccccgatt gccgggcatt aaacgtagcg tgtgtgtttt caaatcggaat cacttgtcac 600
cgaaacaccc ccgggaacgg ttggaaaatt catctcgccg gcagttgcct ttgtttttga 660
ctgggaaaat atggtattca taacgaaatt cgcaaggatt gggctgcagg ccgcccgcga 720
gcttagtgtc acgccccttg ggcgcgtcca ggctcgcgcc attcacctga caagccttct 780
agccaaaggt aaggcaattg tttatgcaat agccactgaa tctcaaactg taatccccgc 840
cagaacgccg atacacaaac aaacacgagt ggggtggaggt ggtatccggc agcaatgcca 900
tagtaggcat cttcagctac gccaggagg ctctcgggga tgtggtggtc gcccaacttc 960
cagaacccgg cacggaactt aagcaggatg acgaatgtgg ggccctggaa agcgttaaag
1020
cggctacgag gtgtattcac cccgtagtgg caaggtaatt ggaaagaatg ccc
1073
```

<210> 323

<211> 501

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(75)

<223> Area matching *Drosophila* EST AA539327.

<400> 323

```
ctctgggtcg tcttgcagtt agccggagct gattcgcccg aggaggagca aggcgttcgc 60
tacgcaaacc gctgcgaagc ctgcaaaatc ctggccaccg aattggaagc tcgacttgga 120
gagaccggca agtcgcacga cgtcatcgaa atcggatact ccgttgacga tgtgaagccc 180
aagaagcgcga ctgaataaccg ggcgcagcgaa ctgcgactgc tcgagtcctt ggagaacgtg 240
tgcgagcgag tgttgggagt acaatctgca caaggaacgc tctgacagca cgagattcgc 300
caaaggtatg tcccagacct ttcagacgct ccatggccct tgtggacaag gggcgtcaag 360
gtgggatctg gggaataccc tacgaagctt gtggggacaa gcccccggtg ggaaggtcac 420
cccaaataaa aaccccgatg gcgaaaacct actggaaggg agtacgagga aaccatcagc 480
gactgggtac ttttaagcac c                                     501
```

<210> 324

<211> 468

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (419)..(468)

<223> Area matching *Drosophila* EST AI539327.

<400> 324

```
gtttaaccca tcgccgcca gttaacccat gacttcggcg gcgagtcacg gatggcagaa 60
ctgtgcggaa tcgaaatgcg agttcgaacg cagagtgcgt gaaaatgagt attatgggaa 120
acattgccac aaattgatgc actacgcagt gctaccttta attgaattat taattatgta 180
ccttaatgaa tgcataattg aataataaac tacgtgcaca cccccccaca attgttgtgc 240
gcacggcgag cggaattggt cgccgttttt tttttttggt ttttggcctt ctctcgacca 300
```

gccactgtta acctttaact tttgtgcacc gaaccgaacc aaaccgaccg gggcgaacca 360
atgtttcgcg gtagtaaaca taagttgggg ctcattaagt aatcacatgg aatattcccg 420
cagccaatta aaccaaaaag cgcagaagg gggttgcggg gcagcggg 468

<210> 325

<211> 422

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (92)..(265)

<223> Area matching *Drosophila* EST AI402854.

<400> 325

gtcgaggcgt aacatttcgt gtctttgaaa tgcatacat cgaagtcacc agtttcagtt 60
ccaagtttca gtagatttcg ggacatcgtg cggatcgaac gtctggcgct gcgttcacgc 120
gactcgtagc ctgcaaggaa tcagttacca gtgaccagta aacagtgatc ggtgaatgtg 180
aacagtgact agtgaatgag acagtgaacg agtaacagcc cgaaaattgt tgcatttacg 240
agaaatcgca tggatattga aaaaggtata gccaaagatg tatggtaaac aaaaaaaaaa 300
aaaaaaaaaa cgcgtgccgt tgttttttag atacacgtgg acagtgggaa tttgtatcta 360
gattgttttg gttgggtttt gcttttagca aagtgtactc acccgtgtgc taaatgcata 420
cg 422

<210> 326

<211> 354

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(222)

<223> Area matching *Drosophila* EST AA441362. This EST
has sequence similarity to mammalian proteasome
subunit HsN3.

<220>

<221> intron

<222> (223)..(290)

<223> Probable intron in gene represented by EST
AA441362.

<220>

<221> misc_feature

<222> (291)..(354)

<223> Area matching Drosophila EST AA441362.

<400> 326

```
tgccccgtcat tctccggcag cgacaaacat ttcaaagtct cgcgttattc cagtctccga 60
ataaattagc atgttgaaca actacaacag cctagcgcag cccatgtggc agaacggacc 120
cgctcccggc gagttctaca acttcacggg cggacagacg ccggtccagc agctaccgcg 180
ggagctgacc acaatgggac cctatggaac caagcacagc acgtaggaac tgcggatatg 240
tttatatgca gatgtaccac ttgtttacac tccttttact attcccgcag tgcttccagc 300
accacggggca ccttccgtgc ttgggcattc gctatgatta aggagtgatg ctgg      354
```

<210> 327

<211> 227

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(219)

<223> Area matching Drosophila EST AA202487. This EST
has sequence similarity to Yeast YFY6 gene.

<400> 327

```
gtcgcgtgtt ttatgctcaa gcaattggat gagtacaaaa acgcagagat tttccgcagt 60
cgggacaaca aggctttgaa ggagaagtgc gatataattg tgcacgtggg cggcgtttat 120
gatcatgcc aaaaattgta cgatcaccac caaataacct tcaaggagac ttttagttcc 180
```

gttcgcccag atgtaagcga ggactacaac gttgtcaggt gaattcc

227

<210> 328

<211> 513

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (328)..(455)

<223> Area matching *Drosophila* EST AA263590. This EST
has sequence similarity to human hRNP F.

<400> 328

agctcgactc acttttcttg ttcttgctac ttttcacacg ggtatgacag atctgagtga 60
tggttgggcaa cactggcttt tccagggatg gacacgttta taactgtcgc tgtcacggaa 120
cagtgaagata tttaaaatgt ttctgcttca gtatatttca aattcgggta agatcacagt 180
tagtttatca ttttccttat atttaatttc ttctatcttg cccaaaaaaaa gcaaaaaaaaa 240
aatcaaaatc aaaccttggt tctttttcaa cgggtccacat tgatgctggc tactgccagg 300
cgggtattttt tgatgattta attgcgggtca cactgcactt tcaacttgac cgccgtgcta 360
tttgattaat ctctctgaaa aataagtcaa attaaccgat taaagtttaa aaaaagggcg 420
atattgggaa agttgaaaca gaagcagaat acgggttagtt cttctgggtc cgcaccaagg 480
tgtggacatt tagaaaagcg ttatattggg gac 513

<210> 329

<211> 247

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (50)..(113)

<223> Area matching *Drosophila* EST AA201496. This EST
has sequence similarity to human oxoglutarate
dehydrogenase.

<400> 329

gtccaggccg tgcgctagca ttaacagtc caccactaac gcaaaagttt tcggctgtaa 60
aaacgtaa atttaaactt taagcaagtt tagtgtaaaa ataatcaa catgtgcgtt 120
aatttgcaaa aagtctgcgg ggctatggtc catttagact tagtactgga ttcagcggaa 180
aactcgcatt tcgctgtgtt ttcacttgtc ccacattcga ggtccgcttt tgcacatgt 240
ggaattc 247

<210> 330

<211> 510

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (281)..(510)

<223> Area matching *Drosophila* EST AA391430.

<400> 330

ggctggacga gggctgcacg tgaattgatt gatgatgagc agaactgggtt cgttgaacta 60
gattatggaa ttaatcgatt tcgtactttg tgtgaaataa acttgtaatg accttttgct 120
taatatttat taaagattta ttcaattttt tgttttattt ttaaattgcag ttttaaatta 180
ttgtttgttt acatatgtaa cgacagccct ggtgtttcct gtctaattggc aacgctctga 240
aattgcgcag caaccccatc tggccacact gaccatttag ttttttggtt atgttggtt 300
gtcggaaaaa tcggctgttt tccgtgtgtc ccgtctgcca tgaaaagctg ctaaaaagct 360
aaatataaaa atcagcgcag cacacacgtt ccgtgcctg cattgggtgc ccattcta 420
gggaaattat gtgagtgccg agtcaggaaa acgcacgtg ggtggtatat atccttatat 480
ccttaagtat gtaactgcgc cccgttggtt 510

<210> 331

<211> 432

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(50)

<223> Area matching Drosophila ESTs AI292722 and
AI534704 (inverted).

<400> 331

```
ctgtaagggtt agaatgcttc ttcttaacga tttgtcattc gcctttcttt agagatgggc 60
ttacgcgaaa cacaactatc gcaagccaaa acgaaaaatgt aggggtgttc aggtgcagat 120
aattgttttag aaatacctta ttgattaaaa ataatgttct tgacaaccta gaaataaatt 180
taagtcaatc aagttactca atgtcggtat ggtcacaatg cgtacaatta gttaaattag 240
ttagtttggtt caatattaaa aaaatccttt ttttaattaa aaaatagctt taatattatg 300
tatcggaataa tttaatggaa catagataac actatttata atattatacc gtgttataat 360
tgtgataggc atacacaaat ttataagggg aaaaataagc cagggaagg cggcccaggg 420
tggccatttc gt 432
```

<210> 332

<211> 65

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(65)

<223> Area matching Drosophila EST AA439393 (inverted).

<400> 332

```
aatgagccta acttggtttt tcgatcacac gcggcgacgt ttgtttcaac gataattcgg 60
aattc 65
```

<210> 333

<211> 529

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (299)..(512)

<223> Area matching Drosophila ESTs AA820797 and
AA438876 (inverted).

<400> 333

```
gcgctgtccc aattggaaaa cgaagagagc tcgacttgcg gtaatcgcag cgcagctttc 60
accatacga agacgatgag ctgacgttgt tagaataact tattggaacg tgtccattta 120
gtttgttggg ggcggcgagg gggtagagc aggagagcgt ggtaatcaca tgtatgtcta 180
tgccttcgcc ttactggcac tcacttacac acatacacac gcgcacagct gcaggtggaa 240
aattaaaaaa caagagcgga aagagtgcga tttaaactcg ctggcaagcg gcacttacct 300
tgtttctttt tacgtggcca atagtaaag gtggtcggta tcaatattag cgccaagaac 360
gataacacca aagtagtagg aacgttcgc cgtctcatc atactgaaac ttttgaccgc 420
ccatctccga cagcgactat atgtattttg atttttgtgg ttttgctggc actggctttg 480
gctcgttcgc ttccgttctt tctctggcgc gttttcctgc cttttcttc 529
```

<210> 334

<211> 486

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(52)

<223> Area matching Drosophila EST AA697891 (inverted).

This EST has sequence similarity to Bovine gamma
COP.

<400> 334

```
ggtaaaacaa ttgaaatggt tttctggctg cgcttacacg tcactcagcg gtgcccagtt 60
ggttcacatg ttatcgatgt gaaaactcca gttaagtatc gatagctccg atgttgttct 120
tatctttaaa agaccacctt tttctgcgt tttgtaggca gtatatattc gccgataatg 180
cacattataa ctttcagttt tcaattaact cgacatcgag atctggtagt tttttttgt 240
tottaaaatt tcttgttttg ctttactgg attgaaaagg aactagttga gattcactta 300
ctgggttcgat tgtatttatc gatagattat cgattgtgaa tgggcggaaa aatagctaag 360
```


ctttgaattt gctccacgtt gactttataa cgaaattgct aagaaattgt atgaatataa 420
taatggttta aaatttattt acattttcat aatttttacc attaagttgg atccgttttt 480
aatgg 486

<210> 335

<211> 473

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1) .. (31)

<223> Area matching *Drosophila* EST AA696845 (inverted).

<400> 335

ctccagtctg cccaatgcgc gccgcacacc tcggagccgc aaattataaa caccgactgtc 60
ttcgatttaa cgggctggcc tatcggtcct atcgatgact cgatagtgcg agctggagtg 120
tgaccatttc ttggtaaaag caaaatcgtg aagagtaagt gtgcgatact atcgaactgt 180
catatactca accaaataac atctgaaatc tgtttctcac taaaaccgaa atttccatca 240
gggttaggaa aatatagttt acgcacatca agttgcatag gtcaatccta cgtaaaaaag 300
gctcgatata ggtaagggtg gacctcagcc tgaacagggc ctaatgcaa tacattccga 360
taaatagatg ttatcgataa ccatttggtg tataaccagta aatgctttgt tttggttttc 420
attcagaaaa ttgacatata tttcttagtc tgcctaaagt tccttggtt gaa 473

<210> 336

<211> 384

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1) .. (384)

<223> Area matching *Drosophila* EST AI259031.

<400> 336

atttaaacca aacaaagggg tagtttagag ggttcttcat cgcgagaaaa aggtactacc 60
 atgtcattgc ccacgaccag agccaccacg gccacgacca ctcacgctgt ggtccaggct 120
 gtggaaacgt atattcagaa ccagaatttg cttggcgaga tcgctgagct ggacgacatg 180
 ctgtacgatt tgggtgtccat gcacaaagac aacgagctgg ccctgaaacg ggtgcttgca 240
 gtgcatccac aacctgttgc agacgaacag caagttaaac gtccgctttg gccaaaagtg 300
 tttcacaac tggtctcgt ggtgattgcc gacagtcgtg aggattcggc agcccggcgt 360
 caaatggtgg ccaatttact ggtc 384

<210> 337

<211> 314

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(82)

<223> Area matching *Drosophila* EST AA803464. This EST
 has sequence similarity to Huamn hypothetical gene
 KIAA0258.

<400> 337

cactggactc tctcgcccg ggcgtagatg gccgagtcg cacgcagcag tttcgctta 60
 atttcaatca tttatttact tttttatttg gtcgcgactc ccgtagagt accgtctgca 120
 ggaattgttc gataggcccg ccgatatga tagcagccgt gcgcgtacgc caaccacttt 180
 ttaaagtcc cacctctgat aagtcgtgtt actgaattta aattttcttt ttactctagc 240
 agaatcccag gtaggccttg ggtataagct cgaaacattg tcattgctgt cgcgcacgag 300
 aacaaccaga attc 314

<210> 338

<211> 489

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (169)..(489)

<223> Area matching Drosophila EST AA539974.

<400> 338

```
ccctagcact ctcgcgcact tttggcgctc tcctaggcca attcgctcgc tctttttctc 60
ctctgctctt tgtcgtggtg cgatcatgtg tgggggtccgg ctcgcgctcg ctaaactctt 120
aaccagtggc tttttaacca gtttaagttt acatttgctg gagcgcagac gtgtccggaa 180
agcgaacgga agacaagtgg aacggaacac ggccgtataa tcagaaatca aacagagtag 240
tggtgtcgtc acttttgca ctctccataa aaatccgtct gccagtgtt gttgttctt 300
cttgagtgcg gggttttcat gtatcgccgc cggtattccg ccttcgagcc cagcacaccc 360
cgcgtgggag tgctaccctc tccgccggt caatatgcca acccccccg cgacactgcc 420
gccccgaaaa cgccaccaa ctgagcgtac actttggacc ccaatttgcc gaagaaaacg 480
attgcaaca 489
```

<210> 339

<211> 524

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(46)

<223> Area matching Drosophila EST AA941993.

<220>

<221> intron

<222> (47)..(431)

<223> Probable intron in gene represented by EST
AA941993.

<220>

<221> misc_feature

<222> (432)..(524)

<223> Area matching Drosophila EST AA941993.

<400> 339

```
ctcgagcatt tgtgggacga gctgagcgga gcgcacaaac tgccaagtaa gtggagcatg 60
tggatgaaag gagttcccag aacagtgttg ccaacaaaaa aaaaaaaaaa gttaaaaagt 120
taattttaat agtgtaaata aatatgaatt aaattaaatt tttatgtaaa cagtattagc 180
tttcatgag attaccaaatt tgtgagtgtc tgtgtttgtt tgtcttttaa aaacttttaa 240
agcacataaa gaaatatatt ttaaatttaa ttaaaaagtt cgtaaaaagt aacaaggtag 300
ctaaattaaa aagtttccta ttcaaactag atttggcgaa caaagagctc aagttggcaa 360
cactgacaat gactccaagc gcgaacaaag cgatttctat cgttatccca ctctctctcc 420
cagaagtatc ggttctcaag gccaaatggg aaggggactt cgagacaatt ttccgggtng 480
gagtacaaaa ggataccgcg ggcggtataac ggtgatttta tggg 524
```

<210> 340

<211> 431

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (43)..(431)

<223> Area matching *Drosophila* EST AA803074.

<400> 340

```
ctcccaacga atcgaaatca gttgttcggt gtgcgtgtgt ggaaaaagtt cgagttcgcc 60
gagagaagcg tgaaaatccg atatcgaaac tacgtttttt tttagtcata ccgattggct 120
atgcaaattt aattgcggat ctcccaaate atcgaaaagc caacaggtcg cccctcaacc 180
aaaataaaca caacaatcga gccgcaaatg aaacgggcaa aaacagcaaa ggcaactggc 240
gaaccgctta accggtttcg aaatatccat cgtagcacag tttcctcgtc catataatat 300
tccgattgca gtggatcaaa atataaacac acacactcgc atataaatte gcagatatac 360
gttgtttgtg tgagtttctg tttgtggttc gcgtgaaaaa tagttttgac aaatatatac 420
aaagccacac g 431
```

<210> 341

<211> 589

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(197)

<223> Area matching Drosophila EST AA695870. This EST
has sequence similarity to mammalian/yeast signal
peptidase 18KDa subunit.

<220>

<221> intron

<222> (198)..(267)

<223> Probable intron in gene represented by EST
AA695870.

<220>

<221> misc_feature

<222> (268)..(534)

<223> Area matching Drosophila EST AA695870.

<400> 341

```
actcggccta aacatacgtg tcggaaattt tctgtcttcg tggacgaagc cgagaagttt 60
tgttaaggac cttttcaatt gcatttaaaa aggtattttc ctccacaagc accgcaataa 120
cagccgcagc catgggcgta gccagcatgt tgcagattga cgagatgctg ggcgacttca 180
acagaatgaa caagcgtcag gtgagcagcg ccgctttctcc gggcaatgca cccatatatc 240
atcctgattc gtgccctttc cctcccgtag tcgctgtacc aggtgctgag cttcgccatg 300
atcgtctcct cggcgctgat gatctggaag ggcctgatgg tggtcaccgg cagcgagtcg 360
ccgatcgttg tcgtgctcag tggcagcatg gagccggctt tccaccggcg cgacctcttc 420
ttcctcacta actacaagga ggagccggtg cgcgtcggcg agatcgtcgt cttcaagggtg 480
gagggcaggg acatacccat tgtacaccgc gtcatcaact gcacgaaaag tgagtttctc 540
ggggctacgg atatggaaac caatccagaa agcgtcttta agatgaatg 589
```

<210> 342

<211> 911

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (775)..(911)

<223> Area matching Drosophila EST AA433251.

<400> 342

agtgaagccaa aatgggcat aatgtgattc ctgctccgct tagccgtatc ccgggcacca 60
gccaggcgaa ggagaagcac agcaaggacc tgaagaccct cacctatccg cagctgctgg 120
agattaagga caggcagtct cactttctgt cgttcaagtg agtttttagtt tccacctgtg 180
gagttccctg tgaatttatc ttatttaatt ttatctctat ttagaaagcg tttgcaccaa 240
ctgccggaca agggaaagcg tctgcaggag tcgtacgaca aattactggc cgagatcagg 300
aggcgggatg aagtagagga agcgactcga atgttgagcg gtctcaacat tgtcgaaaag 360
ggcaaaattg ctctcaacaa tctggagtgg gaatggcaga aacacggacg agggcgccca 420
tgtggacgac attctggtac agcgatgatg aggtggagat ggatccgttg cggattatag 480
cgcagggaac aatgcacgag aagaaggtca aggttttgcc tccgccaacg agtctcatta 540
cggcagatga cctggcggat atcgaggagt ttaagaaacc aaccgactcc ccagattccg 600
ctttggcagg acatagtgc accagttccc ttccagccga aatcgtagaa atcgacgcca 660
gtcaagtggc cgcaaagctg agcagggagc tgcctcccga tcagcatgcc ctctacctca 720
tcgataagac ggaacacaaat gtgaatactc ctagggaaaa gtttatgcca ttccgcacca 780
cgaagtccaa tgtccacaat cccgacaagg agcgcgtgcg caaaaagggc aagcattggg 840
aaataacggc agcaactccg acactcatcc agcacaatag aggcccaagt tgggtgccatt 900
ggctgagtcg g 911

<210> 343

<211> 1176

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (718)..(1007)

<223> Area matching Drosophila EST AI297203. This EST
forms a 1122bp contig with AI455195 and AA438815.

<400> 343

ctgtggtcgt tgccgccatc ggagatctta cactgaaact tgaaggcgga ttctgaatat 60
taattcttct tgaaaaaagg cttttatata tatacataga tctatagctc cctcaaaatc 120
attgcagctc attatcaaac atgctttaat gctgattcgt ctgtataaat atttaattat 180
tgtctaccaa gtcattggaa aattttcacc actatgctta ttcgccaaca ctctcggaat 240
attttatttt ttccatgggc tatttgtata atttcttacc ttaatgcca gaccatttga 300
atatttatac cctgtccttt gctgttttgt tctcttatca atgcccttcg cattgacctg 360
agttttcaga tttccttgcc tttggcatca ttaatccctt tcaacatggc caaaagccat 420
tcaaaactga attgttgaga gctgtcactt ggcattttat tgccatcaga tagctgtact 480
cacaacaaaa ttctacgaca acccaaccga caaagccac acgatgatag ttaattaaaa 540
agttgttggc acactcagaa tatcatgcaa aattagcctg gctaactggc cttatcataa 600
ttatcagcaa tccccaaaca aaactttaca acatgataat tattaaataa aaagcaaata 660
accactaaca gtagaaccga attaacattt gtgagctcag aaaacaaaag caaaatacag 720
gtgaaacaaa atgcagcagc atccgtttac taatttatac gcaatctcaa ataatttaca 780
aaacaaatgg ttaaccgaaa gaaatatttt aacaagcttt cttgaggcat tacaaaaatt 840
aaaataatat atttcagaca gagcaagata tctattttaa tattatttta tacaaaatga 900
agcaattggt aaacaatttg gacaacgc atgcaatgcacc ctatttgtaa ttaattgat 960
caaaagcgaa tgtgtcttaa agcagtacct ctctactaca cgcttggagg taattgaatt
1020
tttgcatttt tattttccgg gtcttttaaat atatataata taatatataa ttttcagctg
1080
atttattgag tttgggtttc tttgattaac tatatgtgag ctgtgtggac tgctacttta
1140
agggtgaagct aatcattttc atattttata atatttc
1176

<210> 344

<211> 106

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(106)

<223> Area matching *Drosophila* EST AA694869 (inverted).

This EST forms a 1632bp contig with ESTs AA735812,
AA568063 and AA695306, and has sequence similarity

to mammalian transketolase genes.

<400> 344

gttcggcatc tccgcacgtc acgtcgtcaa cgccgttaac gagatcctca aggattaggg 60
gaccagtcgt gatctggcta cattcattta ccgcctacag gaattc 106

<210> 345

<211> 143

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(99)

<223> Area matching *Drosophila* EST AA392932 (inverted).

<400> 345

accagtccta tctaaatttc tggttttcag atactagaat atgcgtgcaa tttgcggatt 60
tggacagatt ttggacccga aaaaaaacta atgcggatcc agtgtgacca ccgctcgacc 120
gttcaaatat accatgggaa ttc 143

<210> 346

<211> 510

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(260)

<223> Area matching *Drosophila* EST AA391707.

<220>

<221> intron

<222> (261)..(309)

<223> Probable intron in gene represented by EST

AA391707.

<220>

<221> misc_feature

<222> (310)..(510)

<223> Area matching Drosophila EST AA391707.

<400> 346

gtctggacta cacagcattg ctgctataag gagtcgggac cagaggagta agaaggaagg 60
aatcccgctcc ggtaggggact actagcattc gcaagtgcg tccagcaacc ggaggacccc 120
caactgtaga atcagcatca ccataccta cccaacaaac caatgacatc ttgagacctc 180
accagccatg gatcccttcg tgttcttcat agtactggca tcgctttatg gcgttcttta 240
ctttttcgac cgcttcttca aggtgtagta tatccagcca aagttcgtcc agataactta 300
tgtaatccct tagagttgca tgcactaccc gtacgatgcc ttcctcaaga acaccgggct 360
tgagtataaa tttcatgagc ctccactggc acaacgagtg cctttaacag gaccctctac 420
gctgggggat ctggccggta acagctgcac ccggagagta atgatcacca gtttatgtta 480
ggagtccttg gtcacctttt ctctgttccc 510

<210> 347

<211> 528

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_difference

<222> (45)..(141)

<223> Area matching Drosophila EST AI294564.

<220>

<221> intron

<222> (142)..(444)

<223> Probable intron in gene represented by EST
AI294564.

<220>

<221> misc_feature

<222> (445)..(528)

<223> Area matching Drosophila EST AI294564.

<400> 347

```
atctgttcta ttattgtttt ctttttgta agagtttgat tgaatcggat tggatagaag 60
cctggtgaaa agacaaagaa ccagcgtaaa gatgcctcgc cttgtcaatg gccgcgaagc 120
cgcgcccacg tactcgaatc tggtaagttg aacttcaatg tgtggagcca gcgactcctt 180
tcaccaaaaac aaaggattgt atgcatttgt tgcattgttg ttatgctggt tgcgcaacaa 240
atgtgcattt ttacaaaagt cagaaagatt tgtgcttata tttttgtata aaacgcctta 300
agtacatata ggtgtgccag tggaaatata agaatctact ccataacgcc cacttgcaaca 360
atTTTTgcgt tgtgtgcact tattttcggt ccacaatctg aacacctgtc gctccgtgag 420
ttaaaatttc cttttctatc cacagggttg cttcatattc attttcaatc taatcgttgg 480
aaccggagcg ctgacgctac ccggagtctt tgccagggca ggatggat 528
```

<210> 348

<211> 551

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (345)..(460)

<223> Area matching Drosophila Karyophilin alpha 3 gene,
Accession number AF152928.

<400> 348

```
gacagaagtt tcaataatag cgatgacact cgtaatggta tctacagttc gcagggtca 60
aagatatcga tactttgcta gggttgtgta atagtaccgt cagcacaagc gcctgcttga 120
aaaaacctaa ataatatgaa ttgctataat gctttttaag acaaatgaaa tatttcctaa 180
ataatgttca actggttcat aagcttacaa ctccaactga gtaaaacttaa aatttctaaa 240
tttaaaaaat aagtcgacat aaattcagat ctgacgattg gtgcttcaat cgaccctgcc 300
tattaagtgg ggcagtcccg aattgccaac cgcagccaac ttctctacgt tcgttgctcac 360
tgattgcaat tttaataaaa aggaaaggaa ttttatcact tttaaaaaga cgtagaaagg 420
tgtgtgtggt cgtgggagaa acccgattta cttgctaaaa ccgtaagtat cctctaccgc 480
```

aggaccaaga gaaacctttt tcggcccggtt gcattgctat tttcatggat ttttcgcat 540
ttcctttttt c 551

<210> 349

<211> 177

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(177)

<223> Area matching *Drosophila* EST AA540743. This EST
forms a 1129bp contig with ESTs AI064582, AI519458
and AA568024.

<400> 349

tgcgtaatta acgctaatta ggcagaggag acaatttagt tttattcgat cagcaataaa 60
gtgcgggttg acacgtcacc gaacatttgt tgcccaacac cgcactgcga acttcagctg 120
caagtggagt ggaaaaactg ctgataaccg atgaaccag agacaactaa ctagccc 177

<210> 350

<211> 328

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(325)

<223> Area matching *Drosophila* EST AA539054.

<400> 350

gcccgcgcta tccgagtgcg ccccatgatg cgtggcatcg cctcgtcgtc agtgtggaac 60
cggaatcgtc ccgttcagag ttccctgatg caatactgcc gggatcggtc gttgcgcctc 120
cagcgggtcc acggagccaa tttgatgggtg cagcgcttct acagccgcaa gcgggatgat 180
tccaacgggg atattattat gggaccgatg cttatgtccg atcaagatac ccatcttccg 240

gcaactgtgg cgggtgcccgg accgtgtggc cacatgttcc gttgttggcc atgcgcaaag 300
aatcctctct tccccgctt tattgaaa 328

<210> 351

<211> 531

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1) .. (73)

<223> Area matching *Drosophila* EST AI062939.

<400> 351

acccgagcca accgaaagcg ccacaaagag ctcttttctc tcccggtcg gttgactaaa 60
aaaaaattaa aagggtgaaag cgcgtctcgt gtcgtctttt ttcacattat tatttttttt 120
cttaatctcg tgaatgctac ctactactgc agcatctcat ggaaaaccat tcttaagctt 180
tttttttttg gttttttgga atgcaaattg cgcttatata ataggccatc gcgagccctg 240
tgtgtctgtg tgtgcgagtg agtgcaagca tgtgtgtgtg tgtgtgtttg tgtttcaaga 300
atcgaacttt atgctttggt tacatttccc tttcacaatg accaaatgtg tgtagagaac 360
ataatttggt taaaggtttc cgttttgtcg caccaacgag tcgcattgcc acccctgtga 420
gaaggggctc catagccccc aacacccatt cccacccct gtccctctgc tgctgcgccc 480
ttaaaatttt caattgaaat atgactgcac acaggccagc cccaaacgca g 531

<210> 352

<211> 1109

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (927) .. (1070)

<223> Area matching *Drosophila* EST AI109224.

<400> 352

gtccctgccct tcgacggagc aactccgatg gcctcagcac cgactacgcc cactcccttc 60
 ccaagaagga cgatcagaac gccctctcca gactgggtgca gaatactgcg atgtacgtag 120
 ttgatagtgt atagggtcca catttggtcac tatcatatac aattccattg attggaatgc 180
 tagcatttta cagcgattgc tatactatac tatactatag tagtatacct acgtagtatt 240
 agcgatggca ggatctagta tgtagtatgg ttatacccaa gcatttatcg ggatgttcaa 300
 tgcaacaaag caacacagcc ctaattatcg cttatctata ttatatttgc attcgcttat 360
 acgctacttt gctctccaga aacatgataa acgttggagc catggactgt cacagcctgg 420
 agcaccagga gtacgccgat agaataagat tgtactcgca gcggttgcac caacagtggg 480
 aacaacggcc agcagccag tatcgcccaa aaagggttgc aatatagcta gattgaaagg 540
 gtgaatgatg actaacaatt aaatgaacaa caggtctcct taaagatgta ccaagccatc 600
 agttctatct gtctaagcca acctatccag atgacactgc tcaagtgagt tttacttttc 660
 gcaaattgct tgttgcttac caatttcgta tgtttttaga tgaagctctt caccgagaag 720
 gcacacatca gtgtctcgca catacagatc gaccacaaag aggccgtggg tgttcccttc 780
 cggattccct gattatcgta tcttaagtga aataaagtga taaatttata taaaatcaaa 840
 atctatattg gtactaagta gcccttgaat aaccaggtaa tcgacttatt ttcattaagt 900
 gtacagaagc aaataaatac atactatatt cttaacacgg caagacattt tttttattta 960
 ggaaggcaca cacacacaca tatagctaaa atccaaaatg tcgttcgata ttaaccataa
 1020
 attttgggtc tacacgcgca aggaaattgg tcaattaatc aagaagcaga ccgctgaaga
 1080
 agatgaccgc agaggaaaag catatcgat
 1109

<210> 353

<211> 382

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (43)..(146)

<223> Area matching *Drosophila* EST AA696728. This EST
 has some sequence similarity to isopentyl
 pyrophosphate isomerase genes.

<400> 353

ggtaatcctt ttattacaag gtccataatc ctctgtatcc ttagataacc ttcccaaaca 60
 cctacaccaa cgcggtgctgc agccatccgc tttacgagat cgaacaggaa cgtcaggagc 120
 gcaacgcaca gggcatccgt gtggccgctc aacgacgtct caactacgaa ctgggcattc 180
 ccaaagagga actgcagcca caggactttc gctacctgac ccgcatccac tacgcagaca 240
 cgggcgacgg cgtgtggggc gagcacgaga tagactacat cctgttcctg caaaaagacg 300
 tgacgctgcg tccaaatagc aacgaggtct gtgaggagcg ctacttgccg cgcgataatg 360
 attgacgagg cggtggccga ag 382

<210> 354

<211> 533

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (59)..(533)

<223> Area matching *Drosophila* EST AI518328.

<400> 354

ccctggcctg agttttcctt cattttcacg cgaagttcac actatttcgc gccaaatggc 60
 aaataagcat aatttgtgca aaaaaagaag tttggatttg agcgaggaat caacaagcga 120
 aagccatgcc aagcgtcagt gcaccgaaaa cctcttttgg ccggagggcg aagacgacga 180
 cagcttcttt tccaacgcgc atctggagga tttgctggac ggacgaaagg aggagctctt 240
 tggcacgcaa gcaaccacaa gtaccaacaa gatgacgcaa agtgggtcgg atgatggact 300
 gggactcttt gcggacacat cctttccaag tgcacaggag tgttccaccc aacagtgcct 360
 ctaaaccgga tgaagccagt gcaccaactg ataaacatca aatcgacctg gcggacgagg 420
 aaaacgccga caagctgttt aagaaaatca acctcaacga tctgagcatt gccgaaatgg 480
 aggatatttt tcatggcgcc gatgatattta gtgatcccat gggtcaaaac aca 533

<210> 355

<211> 457

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (43)..(432)

<223> Area matching Drosophila EST AA263622.

<400> 355

ggtcaatctg acgccagttt atagaaatct tttaacgttt cggtcgtaaa tcggctcgaa 60
tgctagtaga aaattagtaga ccagcgcaaa acgggtcgaa aggcaatgag gcatcaaaaa 120
gttaactaaa ttaatcacia ttaccgtgag aaatcagaca gtgcagcgcc acagcgactt 180
taattcagaa aatttgtaac ctggagcgca ttactaagaa ggactgttgc ccataggaat 240
ttgacagact ctggcgactg tcaaagtgtg atgtaacatt ttttaagtga gcgtgatcta 300
ggaaaaattg tgaaaaactgg ctaccagcga taaattgtcc aaatatttcg tgggcatgga 360
cgaagaggag gaggaggagg ttaccggatc taaagctgca attgttcac aattacagta 420
cgcgagcaca ttgtaagtgt ttttctggat tgaattc 457

<210> 356

<211> 489

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(164)

<223> Area matching Drosophila EST AA539661. This EST
has sequence similarity to Human proton ATPase
like gene.

<400> 356

gcctggtcaa tctgttctgc ggcattgctg tgggcattgt gggttcgggt gccgccctct 60
cagacgccgc caatgccgc ctgttcgtca agatccttat tgtggagatc ttcggttcgg 120
ccatcgggtct gttcggcctc atcgtgggca tctacatgac ctccaagtcc aagatgggag 180
acaaggagta ggcgccgtcg ccagccatcc agtgtgagta tgaatcattg cagagacagc 240
caaggtcaag agaatagcac tcgcgacgga gcaactgaag cttatcact tgtaggctgc 300
attgcgcgat tcgcgtctaa gagaatgttg taacgcactt gttcttgcgt ttgataaact 360
cagtaataag ttaatttaac cgcataaaca tagaggagct accagctctt ctctgagatg 420
cattttatga aacctaaagc aatacactcc tgattgccat ccttcggttt tgccaagtgc 480

tatagctcg

489

<210> 357

<211> 1043

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(152)

<223> Area matching *Drosophila* EST AI388964.

<220>

<221> intron

<222> (153)..(213)

<223> Probable intronin gene represented by EST
AI388964.

<220>

<221> misc_feature

<222> (214)..(579)

<223> Area matching *Drosophila* EST AI388964.

<400> 357

ccccatgtca agttcagatg acgatggggtt tgaccaggat gagaacaaac tgttgcaggg 60
cctggagaag tccttgaagt ccctggagct gcagaagaat gaggagtaca tcgaatgccc 120
cccatctgag cgtaaatagcc ccccatctga gggtaaatac caccttatgg ttaagcagcc 180
ataatattgg tactatcaag ctttttgatt tcagtggggg agtacgtgat gcaacataca 240
cggttctccc tgaccgagtt aacaaatgcc ttaaaaatgc cagccatcga catgttctta 300
tactttttgt ccgataagcg agatctcttc gagaatcaaa gtgttggcca ctgacaatgt 360
gaaacgagtt ggctgttcg tggatgtcct gtggtcgctc tgtgaactcg aattgggcgg 420
attcgatgaa gtctttctgt ccgcattcag ccggcagacg gcgcttctgg acaagatcaa 480
gaatcttttg caggccaaag ccgctgtggc aaaatgcgat gcggagtcgg cactgatatt 540
aagccatagt aagtggatgc ttctacgagc ccataagcat ggctcctta gtcaccaggg 600
ctacgaattg gtggaacttt ataagaaatt ggcaccttcc tttaaaagcg acatgattga 660

tgggtcttgaa gcattcaccg gtaacttttc acataacgtc aagggcctaa tttatccaac 720
 gctggagacg ttactgggca aagatgcaac taaggctccc aatgaagaag aggatgaggg 780
 cttggtgtcc gacaaagtag tcaaatatgt gaatgcactg cgaaatttac taagggaaga 840
 ttttttagca ccactagttg agtttgtgca acagctgcgc agcgggaacgg atgtcgatga 900
 gttgaagcaa cagggccttc tgtggtecca tgtgcatctg actttaaatc cacagtttgc 960
 caacgctcag cgtcatagcc ttgttttttt gaaggttcaa tttactaaag aatccaagaa
 1020

tgcctataag cttggctgaa ttc
 1043

<210> 358

<211> 536

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (365)..(462)

<223> Area matching *Drosophila* ESTs AA438987 and
 AA264877. These ESTs have sequence similarity to
 Human FXR1 gene.

<400> 358

atcggagtga acgaacgaac gaagcatttc ggcggcgaga gagagagaaa aagagagcga 60
 gagcgcacac gcttggtggt ggtcatgtgt gtgtgaggcg gcgggctcac acacacaaag 120
 ggagagagac aaagaagaag aggaagcact gcgctgctgc gctgccggca aagccgacgt 180
 cgctgccggc ttcgccgcca gctgcattta gtgttttagct aggaattatc tggcccccaa 240
 aataacttca aaattttctt caactatatt ttttattagt gtgtcaatat atagtctccc 300
 tctccagata caaaaattca aaaataccaa aaacaaaacc attccatatt atcattgatt 360
 acaggcaaca tttgaagcag cagccgcca gcaaaagact gatttgagta caaggaacta 420
 gaagcaggaa cgcgagggtt ctgccactgc aactgaatt gtgagcatac ccaccatac 480
 ctagctatat ctatagccct aatatctcca ttcttcccc tcaggagccc cagata 536

<210> 359

<211> 257

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (6)..(257)

<223> Area matching Drosophila EST AA392117.

<400> 359

acctgagcaa gggtttatgc cgatgatctg cgcataaacc agcagcagct tatggacgag 60
atttcggccc tcttgacagaa cacagcgaag ccgagcgccg ccaacgcact gcagctgaat 120
caggagctcc agcgccggct catgcaagtc cggacacaaa ttctggccat gttacaagta 180
gtaagggccc gcttctctcg gaacgaggac atcctgggtgc gccggctgcg acctagttcc 240
catttcggcc cgaattc 257

<210> 360

<211> 591

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (45)..(120)

<223> Area matching Drosophila EST AA821194. This EST
forms a 987bp contig with EST AA736168 and has
sequence similarity to Human 40s ribosomal protein
s29.

<220>

<221> intron

<222> (121)..(544)

<223> Probable intron in gene represented by EST
AA821194.

<220>

<221> misc_feature

<222> (545)..(591)

<223> Area matching Drosophila EST AA821194.

<400> 360

```
ggtcggggtg ccacgctag ttcttttct tttcgaattt ctctggaaa acgccaacat 60
gggtttcgt actctctggt actcgcatcc ccgcaaataat ggccaaggct cccgatgctg 120
gtaagaattg tgttgccgt tgtttttcgc acgttttgggt gtacaatttg tttaaatgct 180
tgtcccgtaa ccccgatatt tgcacgattt ttgcttggtt gtagaaagtg gggttatacc 240
cgaccgcgtt tttttttaac gcatggcgct taccaatttg tatttgcttg tattgtcaat 300
tgtttcaatg ttccaaaggc ttttgcccc gggtgagtag ggaaatacgt gtttagcatc 360
tagaacagtt tccttaatta aggggtggcca aagtaagagc tgcgcgaggc aaaacgagcc 420
atttcogaat ggatttggt cagccaagt cagcgacagc tttgctttta atgaaactgt 480
tccatgctac ggagattctt tgatggaacc gatctaacta tgatatacca tctcattttc 540
agcccggtgc tgctctaacc gcacggctctg atccgcagggt atggcttaac a 591
```

<210> 361

<211> 555

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (12)..(469)

<223> Area matching Drosophila EST AA539752.

<400> 361

```
gttcggacgt gctacgggt ctctctgtg tgtgtgaggt agtgtgctg agcggagcgg 60
cgaaaaagca caattgaaat taaatcgagt cgttatctgt ggattcggcg gatacaatac 120
aatatcgat cgttatctat ttacaaacaa atcgacgtgg attaataaaa tgccgcacac 180
gaatgcttaa agcggcctat ctgtgtgtgt gtacgtgtgt gtctatgtct ttgtgtgttt 240
cactctctct ttgaaatagt aaacaaattg cgtataaagt ttacagcaaa gtaaaagaca 300
aacaaaaata tttatataaa acaaagtata ttctgcagt cgtgtaaaat atttcgaaaa 360
gtagccgcaa aaaggcagcg gcgtcgacgt cagcagagcg cgggctgcaa gtgtgttggt 420
gaggcgata tacatacata ccacgcataa agtgcataa taaggggggt acataagcag 480
tgtaattaat taagtgaat ccaaatagtt ttgtgcatgc gaaattggaa aaatcgagag 540
```

gagttccgca caaca

555

<210> 362

<211> 526

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(382)

<223> Area matching Drosophila EST AA803203.

<220>

<221> intron

<222> (383)..(455)

<223> Probable intron in gene represented by EST
AA803203.

<220>

<221> misc_feature

<222> (456)..(484)

<223> Area matching Drosophila EST AA803203.

<400> 362

ctccccgacc gtactactcg accaacgtgc ttgtgtgcag aatttcctcg gctaaataaa 60
accaaaaatt ggcaaagcgc cgtgtcagat ctagccgtcg attgcacaat tccggagcag 120
gacgtcgtcg ctggagccac cgaagcggag tcaccatcag aagatcacca gcaccaggag 180
aaccacgtgg acagtcctcc tctttttctt ggctgccgag gcgtcgcgtg tgcgtatctt 240
tcagcgggtga ataaccacg gctttttgtt ttcggccaga ggaggagcgt gttgcagtcg 300
caaacgggaa gatgggttaa gctaaaaagg gcaagaaaga gatactgacc aaggtcgaag 360
gcggttcctc ggtggacgaa atgtgagtct tgtgcaagtt catgcccacc tgccaacttg 420
gcaaactttc tatcgcaaat tattcaatct tacagctccg atgtggacag cgaccagttg 480
agcctcaaca accagcagaa tcatgccctt gaagggcaat caagct 526

<210> 363

<211> 401

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (105)..(154)

<223> Area matching *Drosophila* ESTs AA802887 and
AA820871. These ESTs have sequence similarity to
C. elegans protein B0336.11.

<400> 363

```
cgccagacgg gaagcggcag caacaacagc tggaagaagc tgatcgagtg tgagcgagac 60
agcagtcacg gagcgagctt ttgggtgtgc tttcaattca gtagtatttt cacttttgcg 120
cgaactagtc acaaaaacct gcaaagcaat cgcaatttac gtttgtttct gtctctcaact 180
tgccgtaatc gtcattgaaa tgtgcaatct gtaattgtta ttaacaaagg agcaaacata 240
agtggaaact gcattgttat cgtaccaatt gatattcact actcaaagtt taagcaaaaa 300
caacaaaatg cccagggtat gtgtgtgtga gtgtgttcgt gtagaatgtt ttttgtgttt 360
catgttcatt gaatttcgct taagaaatcc tgcgtcattt a 401
```

<210> 364

<211> 177

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (22)..(177)

<223> Area matching *Drosophila* EST AA817394. This EST
has sequence similarity to Dead box DNA helicase
genes.

<400> 364

```
ggccaccccc agtaagcgga ccgcattttt ttctgtgaaa gtcagaaaaa ttagccgaaa 60
aagactgtaa atatttatta atatcagccg aaaccgcacg cgaacaaatc gtgaacatgg 120
```

cgcgcaagaa tgcccaggcg gaggacctct ccaacgtgga gtttgagacg agcgagg 177

<210> 365

<211> 546

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(77)

<223> Area matching *Drosophila* EST AI064638 (inverted).

<400> 365

ctcccggttc tttcgatcct gatccctccc ccaaactaat aattttaagt gattttgttt 60
ttatcaatga gtttctacgc ccatcaaagg actgcccact cgtttgcata acagatgtct 120
ttaggttgct tatcggtttc tggtatcgat gattttatat aaaaataata caaataaaga 180
caaataatag aggtaaagat aaattttaaa ttctgaggaa gccatatatt tattgttggt 240
cctttaataa gcaggaattt tcaagtattg attcagaaaa acgcttataa ctggaaacaa 300
tctacaactt aatgggagta tacaatttaa tgattagttc ctttcgatga tgtggattca 360
aagttgctca accaaagtta aaaatctaaa atcgaaaatt taaaaactta tcgagtgaga 420
ggaccaatcg actactcgac ttagcaaaca tcgaaatatc gcagggtggg acctcacatc 480
gccatctggt ccacgctag ttcattcttg gttcatcgcg ttcgggtcag tgcacggaac 540
gatttt 546

<210> 366

<211> 547

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(37)

<223> Area matching *Drosophila* ESTs AA736157 and
AA140746.

<400> 366

acatcaccat aagcattttg ttgtgtgacc ggagttagt gttgccaaat accaaagcat 60
gaccgcctac cagaatgttt gcactacgat agataaaata ctaaaagtta caaaaaaatg 120
atatatatct ttgtttaatt tttttgtata tttgtttttt tttttgtatt atattttgca 180
tatttgtaca tttctctatt ttataacggt tactccgtaa atttacttat atgtaaatta 240
tatttataca ctaaactttc tttaagacaa tttcctattg ttcattttat tgcgatatat 300
ggatttatgt gccagtggat gtctcagtag tcaaataact gatttcttgc attggtggta 360
acagaaatat catcaagtca gcctgtatat aaaagaacat atgtagatga aaattttaa 420
tgattgtatt ttaaagacaa attattttcc ctgattttgt agagtgggat tttttattta 480
actatgcgtt taagtgggaa aagggtctata aacaaaacga gttgatagca gagtgcctg 540
tgagttt 547

<210> 367

<211> 559

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (7)..(369)

<223> Area matching *Drosophila* EST AA820427.

<400> 367

atgtaaacga aatgcgagtt ttaggaaagt gcactgtttt ggtcaggcaa acccgagct 60
tatccacgcc atctgggcgc cgcagagtgg tggtcacggg aagtggcgca gtcactccgc 120
tgggcaacaa tggaccggat tcttggcgac gcatcctggc cggcgagtcg gcaatttctc 180
ggctgagtgcc ggagtttaag ggcttgccct gccaggttgc ggctcaaata cccgaggaaa 240
acctacagct ggatcaacac ctgaccaagt cggacattaa gctgatgagc cccgccacgc 300
agcttgccgt attggcggtt gaggaggcct tgtcaaccgg aaagctgtgc cccaagcaat 360
tgagcgagga ggagcttgag cgggttcggag tgtgcgtggg catgggcatg ttogaccttg 420
cagaggtcta tggcgcttgg aaccagctgc aacgaggtta caacagagta agcccccttt 480
tcgtgcccag gctgctgccc atatggcggt gtgggtcacat aacatgcgac atggctttaa 540
gaggacctac cacttcggt 559

<210> 368

<211> 533

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(533)

<223> Area matching *Drosophila* EST AA391736. This EST
forms a 1692bp contig with ESTs AA202259 and
AA820861.

<400> 368

ctaccgactg tctgtgtgta agtggg'gcgcg aacgtacggt cgaaaaggaa gtgaaaatag 60
tgcaaaaagg ccaagtaata ataataataa taaaataggc aaaaagacag gccccaaaag 120
agaccgacca gaccagtttc aaaaagcgcc tatttccagg ctctttgtgt tatgtgtagt 180
ggtaagtgtg tgagcggcaa caacaacagc agcagaagca acaaaaacaa ctagcagcga 240
ccacatacgg tggaaaaggc cttttttcaa ggagcgaaag gcaatgcgcg aacgagcaat 300
aagaataata aattacactt tgctataata agaataaatt tatacatata tacacacaag 360
cgggagaggc ccacacacac atgtgttttt cctcgttgag agtgtgtgga aaattgtaat 420
actaatatga accgcagaag cagcagcaca acgagaacca cgagagaaaa tttcgaaata 480
tcgcatgtgc cattttaagc tttaaataaa ttataacgta cagtattaca aat 533

<210> 369

<211> 612

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (158)..(470)

<223> Area matching *Drosophila* EST AA567184.

<400> 369

gctccgggca agaagtccat taccaagtgc gccgtgaatc agcgccagggt ggtcatcacc 60
ttgtcgggca gggagttggg ctacttcgaa atggatccgg taagtaattc tactactata 120

ttacactcaa cttttgactt cttgctctga tgacaaaaaac acgaaaagaa caatcatggt 180
 gagacactat gtgtcctgca gtgctgagct tcaaaatcaa ccaagagcct tatectcggt 240
 tacttaactt cacaactaat gaatacattt tatgcttgca gactggggag ctgaacgagt 300
 acacggaacg ttccgagatg cctgctgaga ttatgtgcat ggccttgga actgttccgg 360
 agggcgagca gagatcctgg ttcttgccg tcggcctggc ggataatata gtgcgcatct 420
 tatcgctgga tccaacaac tgtctcactc cctgctccat gcaagccctg ccttcgccag 480
 ccgaatccct ttgcctgggc gaaatgggtc acacggagag cagactcag ggaggtttgg 540
 atgacgatgc ttccgctcag cgcagtggca acaataaggg aaccatttac ctaacattgc 600
 ttgacaacgg tg 612

<210> 370

<211> 462

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(122)

<223> Area matching *Drosophila* EST AA735277. This EST
 forms a 1176bp contig with EST AA697907.

<400> 370

gcccaaactg ttggcattat tacaactttt attgcctaa aaggcgattg accgggagga 60
 gtgtttgatt tgccgcat tcaccaattc gtcagcactt cagagaaaga aggagcaatt 120
 aagtaagcat aaattctgaa ctactgtaca gtcgccgat ttaagacaag ggaagcga 180
 agagggcaac acttgaagca catggcagaa acacagaata aattgggttt gtctgaaaat 240
 agcatgtatg ttatgtattc aaaaaacatt cgaaatggga agtatagaat taattgacat 300
 tgtaaaaaaa aaaaaacttg gatgtgccat ggttgtaaga tgagaaccac cgaaagcaga 360
 cgaaaaacaa aaagcaggag aaaaaacggc tttagcgaac cataatgcc gaagtga 420
 ttttaaccga aaccttttca taaaaccgaa attcgacagt ca 462

<210> 371

<211> 616

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (514)..(616)

<223> Area matching Drosophila COP 9 complex homolog
subunit 1-2 gene. Accession number AF129080.

<400> 371

```
gcgtggtgcg cttcttcttc tgaaattagg gatgggaaaa atatatcaat ttatcgatat 60
attaaaataa atgtaaatat ttatatcgtg atagtctttc tatgatatat caaatatcgc 120
tctttctgta aaatatttta ttggacacat gtggattcat aaaaaactga aaactaagtt 180
attattctta aaggatcact aaattattat atttatgatg aaatatctga tgataaatga 240
taatatatta taaaatgtca agaataatth gtttgggtac tttatcattt tgataatttt 300
tttaaagtaa aagtgtctga taacgacctg tagtcgcgga ttataaaagt atttgatata 360
ggaacttagc ctaaaaccaa ctatctttgt taaatatttt aaaactgata tcagtgttat 420
tttttggtat attatttggt ggaaaagtgg aaaatggtct tctcctacag ttgtcatcta 480
tcgacaaagc cgttggtcaca ttgccatctc tagattatcg gtgtaaaata atttgcgaa 540
cggaaaaatt aattgacgaa taaacaaaaa cgtagcttaa atttttcatt ttccctggac 600
tttcgttgca aataga 616
```

<210> 372

<211> 322

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (140)..(189)

<223> Area matching Drosophila EST AA202581.

<400> 372

```
attcagacaa acacggcaat gcaacttttg tgttatcgat aagcagtgtt ggacagcacc 60
ctgcagctgc ctgcattggt atgcgcaatt atcgatatata acaccctggg gccatcattc 120
tcgttaagcc atctctagtt cgccactgaa ctcgtaaaaa agtgtaaaat ttgtttacat 180
tgaaaaaagg taaaatattg ttcttgaggg ctacctacgg tgctccctgg ctcttagatg 240
```

ggtcagccaa gacaaagggc cgtgtgcatg tgtggcgcgt agccctttat aagtgcgggg 300
ggtggcggga acagctcagg gc 322

<210> 373

<211> 607

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (41)..(377)

<223> Area matching *Drosophila* EST AA390775.

<400> 373

cactgagcca aacaaaatcc gaaattatcc gcaacatgga cgagtcggag ctgctattca 60
atctgtttta tattctgttg tgcattggtga tcatctaccc gccagaggag ttccaacgcc 120
tggtgattcac cattgaacag ttgttcgctc ggttcctggg agaagagtac ctggactttg 180
taggtacca ccagcgccgt acttcgctga atctcttcgt gcaactcctgt ctgcccttct 240
cctactttct tattcatagg ctcaagttct ccgtcttcgc cagcgaggag cccttgagg 300
acttcgacct ggacccgat ttcccatgc cccaggaagc ggtagcggtt aaaacgcttt 360
acgtggaaaa ccgcccagcg gttagtggtg ttggccgttc tggcgatgcc cgtctgatct 420
tcaactgggc accaggaaaa tgggcgtcgg cccccgatc agcaaggcgc tcttcaagta 480
ctccatcacg ccgggcagct acagtgcctg ggctagcgaa attggtatta gagttccggc 540
aaccggaaat ataccagaag aactaattca ttagcttcgg tgattgccac gcagactggg 600
atataaa 607

<210> 374

<211> 488

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (169)..(488)

<223> Area matching *Drosophila* EST AA539898.

<400> 374

cggtgaagtg agcggttgtg gaacgtgagt ggatgctaag agcaagctct cacatacgcg 60
gacatagctc gcacacacac acgcacagac cgcctttttg cgccgccgaa acgaacactt 120
ttacgaaggc gacggcgaat cagtttcagt tgtcagttcg catccaacta gaaagcagtt 180
aacgagtagt ctgtgttttt tgccttgccg ttaaaagcca cgaggtcggt catcgttcat 240
cgttttcctt ttcaacttca agcaaagcaa atataaacca atgcaaaaaa cgcagtgatc 300
ttttgaggcc caaatcgttt ggggccgaac accgttgatt ctaaaacgca aatgtagaaa 360
caaatcaaga aaagtggaaa ataaatatgt ttcgctttca aaacatgtgg aatgtgcccc 420
aactcaaaac tgaaaacgta gaaggaaccg cgttcgtttt ttacatacga caatcgatt 480
aaaataag 488

<210> 375

<211> 597

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(127)

<223> Area matching *Drosophila* EST AA390453.

<400> 375

gatgtgtgca taaaaatcaa gcgctgcagc agccaaaaag cgagaagaga gcgcgaggca 60
gagagcgtgc aaagcgggtca gcgagagagc ggggtggctgc tgcaccttca taactgttgt 120
tgcaaagggtg agtgcggtgc gaatattgtt tttggttcag aattgtttat ttaagtgtac 180
totcaaccag gccaacacac tcacaaccac acgcccgcac gtacctgcga cccacgaacg 240
tgtgtgtgcg tgtgtgttgg cctgcctgct tattttttat gcggaaaaaa cattgatcca 300
aactttttcg ggctcaaga acctcatttt tggctcgccc cacaaggcat taatatctgt 360
tgtgaaccga aatgggttta aataaaagct ggtcagcaga taaaagtga tccaatatat 420
atgtacgtac atatgtatgt ctgtaggag cctttgttca tttcagctac aaacatctga 480
gaaagaataa agtattaaga aatattttac tttggtaatt acttaaacag aaccagtttg 540
gcctctgtgg catatcactt gccagttgaa tccgcggaat taattcttga agacaaa 597

<210> 376

<211> 328

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(321)

<223> Area matching *Drosophila* EST AA568061 (inverted).

This EST forms 1356bp contig with ESTs AA264532
and AA441674.

<400> 376

gagtgggtga tgcttttccc gttcgttttc ttggcggact ttggtcggaa tcccgccttt 60
ttctgactgg cgattgattg ccattcctgg cctttcgggg tggactctga tcggaatccc 120
tgtgcttttg gcgtggcgga gactgatcgc catctcgccc tcgtctgggtg ggactctgat 180
ctgagcttcc cgcccttctt cgcccccttt gaggactctc ttctcgcttt gctggcttac 240
tcgatctcgc tgggcttaaa tccctagagc tgctgcgttt ttcttgctta attctgacgg 300
gtgaacttcg tctggatggt gagaattc 328

<210> 377

<211> 533

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (102)..(311)

<223> Area matching *Drosophila* EST AA141908. This EST
forms a 794bp contig with EST AA802528.

<400> 377

gcacagcgta agacgacgag atcctctctt cgaaatctat ggcatagcca gcatcaaaac 60
aatcacgcag ttcgaatacc aaaatccatt gcatacttgc aggcaactc cgaaaatgcc 120
gcacaaagac gaaacagtcg gtctagttag aacagtgagg acaatgaaaa cagcgcgtcc 180
ggcaccggtta gggaacagcg tgacgaggcg gcgggccgca ccgttctcca gtgggcgtgg 240

catgtggtca aatccacatc cgtggagccc acaatgttcc tgtacatggt cgccttcatg 300
 atcacctcgg gtggtggagc agaacttctt cctctacaag tcctgtcggg ttaacaggaa 360
 atttcacgga gggagatctg caggaaatct caacaagccg gagaacgaag gagttccgaa 420
 cgaaggcaat gttgaccaat gcctgggtcc ttcagtgggg agaacatttc tgcccacggt 480
 ttccccatta ttctggcct tttctgggct cttctcggat cgacgggccc gaa 533

<210> 378

<211> 612

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(100)

<223> Area matching *Drosophila* EST AA539224 (inverted).

<400> 378

gtcccagcga aaaactttgc aaaagggtgat tttccaact acttcgcgag agagactagt 60
 ggaaaaggca agacgaaaac acaactaagc gaagtgggtg gttggccagt gtggccgcag 120
 gtggcgacc gccaatagc cccgcgcga aaaataccac tttctttaaa ataccaatgg 180
 gtcttaattt ttgattcta ttcttttagt tttatttttg ggcccaaatt ttcgaggata 240
 atagttgaat attgtcaagc taatacctat ttcgctatat tattattatt gttaaaacta 300
 atgatgaaga attgtaaagc tgaaccattg tttaaaagta ccaaacaag ccaatttact 360
 tggctttact ttacttttct tctctttaat gaagaaaaga gtttacttat gccaatgcct 420
 gcagagcctt gctgtatcat cagtttctgg atggaaatgg agacaaaaca caataccaat 480
 ctattaaatg acaataacta tcaattaaat gactaatatt ggctgtcacc aagtaaccta 540
 tcccatctat ggaagagtag gcattctcct gggttgaatt aacaaactct ttgggggcta 600
 ttttaatgaa ga 612

<210> 379

<211> 837

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (431)..(622)

<223> Area matching Drosophila EST AA246367. This EST
has sequence similarity to human ribosome S6 PK
gene.

<400> 379

gtcagtagtt ttggatttgg cccaaagagc gaacaaagcc gggttgagtt ttctgggtaa 60
tcgtgtcaag gttaaataca tgtgctccac ttaacaaag aacgatagag acggcacttc 120
atctggcatt gaccagccac cctctgccga catttcaata aaaccttgag acatccaccc 180
ggttaaagtt atcaattatt ccaccacact accatgtttg ataagctctg tggcagctgc 240
cttaaaatgg catgaaatat tcacagggaa gaagttgccg gtttaatttg atatggacgg 300
gaattattaa actatcatat ttaaccataa gtacatcctg acctgcaact tgtaacaaat 360
tttcttatct agcttgtgct tgcagttggc cgggtcttct ttatcactat cattgagtgg 420
aatgactcac cgtagtattt cagatcgggtg accgcctcca ggtcccgttg atgggcctca 480
ttgtccagat caaggggtgt actattgctg gtgggcatgg cgtaggaggg cgtgggtcgac 540
gaggaggcct tcgaggctgc tgctgccgct gctgcagccg ccgccgccgc cgctgcagct 600
gcattgttgg acttggcctt ggacaagctg gagctggatt catcgatctc tatcccgttc 660
ggctcctcct cctccatgtc ctggtccgta gtactcccgt cggaatccg cgtccgtcct 720
cgctctccgc atccgatatg caaacaatat ccgccacatt tgtggtggcc gggatggaag 780
gtgtgggccc gtgatatggc tccgggaaag tgtaatccct tgcaaagctg aaatggc 837

<210> 380

<211> 654

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (46)..(319)

<223> Area matching Drosophila EST AA817295.

<400> 380

cgtaaaacca tggcgttctt ttcagtttca cattggcggt cgttgagcgc ggacgtgagc 60
atgtatttct gtttgagtgt gtgtgagtgt tagtgtttgt gtaagaagtt cggcggcaac 120

gaaaacgtaa aatagtgaag cataaaggca caaagtgaag aaatactcgc acataaaccg 180
 atgttagtgt gtttgtctaa gcccttctac ctcttttttt gctacctgcc aatttggttaa 240
 ctttattggt gctaccgctt gcgtgccgtg aatcaaagta acaacaaccg ccacaacaac 300
 aacatgcaca aataaatgta agtgtgtaag tgaccgtgga gcgatttaat aacagtgcaa 360
 agccaggaat agcaactaaa atctgttttt aaacgcgcga cgaatgagtt taaaatcgat 420
 tgcagctcgc aaaaattggt caacatcaca aatagtagaa tgcaccacac aatgcccttt 480
 agttatatac catgtacatg tagatgtatc atatcccggtg actcatccga tttgcttttg 540
 catatgcaat ctctacgcaa attacttggg tgaccaaag aaactattat aagttgcgtt 600
 gaagatacat aattgtcgac cgaaatttca taatcatggc gagatattaa taat 654

<210> 381

<211> 387

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (35)..(383)

<223> Area matching *Drosophila* EST AA439743.

<400> 381

gtgtggcagc cagttagtcg tgctccgcta gtcgatgtcg acggttcgct gttttctgtg 60
 ttgctcgccg cccgttcccg cctctccgc cgcatatcga agtctcgct attgagtctc 120
 gaaaacaagt ccaatctgat gtacggccgc attccaagg actccctttt aaacactaat 180
 tcaagcacgg catgccaggc ccaataggtc gagtagcagt gggcgcggt ctgcaacaat 240
 tagagcaata attgttgagc gccagcctat gcggtctaca tagaaaccga actaccggac 300
 tatcgcccg taaccaccta tagtttacgc ctggcttttt tggtagaacc ggcccaaaag 360
 cccgttcaac caaaaaaaaa aggtaaa 387

<210> 382

<211> 548

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(264)

<223> Area matching Drosophila EST AA441568.

<400> 382

```
catacgccca ttctgcggga atcgcccca catccaactg gtcagtgcgg attgtgccag 60
cggtgagtgg agatggcgcg cgaggacgag gaacgcacg tggacaatga ggaggtgtcg 120
caaccgacgg aggaggacca agtggtcagt cgggccggtc ggcgtgacaa tgaactgagc 180
cttccgtccg gcggctgctg catgccctcg agcacgagcc accggttcat ggctctggtg 240
ttcatgtgcc tgctgggatt cggctcctat ttctgttacg atgcacccgg cgcctgcag 300
aactatttca agaaagatct taatctgacc tccgccagc tcacgctcat ctactcgatt 360
taactcgtgg cccaatgtcg tcctgtgctt cgtggggagg tttccttacc gatcgactgt 420
ttgggcattc gactgggcac gattatctac atgatgatct gctgggtggg gtcaattgat 480
cttttgctg cgcggcattc tggacgcttc tggatgatga tctggggacg ggttatcttc 540
ggattggc
```

548

<210> 383

<211> 579

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (337)..(408)

<223> Area matching Drosophila EST AA247082.

<220>

<221> intron

<222> (409)..(478)

<223> Probable intron in gene represented by EST
AA247082.

<220>

<221> misc_feature

<222> (479)..(568)

<223> Area matching Drosophila EST AA247082.

<400> 383

```
attcaagcta aaaaatagtt gtttcgccac tatttggtgtt cggttggtatg cctatcgtgc 60
aactgcgtcg ccggcatttc cttatttggt ctgctgcgca aagaagaaga attgctgcga 120
acggccgttg aaaaatcgaa gcagagagcc aattggaaaa gcaataacaa cttggctctc 180
tcgcaaaaca aacagtttagc ttgtgataag ggaaattaaa ttactttgtg tgcgaaaaaa 240
gagcgctaatt cttaggtgga attaccaata aaacagtaaa agaaacaaac tgcaaacgct 300
ttccagcgct ttgactcatt tagtgccaat atttcagagc ctgcaggtga caaaatgcgt 360
tgcagtttgc aaaaggactg cgcagctccc acgcaggaaa attttcgtca agtaagatga 420
tacatgctga atacatttaa actgaactaa aaactattca ttgcatttac tgacattcca 480
gcagatgcgt tccaattgt gatttgcttg ctttgctgct tttctgcagc ggtgaaagtg 540
tcgccgttga cgcagccaat cagctggtaa gtgggccgg 579
```

<210> 384

<211> 828

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(321)

<223> Area matching Drosophila EST AA201685

(inverted).This EST forms a 868bp contig with EST
AA540405.

<400> 384

```
ttctcggeet tttttgttgt cttggctgct tcttcttcca ccaaacgaat gcgctgcgcc 60
tccagttccg cctcatcttc gctgtcgatt tggagtgcta catccggcag atcgtectec 120
tctcgtctt cctcatcttc ctctcttct tccatategg actcatcgga ctctcgtcg 180
ccgtttgctt tcttcattgt ttgcagcgga tttgcacat ttgccattgc cattttcagc 240
atgtcagaca cgaaacgctt gcttttcttt taacaaatcg gcaaaaactg cggcgcagcg 300
ttcagaacaa atccaaatcc accgacgcg ctggaaattt ttatttttct gcctctctct 360
cactctctct ctctctgtgt ctcttttagc gttcttacct ttgtttgtgt tcgtgtgcga 420
gcgtgcgaaa ttcggcgtag atgtgtgttg gtgagcgtga tcgcttgcaa cactgtttga 480
```

gcgtgtcagt gttatacagc gccttcccaa aggacagtgt tggaagtcgg agctgccgca 540
 cgcgctataa ttcaaataaa aaggagcggt aaatgcgaat tgtaaagta aaagagcagc 600
 tgccgccact aatgccattt tgatagatat ttgacttttg gcgcagaagc ggccaactat 660
 ttgtgtattc cgttcacgcg ctcaaattggc acgtattttcc caatgcactt aaaaaaaaaa 720
 ccatgttaaa tatacattaa aattctaaga aggaccaaag ttttggataa tatactcctt 780
 ggaagcttct tttaacattc ctttggagtt agccactttt ctatataa 828

<210> 385

<211> 472

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (83)...(218)

<223> Area matching *Drosophila* EST AA540693. This EST
 forms a 1450bp contig with ESTs AA441321, AA440080
 and AA392794.

<400> 385

gccgccgcca aagctgccca acacatacac gaatgttaga cacttcgcgg tcggtcggca 60
 gaaacaggca attttatacg ggcgaaaagt tacaaaaaat aattttccca cttttcgggtg 120
 gcgaaaacga agaaactgta aaaaatggac cagagattta agtgcaaac atagaaacat 180
 cttgcgataa agcgtgctaa tccggggcat aaaactggta ctgccattat ctgcgttttt 240
 taattgcttt tgtttatttt ttgtatagga cacagtataa tttttctttt gcgctgcgcg 300
 cgtgtgagtg agtgtgtgtg tgtgatttgg ccactcgctg gtttctatgg tatgtgcccg 360
 tatcgccgaa cagagttgcc gccttcaggg caaatcataa aaaatatatt gggctgtcaa 420
 ttgaaaaata ttgaaaaggg ccaagcaagt gaattatatg ccgataagcg gg 472

<210> 386

<211> 1082

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (452)..(1044)

<223> Area matching Drosophila EST AI295950.

<400> 386

gcccagggca ttatcagttg agttaccagg aactcgtttt gtggccccga gagacaagca 60
tggaagactc aaaccggcat cacatttgct gctatcagcg ctatttatac gcgccatcag 120
cggaaaaacg agttgggaat cataaccagc cgaacgcgat atgaatagca caccccaatc 180
cgaaagatac ggggttcaaaa cccgcgcggg gcgaactcat taaatatttt tagatctatg 240
tgaaccacat gtttttgtgt attttattaa atatacattt cccatttttg attgcagggga 300
atcacttggg gctgcgccta cagaataaca ggcagcacgg cactggatta tctcaagcag 360
cgggagtgca cactgggtaa gttaaactgaa ttgaagagaa gtggggacca tcatttgagc 420
taaccacga tgactccaac aggtggctat gcaacaatcg ataccaagtt cttcccgcgc 480
gtcgcctcgc aggacacgcc cttcagcggc gaggcggctg aggtactggg ctatgtggcg 540
acgccagaga atatctattg gttgggcgat gacccggtcg aggagattgc ccagcagatc 600
gtatcctgcc gcggtcccag cggacacaat gccgagtacc tgttgccctt ggccctgttc 660
atgcacgagg agattcccgg cgtgaggggac gatcatctgt tcgagctgga gcaattgggt 720
ttagaggaac tgtaccgccg ccaaatacct ctgtcatctg tgatgggccc caatccagat 780
aggatacgcc gcgactcgca cgaggacatc cgccgcccgc catccttcga gttcacctcc 840
cgtgtgcccg acaccaagct gcgttgccctg aacatttgat ttctgggtgt ctggcggcca 900
agtgttatgc aggtcgcgtt ttttgctaca gcaaattcca aattattgat cgacatttta 960
gcttggtagg taaccagagt ctattgcaa atttgacgta tttctttaa ttgtaaataa
1020
tcctaggcct aatcataaca gcaactctca taagtgactg attagccata actaggatta
1080
ag
1082

<210> 387

<211> 505

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (2)..(339)

<223> Area matching Drosophila EST AA439667.

<400> 387

gtcgggtacgc ggttcagcgt ttttgttcaa cggattagcg caagttaagc acgatggcgg 60
cccagacgat actgtttgat ttcacgctgg acaaggacaa gacggcggat gaggaggcgc 120
gcctccaggt ggccaaaatc ctgcgtaacg agctggagca gctgttcccc cagctggagc 180
tggcctactc gatggagtcg cgggaaaacg gctactttgc ggtgctgcac gagaacaagg 240
acacggtgat tacctgccgc atcttcacgc acggcctgct gacgctcaac gtgggagtac 300
ttcctgcccc atggcaagga gccgagcata tccttcgacg gtaccgtagt tcagtgccat 360
tttaggttcc tttaaaaaac tcaaaaaaca agcaagcaaa caccgcacag cagcaccacc 420
accacatct ttcttacctt cccattttcc gtgtctcgtc tgaattattg gggaaagggg 480
tttttccacc acccgggtna aaaat 505

<210> 388

<211> 637

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (12)..(394)

<223> Area matching *Drosophila* EST AA539198.

<400> 388

cctcggcgca tttttttcaa agcgaaacgg cagaaaaatg ctctggcatt ttacggattt 60
ctaattgtat tatttatgtg agaaaattgc aaataaaaagt gagtccatca tgccacccaa 120
gatggagccg attagcgtgc gcaccgcgcg tctgaacaac ctgattctgg gcaaaggagc 180
tggcgtctgt gcgaagcccc ctggaagcgc ctccggatca ggtattcccc cctccaccag 240
gagaagcatt gtaccctga gcaccactag cgccgcctg gccgaggcca tctgccgcga 300
gggactcctg gacgccttct gtctgctgta caacgagtgc gacaaggata cgctgaagaa 360
gcgcgategc aacatcgccg agtttgtaa caaatgtgag tcaactgcat tggtcagcag 420
ggttttogga tggactatct accattctat agaaatggaa ctcagaaccc catttttact 480
tcttgggtct gagaatctac ttttgcta atattccat tattaaagcc cacaaaatta 540
ttgggagtag aatctcttat agatttacct gtatgttccg ggttccctct tgaaatagac 600
tatgcctagt taccattat attactatct aatttct 637

<210> 389

<211> 518

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (83)..(227)

<223> Area matching *Drosophila* EST AA696927. This EST
has sequence similarity to *C. elegans* ADP carrier
protein gene.

<220>

<221> intron

<222> (228)..(497)

<223> Probable intron in gene represented by EST
AA696927.

<220>

<221> misc_feature

<222> (498)..(518)

<223> Area matching *Drosophila* EST AA696927.

<400> 389

tgttgggggc tctgattccg gcggttcttc gctcgccagt acgtccact cgcagttagt 60
taatcgcgga acgaggacga ggtggtttcg actcgggcgg attggattag atcggcttgc 120
attgatgagc taattagacg cgggaattgc tcgcggaaac aacactgaac cagaagcagt 180
caaagctaaa aaacaggaat gccgttgacc aagagtttgc caaatgtaag tttcagctgc 240
gattgccgag cgactgacac gtgttgcttt tgcaattgac tgtcagacgg gagagcgcag 300
aaatgagagt gcgactgaga cagtggcggg tagcgaaggg ttgtttgtga actaccata 360
aagataaaag tataagtaaa tacgtacata tatacagcaa aaagatattc aaactaatca 420
agtagaggag aagaaacccc aatgaagcaa ccctttacca caactaatta tttactttgc 480
aattcttctt tgcagtctcc gtcgcttttg aagcgcgc 518

<210> 390

<211> 500

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (360)..(500)

<223> Area matching *Drosophila* EST AA438961. This EST
has sequence similarity to Human KIAA0160 gene.

<400> 390

```
catgtgagtt taccgtgcag tgtgccccaa tatggttttc actaaatata ccagcaaatt 60
gtgtcggttg cacatggctg taactggcgt gctttacagc actgaccaa acagctgtct 120
gaaaggtgca ctaattactg tctttcattc aatttactaa ttaaaatagg aaaaatatat 180
aaagtataac ctttaaaaaa tgttttgtac taaacggaga agtaaagca tatgaaatca 240
aattgtttga aggactatca aaacagtgtt ggcaaacgcg caatgtatta ggactggcgt 300
tttacatgat tggcatgacc gcaaaaaaat aatgctttca tttgcaatgt ttgtaagcga 360
ataaagtgct tgaactcatc aacttaaaca agtacaatgg gcatatgaac aaattattta 420
gtcagagtgc aactggtgaa cagtaaaaca aaaaaattcg tcatgcagtc gtacgtttgc 480
tagtgcgccc ataataacgc                                     500
```

<210> 391

<211> 641

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (53)..(260)

<223> Area matching *Drosophila* EST AA735138 (inverted)

<400> 391

```
gatggatgga tgaatggtca gttcgcattg ccagctctag cgattcactt acattgctgt 60
atgagactcc caaaagttga atcaacatct cgttcggcga ttctcgcct tctcgcgga 120
tctcgtctag gcgctgcagt cgctcactct gcgccaggca gaccggcac gtctgtgggg 180
```

taagctcgac gcgcattctg gaatcctgct cgaaatttaa tttaaagaac cgctcgcgta 240
 gtattgtagt gttaaaatct gtgttgctaa agtggtgtgt aaagcgactg aaaaaagaaa 300
 cgaaaagaca tcgccatttt ccttaccagg gctgcatagc atcggcgaac acgatgtggt 360
 tcattttgct gggtccggga agcggatttt tggttaaata tctgataaac atgtttgctg 420
 cttgtgacaa tacattggaa atatttgctt ctttaaccat ggctaaacga tatgatatga 480
 taactgaaag tattccccag tgtgcctata aacaccaacc acttgtaaaa tgagaaagaa 540
 aatattaata cttcaaatat tcaaatatta tgaaaacaat tatatatata tttatatatt 600
 tctttcatat ttaccgtata tttagataga gtaaagaatt c 641

<210> 392

<211> 287

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1) .. (237)

<223> Area matching *Drosophila* EST AI064414 (inverted).

<400> 392

ggctcgacaa aaggcatttt ttttaattgtt taaaaatcat ttgactgcaa cgtttaaaac 60
 aacaaatatt aaccagggtt gcacgatcag cgggttcatt aatatatgta tcttcaaaaa 120
 cggctgattg gtggcaatgg aaaagttggc gaaatttggt tttttatttg aggaaacttc 180
 gattaataat ccaacagttt aacaacaatt cggaaaatac gttggaggga aatctttcga 240
 taggttacta ccagggttgg tcgagggcag ttaggaaaat ggaattc 287

<210> 393

<211> 543

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1) .. (67)

<223> Area matching *Drosophila* EST AA540712 (inverted).

THIS EST forms a 809bp contig with ESTs AA440879
and AA440431, and has sequence similarity to Human
Cyclin G associated kinase gene.

<400> 393

```
gctgtaatcg acaagtgata cacctaaaat atctggcgcc cgttaactga actaaaacat 60
tttcgtagcg ccgtggccac aaaaaataa aaagaatcca gggctgcgga ggagcagggtt 120
cctcagcagg gtggagcgga atcagtttgc tccgatagct tgatcgcgca ggcctggctc 180
accatcgata tgtggcgctg tgctcttata gatatttgac gctgggctct tatccgatgt 240
ggcgcgcgga taactagatt atgaatttcg actaaattta gagtgccttt aagcaaacat 300
tttgatatgtt gactcttcaa aattcaagac gtttaatcct ggctttaaga ttgcacctgg 360
aggtggattg tattatatatt aaaatgcgtg gcagtgccaa cgcccttgcc gaggttttaa 420
ggagatcaca gtttttgcg aagcagtcac gtcaagatat atgctctaaa agagttcttc 480
cggctagttc atactcttca acaagtaccc atttagcttg ataccggtta aaagagcgca 540
cac 543
```

<210> 394

<211> 682

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((596)..(682))

<223> Area matching *Drosophila* damage-specific DNA
binding protein, Accession number AF132145.

<400> 394

```
ctttggacta gtcagccgcc acgaggataa aaatcgtttt cgctgacttt taacgcgcta 60
aaatgtttcc tgacacttag tgtgaccgtt caactgttaa gaactaatac tgtccggctc 120
aggaaaatat actttttatt ttggaaggta ttccatttat gttcaatata aattatgttg 180
cagagagcgc gtggatttta taagcttggt ttgattcttg tacaagcaaa tgacacattt 240
aagatttcca taaaagtcta gaagatcatt tacagtcac gcataagcca gaaaaaacg 300
aatatcgata tgtgtttgtg ttgccccaac tctctctttt ggcaagaaaa atcgatttcg 360
tttttttgca gctctgggac gccttcaaat tgcggttaaa ctgaaactgt ttgaaaatag 420
```

cttttgtaat aagtgccctt aataccacta ttaccacac ttacttaaa tttctaaagc 480
aatcattggt attacatgac aggattgttc agatattccc ttacaagtta ttacttggtt 540
acttattttc ttggatggaa tacgtataat taaatataat atactaatta aaaataaata 600
cgaagacaga gaaaagtcta aatagaatga gctaatttaa gtaaataaat atatagctta 660
cttagggccg tgggtggttg gt 682

<210> 395

<211> 513

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(513)

<223> Area matching *Drosophila* EST AF007159.

<400> 395

gcctcgacgt tcgctaacag agctgagcac tgtaagcgg cgcttcgtga ctgtgagccg 60
aacgcatacg aacgacctac gccagcgcgc tcaaacctgt tggccaactg agtgtgcaac 120
aaacatgttg tgtttacgtt ttttccttgg cctaagcggg ttgagcgtgt tgctgtcctc 180
catcaacatg ttgcactttt cgggcttggc aacaagtgct ttttgtttcc aactaccaga 240
tactctttct atttaactgt atttatggtt gtagttatat tatgccgtta attgtgaaat 300
gttaccaatg agtattgcat ataaaaatca tttaaaattt acatattaca aactcaagct 360
gattttatta aaattaaatg tatatatcta agtcctattc aaaaaaaaaa cgtatcaaca 420
gaagctgcgt aatatattgc ttaattcaaa ttggacattc agcccgaata aaatattttt 480
gacagatcac taggaagctc tgacacggaa aaa 513

<210> 396

<211> 958

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (13)..(235)

<223> Area matching Drosophila EST AI511691 (inverted).

<400> 396

```
tatgtaacca accttttttcg ggttttcttag aagattcagt ggaagtggcc agaggtgcag 60
gagtctgcaa atcaggaact tcatcaaaac gatttttgccg cacagaaaat gctgccgcct 120
gcaactcgct cagttgcgtc acaataagta gcaacaaaat aaataaaatg cgactcatta 180
tgcgtttaat gaaacatttg ttggcttata cttaaaaaag aatcgacaag ctcaacctaa 240
tcgtgttaaa ttgaacttaa aatgccgccca ttttgcactc gataccagga atgctcgata 300
tcacagcaag tcgaaagcag tgtactgtaa ttctcgtacc gtgtgctggt aatgtcagta 360
acattttact gttaagcgca acttctctta ttagcaaatt gtgcaagcag ttcaaaaaat 420
aanaaatggt caatatagaa tttcattaat attataaaaa aataaacaaa tattttttta 480
gttgatatcc ttggcaaaaa atatttttaa aacctatgag tagaaatccg gaagccagta 540
aatcgaaaac ctagtgttct accaaaataa atttaataaa ttttaacaat gtttgtgaca 600
atgatcaatg catagggcga ctattgatat ttagagtttc acaaaaatta aaatgtattg 660
catcaattaa aattaataaa agaatttggt tttgtggatt aattacgttg atgttggtta 720
cgtctatttt aaaattgctt atgccggtag ttttgtatgg gaatcgataa taagcaaacc 780
aaaaatcacg aatatatccg gatgtttaac tcccttgga ttgccataag ttctgcccct 840
ctaactctca ngtgggttgt accggggggg tataaacttc ataattggat tactctctta 900
taacttccca aattttataa tattatatta ttgcaattat tgcaatttgc atttactt 958
```

<210> 397

<211> 289

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(61)

<223> Area matching Drosophila ESTs AA264883 and
AA392712 (inverted). These ESTs show evidence of
alternative splicing.

<400> 397

```
gtctcgcttc ttagcaaaaa tggacgacga tgcttgctg acgggacgtg aacagagtga 60
ccgcattggc accgttaata ttggttgccc tgctaacgga tctataccaa aaaatacttt 120
```

atggttctac caaatatagc aaaaacttca aataaccgaa aagtctgggg agaacatttt 180
tcaattgcat attctatgta ctttcttgag tcctataacc ttaagtcatt tgtagaaagt 240
tagattttcc ttttcttagc attattgcat ttttattttt atggaattc 289

<210> 398

<211> 538

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (30)..(451)

<223> Area matching *Drosophila* EST AA438399. This EST
forms a 821bp contig with EST AA439438.

<400> 398

gttttagagta caaattgtgc agcactagca agaagcagtt tagttacgtt tactccgtag 60
aagcgcgata caaaaaagtc aataaaaggg tgaaaagcga acgttctaga cacagaaagt 120
attcaaaaat actgactcag tcctggcgca gcatcggtga caaaagagc ggctcttcac 180
ggtgaaaagt ttccgcaaaa tcggcatttc tgaaagttgc gcgttcacgg tatgcgaagc 240
gtggcggtgtg tgtcgagttg agttacctgt aattgtgtgc gcctgcgaga gtggaagtgg 300
agtaaacctc gccaccgttt tgaagttttg gaaagatata gggataaccg ccagcgttt 360
attttaaaca atgtcggagg caactgtggc caaaagccg gaggcggtgg aagatgtgaa 420
tgcgctcgacg ggggacgaga agcagactcc cgtaagtagc cgcacataca catatttagc 480
gacaattaac atagcacggc gatacgcaca ccaacacggc ttccgtttgc tttgccga 538

<210> 399

<211> 627

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (600)..(627)

<223> Area matching *Drosophila* EST AA440272. This EST

forms a 1324bp contig with EST AA438941.

<400> 399

```
attcaggtat tctcgcaaaa taaatgtaca tatgtatctt tatatatata tgtgggggtcg 60
tccctctgac gtaccaagtt tgcttgaata gccaaacaaa caccttttgt tgacgtaaat 120
agcacacaca gtctacacac agtcacacgc taaaacgata atgcagccgt tacgtagtta 180
gcactacggt acaggttggt gctacctgga aatgtaatcg ttacatgtct tatttcccct 240
tttcgggttc ccgtttctta ttatacacac acacacgcgg ccatcgaaat agaactgttt 300
tgttttacct ttggaacggt acatttcgta ctgaggtaaa aaaggatttc tgtcgtatac 360
tggaagtttt ttccatgtgt atatgtacat attatctttc ttactcaacc taaatttaaa 420
tatagacctt ttaacgtaag gaatgtattt caataaactg cattgtaatt aatgcggttg 480
atgctgattt cataaatagt tcataagaa ataagacttc aactattttc ctggtaacat 540
aagccaatat gtatcggttc gaatttcaat gggttctttc gctcttctcc aaaaaccagg 600
atcagcacgg cttggaatgc gaaagca 627
```

<210> 400

<211> 682

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (65)..(483)

<223> Area matching *Drosophila* EST AA264865.

<400> 400

```
gccccgatca agtcttaacg gcaagttgca gcaacaaaca ttttcattcg ttttcgcatac 60
gtcgaagcgt acggttcata ggaggaacgg aacgaagcgg ggaacgcgac ggaaactagt 120
tgctgttttt ttgtccgtgt taaataattg acacaagaaa atttagctac acttaagcaa 180
agtccgcgaa aaatctatta aaaatcggtc gtcgttttgt gtgtgtgacc acgaaaaaag 240
tgccccgata ggaggatttt aataaattca attaagggtc cgtcccaacg atcgtttttc 300
attgtctgac gctcacgcgt gatgtacaaa tgaaaaagta aaaatttaaa taagatcaaaa 360
gaaagaaaga tcacagtaaa atttaaagtg ggattgactg cacaagaaaa agaaaagtgc 420
cttacctcct agccagaagt caaaagtga gcgaaaaaca gagtgggaga taacaattaa 480
cggttaagtt gttaaagctaa aactacacaa taaacatatc atgaaaaact ttataaaaca 540
```

taagaagggg ggcattttat tattttgggg tatcagcatt tacatcacct tggttcgaat 600
caaactgatt ttaacatgca ttgggaccaa ctacaccgtt cgaatgtatc tcttatggaa 660
atggtattgc tatattatcc at 682

<210> 401

<211> 668

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(246)

<223> Area matching *Drosophila* EST AA263693.

<400> 401

gtgcagtgcg tgtgttaatt aattttgggt gccatttcgc acattctgta tttattaatt 60
ggcagtgcac agcttccggc ggaagagggc aactttccgt tcattttcga gcttccgttt 120
gtcggccaat tagcagcagg tcgacaaaga aaaagcaaaa acaagcgtaa aggataagcc 180
aacatgacgc actgggagga cttctacaac acacacctgc cggccgcgga cttcgaggac 240
aatcgctccc tgctcaagga gttctgcgaa cggcacaaca agctccagaa tcgaatcgtc 300
ctcgtcacgg tgagctggga ttaatccaaa tccgaattag gattaggatt agcgctaaat 360
aaccactgtg ctccgttaat taactggcca agctggtgaa agctttcatg gttgagccga 420
gcgcttgggg cattaaaaac aaatgtgtaa agtgtggaag tgaataaatt ttagattggc 480
tagaaciaag ttcgtaaatg ttaaacacat gcagggggcg accagcaatg cataaacaat 540
taacattttg tgaatggaaa aaaccaaagt gtaaagtggg ttttttttta acatacttta 600
aaaagcaaaa acaccttttt ttggtgggtt taaattttca tttcagaaat tatcttagtt 660
aagtttca 668

<210> 402

<211> 563

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (137)..(160)

<223> Area matching Drosophila EST AA698620.

<220>

<221> intron

<222> (161)..(378)

<223> Probable intron in gene represented by EST
AA698620.

<220>

<221> misc_feature

<222> (379)..(475)

<223> Area matching Drosophila EST AA698620.

<400> 402

```
cccggaatga taaactcaac atgcttgcta gtgtgaccaa cgtatctacg cacgatgcga 60
cccacctatc gatagcttct tcgccagtta ttgccctgcc tttctcatca ctaaaaacag 120
cggcatttta ttgtgcaaata tagaatttct taatataaac tgtaataaga actgctcact 180
atgtctttta tgaaccccggt ggatatgggtg gatgaggacg ccgccgacct gcagtttccc 240
aaaggttaacc aacgccctac accaaccgaa atgcaactta caagtgaacac tggctgaaac 300
ctttggcttc gagtgcacca aaagtggcac tcctccacat ttttaccaca ctgaattgcc 360
tctttgcagt tgagccactg gggccacagg ttaagcggtt catccatgca catcaggatg 420
aacacaccag gaactccatg gttttgtata atccgcacac gttgcacagg tacttggagg 480
agatggagga aaagacgcgg gaccagatag ccagtgttcc atcggctaca aaggatgcca 540
atccggtgtg ccacatgtcg ctg 563
```

<210> 403

<211> 618

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(51)

<223> Area matching Drosophila EST AA391350 (inverted).

<400> 403

gtctggacac tgtatcacca acttttcggtt gcactgcact tttttcgccc gcgacagcgg 60
tagagatgta aaataacaat ttggcatcga ctaccgatga ttcttggcga tagttgtcga 120
ttcgcttttt gctatcgaag ttaatcgatt catcggtcga tatctacact ctacaaaatc 180
tccactcact tatgttagcc aatacaacaa ccaagtcgcg gcggtattca aaaaaaattt 240
caaatatata aaaaaatcaa acaaatgatt tactataacc gtagcgaagc tttctcttag 300
gtattatggt taatttcaaa tcgcaaccct taaatgagtt aaacactggt tggatcgcga 360
tagtttacgt ttattttggt tgagaaatgt ctagaacacc aataaagtaa attcagtagc 420
aaacaagttg gattagtaat attaaatc cacttgctgt tcgcatttat tgcttcttat 480
ggctcttctg gacttaagag tatatctata taaataccag taatatgagt ataataacca 540
tttcgggtat gaaaaagatc tacaatccaa tgccttcat ttacgtttgt aattgatatg 600
agtattgcct cgattcat 618

<210> 404

<211> 499

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (100)..(499)

<223> Area matching *Drosophila* EST AA392183. This EST
has sequence similarity to DNA J genes.

<400> 404

atttctacct atatatgcct ggagcataca caaatctgtt cccaatctg ttatttaca 60
gtccccagat agtaattacg cactacttgc tctgttcaca gtaaacagca aacaaaatgg 120
ttaaggagac tggatattat gatatacttg gcgtgaagcc taatgccacg cccgacgagc 180
tgaagaaggc ttaccgcaag ctggccctca agtaccatcc ggacaagaac cccaacgagg 240
gcgagaaatt caaggccatc tcgcaggctt accgaagtgc tgtccgatgc ggacaagcga 300
caggggtgtac gacgaaggcg gcgaggcggc catcaagaag ggcgggcgag attccggtga 360
cttcgcgaat cctatgggac ttctttgaag aagttctttg gcgctggatt cggaggtagt 420
gggcggtgga cgcaggcgca gaaggcgtt caagggaccg tgggtcacca gatggtccgt 480
acagctggag ggaagctgt 499

<210> 405

<211> 489

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (149)..(348)

<223> Area matching *Drosophila* EST AA696390. This EST
has sequence similarity to Ubiquitin fusion
protein genes.

<220>

<221> intron

<222> (349)..(411)

<223> Probable intron in gene represented by EST
AA696390.

<220>

<221> misc_feature

<222> (412)..(457)

<223> Area matching *Drosophila* EST AA696390.

<400> 405

gcttggtccg caacccaca cagtgtgcc acctgtgggc gaaaaagtta cgtctacatg 60
gtgttctggt cacactgccc ccgccgtgac aaacaaaata gaaaaaaaaat aaaacaaaag 120
ataaaatttt agcctcccc ctttgagaaa taaaggggtca tttgaggcag tttaaatacg 180
aaagaatcca taggcacgga gagcccagca cacatagaat gttccacttc agcggcttca 240
acatgatgtt cccggaggga cgcaattttc atgccaaacta ccaagtgtt ctccgtatcc 300
catgttgcca ggaaacgagc gaacccgacg tggaaaaggc cggaagagg tgagttaccg 360
aagtgtaggc ttggcctgaa attcatgtga acaacacatt ccatcccaca gttattatgc 420
ctccctcggc gcttggacac gctcaccgc ttgaatggtc gattattcaa tggctgggtca 480
agctgcca

489

<210> 406

<211> 518

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(267)

<223> Area matching *Drosophila* EST AA802961 (inverted).

This EST forms 816bp contig with EST AA817584.

<400> 406

```
cgccacaca gctcatccac tgcacccctc gccagtaaa cactccgctg cgacggctgg 60
cggttgctgg gacgtttttc ggcaccttcg acggcgctctt ctgttccaat cctcgactgc 120
gtcgcgaacg gcgatccgtt tgttgcaact tctggcctga cacgctgccg attcgtttat 180
ttaggcgttt ttttcacgct aaaacaccca agaaatgtga gcaaatacat gcctctggct 240
tatcgatagt cccccccgca tatcgctcgg ccagcgcaac tgcggcatgc tcatcgataa 300
taaccgcgtt aagctgagat atgccaaaaa tggcttaatt tatgtgattt attaattttt 360
tattacggta acgagcaagg aaaattagtt tgcagggcgg ttcatttgat tataagccaa 420
gttttttagta aaatattctt tttcttttga acacattaag agctggcaaa aaataactaga 480
tggtccggaa tatgccagaa taccaacatc tagaaacc 518
```

<210> 407

<211> 565

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(259)

<223> Area matching *Drosophila* EST AA699045 (inverted).

<400> 407

```
ctatagccca tggccggctg acatcccctg atcttgctga ccttctgct cagcggattg 60
taggtgctgc cattgtagtt gggcatgtcc acaaactggt ggatgaacct cacatctcca 120
```

gtgacctccc gtgccgtgga ctcttggtc tggttcgttga gcagtcccag agcagcatcc 180
 gccagacgtt gacccaagat ctgggtgctt tcgaacatat ccttaccggg tccggaggca 240
 aagcaatctc cctcgccagt gggacaacgg gaggtcagta gatcacactc attgccggag 300
 atcgagcact tgggacccat tatattgggg gacacatcgc caagggttga tgagcagaag 360
 gcaccacga acttgccctt tccgggcac ttgttcggat tgtactcctt ttccaggagc 420
 agggcggtcat aaccacatt gtcgctggtc accagtctgg ttggtattgg tcatgggagg 480
 tggcatgcac cgcataccca gttgaaaagc gccaggaag gttggtttcc aaggtcgaca 540
 aatcgactg gggtaagtg cttaa 565

<210> 408

<211> 498

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(99)

<223> Area matching *Drosophila* EST AA952055. This EST
 forms a 1205bp contig with AA202358, AA202625 and
 AA951416. Sequence similarity to Human SIAH
 binding protein gene.

<400> 408

atcttgacaa aaatttttgc aagcgcataa aattaacaa attgtagagt tgtggacaac 60
 aaatcgccac tagaataact ggaaaaaagc gaaaatggtt agtactagac aaacgcgact 120
 cacttgetcc gcagcagaga ctttttaact cgcaccaaac cgaagattgc gtctttcgtt 180
 ttcccgtaga atttgcgcat tttttcgga ctttcacagt ggcgttgtag cgaccgctct 240
 tgggcggcat aagggttaag gggcatgtgg gtggctacgg gtgggagggt tccgcggagc 300
 accccgtcgt gaccttgctt ccatttggga ctaccgacgt cacagctgcc agctccgggc 360
 gggtagatac acatcccgaa ttaacaccac gcgctccgc acctccgatt cgccgtctca 420
 tgggaagtgg aaatgggaag tacagccctt ttggtccac atgcggattt tacctggggg 480
 gtggaaaggg aaaagggt 498

<210> 409

<211> 601

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(601)

<223> Area matching *Drosophila* EST AA142266 (inverted).

<400> 409

aagcagacca agaaaaggaa taaagataag ggcgtcagaa tcaagactgc aacgaacggg 60
aatgccctt tggctctggg aagaaagtaa acaatcggag gtgaaggcgt ttgcgagttg 120
catttatcaa aacggattat tgtgcaatag agaaaggtgt cggacagggt gtgttttttaa 180
tgacacttcc cctcgaaact gcaacttctt catgtcaaaa cataactcga cgaaagacag 240
gacggatcaa ttcttacttg aagatttcac ttcttatagg gagatttgta agtcatatta 300
atggagttag gcgtatgttc atatatcacc gggtataaga gttaggaagt ttgaaaaacc 360
cgtgttatcg aactacaaga tatacgttag tattatatca ttttatttat ctagtttttaa 420
ttctacagtt ttttaatcca cctttaatgc aatacagtaa aactatTTTT ggagttctac 480
gtactgaccg gcaaattcaa catgaactaa acgcatagta caacttttct tactgtcgaa 540
agactaagaa attaatgcga gctgctccgc tggccgcaac gaaggagaaa acgtaacaga 600
g 601

<210> 410

<211> 628

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (52)..(534)

<223> Area matching *Drosophila* EST AA696974. This EST
has sequence similarity to hypothetical proteins
from yeast and *C. elegans*.

<400> 410

ggccagatgg aacatattgc ttccgggagc acaaggatcg ggtctactac gtctcggagc 60

ggattttgaa gctgagcgag tgcttcggct acaagcagct ggtgtgctg ggcacctgct 120
 tcggcaagtt ctccaagacc aacaaactga agttccatat cacggcgctc tactacttgg 180
 cgccctacgc ccagtacaag gtgtgggtga agccctcctt cgagcagcag tttctctacg 240
 gcaaccacat acccaaaacc ggactgggtc gcatcacgga gaacgccggc cagtaccagg 300
 gccgtggtgg tttactccat gaacgacctg cctctgggct tcggcgctcct ggcgcgttcc 360
 acaacggact gcaagaccgc ccgatcccat gaccaccgta tgctttcatc agtcggatat 420
 cggcgaatat attcgcgccg aggacacgct ctttttagatc catagatgct aagttttaca 480
 tgttttagtc aataaccatg tttaggtaaa taaataagta tgctgaaaaa cggataaact 540
 gcttttgatt tatattttta tggttaatact gataataata ataattgata taaaattacc 600
 tacatttcat aaattattaa aaaaaatt 628

<210> 411

<211> 1139

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (503)..(626)

<223> Area matching *Drosophila* EST AI532170. Forms a
 1565bp EST contig with AI544333 and AI062662,
 sequence similarity to MTF-1 gene.

<220>

<221> intron

<222> (627)..(733)

<223> Probable intron in gene represented by EST
 AI532170.

<220>

<221> misc_feature

<222> (734)..(1069)

<223> Area matching *Drosophila* EST AI532170.

<400> 411

gtcaaaacca tccatagtga tgtgattttt tgaaaatcta tcaaaatatt ctgaggtaaa 60
 cttatgcgct tttgcgtcgc gtgaaaaagt taacgcaggc aaacagctga taagcgtag 120
 gtgttttgca aactggcgga gtcagtggcg cctagcctag caatttgata agtgaatgaa 180
 aatacacaca tgccgtaaat aaataatggt ttcaccttac gcagtaaata aaaaataatt 240
 aaattgcgaa tattattaac ttttgatttt gtattgaatc tcagaacaat ttgtttctgg 300
 ttctttaatc gacacctact cgatagttct gggtatcgcg ccgatcttat ctttttcaaa 360
 actaattttt gtcctcttga ttataaaata caaaaatgct ttattaaagc gaaatattaa 420
 aatattcaaa acgagtaaca gccacggata acaaccaacg ttttttctgc tttccaggcg 480
 actacagctt taaatgcccc ggaagatgga tgccacaagg cattcctcac ttcctacagc 540
 ctgaagatcc acgtccgagt ccacacgaag gtgaagccat acgaatgcga ggtgtccggc 600
 tgcgataagg cgttcaacac gcgctacagg tgagtaatca tcttccactt cggaggactg 660
 atagccaccg gaataaacca atggctgcgg gcccggccct attaacttgt aatcaacgtc 720
 gcccgattca caaacagatt gcacgcccac cttcgtctgc acaatggcga gacgttcaac 780
 tgtgagctgt gccagaagtg cttcaccacg ctgagcgacc tgaagaagca tatgcgcacg 840
 cacacccagg agcggcccta caaatgtccg gaagatgact gcggcaaagc cttcaccgcc 900
 tcgcatcacc tgaagaccca ccgaaggaca cataccggcg aaaagccgta tccctgccag 960
 gaggacagct gccaaaagtc gtttagcaca tcgcatagtt tgaaatccca caaaaagatt
 1020
 accagcgaca attgcaaaac aaaggctcgca agaaaggcca ctaaagacca gcagaccaat
 1080
 gcagcgatca ggagcagaag gtcccagcag gaggagcaga ggaagaagga gttcattaa
 1139

<210> 412

<211> 569

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (442)..(569)

<223> Area matching *Drosophila* EST AA567128.

<400> 412

ggttgtagcag ttcggggcgaa ctagttatga attgaaccgg ttcgcgcggt gctttttacc 60
 agagttatca ggccatgccaa aaagcgcgcc tatcgaactg gtttatgtgg tacatataag 120

ggaccctaaa tttaaatttc tggcaattgg gatttcaaataaaaatcaaataattgaaatg 180
 cactgtaaga atgtacactc tactagtcata gtttaattgt aaataaatat ataaaaacat 240
 atagtattat taatttgatc aaattagaaa gcagtcttag ggcccattat ataactctgta 300
 gaaaataatt tccttatttt taatacatct cgcatgtgct tctgatgtat tatcatttta 360
 taaattagta ttaatttaag tgcacgaaca acctattcgt ttattcagtg ggtcctactg 420
 ataacgataa gtccgatata gataggagta ttgtttttat tttgtttaat gtaatataca 480
 atacgaagta attgttttga tttcatgaga atgtcgaacg cgttggaacg ctgccaggag 540
 cctactgtgg gccgatcacc gctaggaaa 569

<210> 413

<211> 574

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(79)

<223> Area matching *Drosophila* EST AA950480.

<400> 413

ccctggggaa ttggcagttc actttcgttg gtggctcgag tgcgacgtaa agtgcggcag 60
 cgaagagcgc ttttccaggc acagtgcgcc actacttgcc tgcaagtcag ccacaacaat 120
 ttctcggtaa ttgcgttgca aagtgcgtaa ttagagcttg ggggaaaaac tgcgttttcc 180
 gcaataccag aacgtgcccc atttccacaa gagcgtacgc agatccgtga gttcagtgat 240
 tcctctaagc tcaatgtggt aacgagagcc atggcgatga ctttgaaatg cggaaatgaa 300
 agtacaaatt cggttgcgtg ctggggaaac ggctctgaaa attttacagc caataacaac 360
 aaaggcaaaa caaacgcgta attgcagaaa tcagcttggt tacctacgga cgaaccagag 420
 ccccataaag aagaggggca catgccccct accccgcgac ccattatccc ccctccgtcc 480
 acaactatgg agcccaacag cttgggtcgc aagccctctc tcgcgctctc tctctctctc 540
 tctgctttgt ctgcctttt atggactaac tttt 574

<210> 414

<211> 360

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (2)..(360)

<223> Area matching Drosophila EST AA950161. This EST
forms a 1217bp EST contig with AA950864 and
AA950181.

<400> 414

cctccggcca agcgccataa ctccacaaaa ctcgatccgg aattatattg tgagtttgtg 60
tgaatgtcta ggcttgatcg agtcgacaat atcggcagta gcgaacgact caagttctag 120
ccagcacaaa gaccacattc tgcaaggaat ccgctagcga ggatcttgct gaaaccaagt 180
ggaagtggag gagacgagga ctccaggcgc cgcgcacaaag aacacaaaaca acaaacgacg 240
agtgcgctca cagcgaacaa cgcattcaaa atggcgccca caaaagcaac aacgcgcgcg 300
gccatcacia gcgggcatca tcagctgcag caggcagtga atcccatctt gggagccctt 360

<210> 415

<211> 649

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (30)..(194)

<223> Area matching Drosophila EST AA539625. This EST
forms 882bp EST contig with AA202440 and AA390927.

<220>

<221> intron

<222> (195)..(290)

<223> Probable intron in gene represented by EST
AA539625.

<220>

<221> misc_feature

<222> (291)..(366)

<223> Area matching Drosophila EST AA539625.

<400> 415

agacgtgggtt ttcccaactt gcaatgcagc gaattaacgg atgtaatgcg acgcatagct 60
tcccgatttc tggaacaag caaacgaagt tgcagcccg aggttgatcc ttgcatgaca 120
accgattgaa tgagagagat tgagacatca acgcgcagtt acgacatcgg gggattacag 180
tctggtcaga tattggtgag tccgagattc agatgcgaat tgggtgatgg ggtgtctgtg 240
gttactgcgc attacgttgg tcgatcccc ctaaacgac tgctttcaca gggcaagcta 300
gcaaaaggaa aacaaacgcc atgtcgacag agcgaagctc gcattcagct gaaccagcgg 360
at ttggcgct tttgttgac cgcataaca tcaacaaca caataataat aataagaata 420
ataataataa taataacaac aacaacaaca acaataataa taatgacaat aacaattgcy 480
gtcgcagcaa gaaccggtgg gaactcacag ggaaatatgc aactgctgaa gccccagct 540
cattagaatg tgccccgcag caatctgaca gcaccaagca acaacaatt tactcgattt 600
gccagcgggc gcagcgggca taactggatg atcatatgcy cggccttta 649

<210> 416

<211> 572

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(255)

<223> Area matching Drosophila EST AA951297.

<400> 416

gggtgggactc ccgatatttt gtggagcggg aggtgttttg atttccttag catttagcac 60
aaaaaaatgc aactagtata aagtactgtt cactataaca atttttaacc accgatagcy 120
agtgttcac tgtgtgtgcy agtaagagag atagagagca actagctcca gcatcatgag 180
aatacaaaa agcgccttgt tgttgttgc gctggccgtg acgtcgcaag gagatgccga 240
gtccaattgg aatggtttgt tcttaatttc taactagaat gagttcatca gcagccatag 300
aaaattatat tgcattcatg ttttcatatt tttcgatctt taagtgcatt ccactgccgt 360
acttattaca caaatgcaca gagataaaaa ggggatgtga tgcggttggg tttttctta 420
tcattcttga taagaaacta gaacatcctt ttctcgttca aaacatacaa aagtccgaaa 480

tgtaagtttc ccttactttt ttctggggta tgcgcagtag atatctcaaa gaatttgttt 540
atgatccata taccaccgac ccattctctt tg 572

<210> 417

<211> 654

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (20)..(95)

<223> Area matching Drosophila EST AA948996. This EST
forms 781bp EST contig with AA541068 and AA950730.

<220>

<221> intron

<222> (96)..(478)

<223> Probable intron in gene represented by EST
AA948996.

<220>

<221> misc_feature

<222> (479)..(654)

<223> Area matching Drosophila EST AA948996.

<400> 417

atccaagggtg cataaaacga caaagtaaga aactgtgagt gctgtggaca ttaaaccagc 60
ttcgatttca agaagtcgca ctccctgaaa gcaagcaggt aatgtaaaac attcatcgcg 120
tgcgatgcaa gggttatttt gaagtgcggg atcgcaacgt tcatatgcgt acaggaatcc 180
tcgcacttgc atacatactt acattgcata ttctactgat gctaagggga tatttgaaat 240
gcaaaagggtg tcacgagtgc atttcgtgtg ctttctgtct aaggattgcg gaaactcccg 300
aacaactgtg gtttaagggt acacgggctc tgtttgccga atctgcgtat gtaccgcagt 360
ggctgtgtct gtaggtatgt tcgtttgggg gtaagaacgc ttgagactgg gaggtcacat 420
tttctgaac ttaccattt tgccttagcg tcaatcgcta acccctcgcc tttgctttca 480
ggatcatcagg tccagacttg tcagtgattt gaaaaccgga aaaccctttt gcgatcatcg 540

taacgaaatg agtgccgtca ccagcagcga tacagccatc agcggcatgg ctcttggccg 600
gagccagaca tctgccgtac tacgtgcgcg gcattgccgt ttggggaact ttgc 654

<210> 418

<211> 378

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(378)

<223> Area matching Drosophila EST AA941568.

<400> 418

ggccagaccg aaaaatagca tcgaaattcg agcgaacgtc gtgtataagt aaaacgaaag 60
ttgtgtcgct ctgtgcgaaa gagagaggga gaaccaata tttttgcaag ccagaagtcg 120
aagggtgaaat taaaatgcat tagccacca attgaagagg agtcaactac gaacaaaact 180
cggatcttta agaatcagcg aaaaatcggt tgtgaacatc catacaacca caaatcggtt 240
ttgcctgctc tcgtgtagtt cctgtgtatt ggtgcgcgcg ccctgtgtgt gtttgtgtgt 300
gcgtgcgtgt aagcattgga atggattaac taccctaata attccaaacc aataataccg 360
caacataatc gcaatagt 378

<210> 419

<211> 552

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (228)..(522)

<223> Area matching Drosophila EST AA801928.

<400> 419

gcacgtacat accaaaagaa gcgaggagcc agagagcgag agtggacagg ctaagagcag 60
cgaagtgatc tgccactcgc tacttccgtt ctctcacttg taataaacga gtgcaaagag 120

agcagtagca gcagcagtag caacaacaac agcaatcgac gggcaaccac ttgaaagcaa 180
 ctcgtttcga ttccatttag cagatacctt ttgtacgttg attaagatac cttggcacac 240
 acagacgcac tacaaaagaa gagaaggcag ctaaaaactg cacttaaaaa acacataaaa 300
 taataagaag tcaactcgat taattcagaa cagttctcca aatgaatgta caacaaaatc 360
 cacttgacca aaaatgtctt gagtaaaagt gtcgcatacg cgtaaagcgt acgtataata 420
 tagaaataga tatatgtatt cgtgtgtgtc cgccagccaa tacaaaagca gcacaaaaag 480
 gtgggttaaaa ggcatttaaa atcaacaat atttaaagt ctgaaattag tgtggcgtgt 540
 gcaaagaaag at 552

<210> 420

<211> 172

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (14)..(98)

<223> Area matching *Drosophila* EST AA951147. This EST
 forms a 695bp EST contig with AA695598 and
 AA540269.

<400> 420

ctattgagca ccgacaacgt tgcgtgtata agacagttta cataaattat tatttacaat 60
 tgcacagagc gttgatgttg tgcgttctaa gcgaaaaggt gaacttgacc ccggtgccga 120
 tagaccgccg agctattggg tgtgaaattc gcgagcgagc cttgtggaat tc 172

<210> 421

<211> 411

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(279)

<223> Area matching *Drosophila* EST AA697191. This EST

forms a 1002bp EST contig with AA392404 and
AA438791.

<400> 421

atcccaagca gtagcaagca agccatcaaa atcgtaacct tgggcgtgtg ttaatcaagt 60
gatecgtaca tccccgcctc tccccctcc ttttatcatc atacatacca ccaccatttc 120
tacatccaac gattttgate tggattactc ggcttggttg attgttgggt ctgtttcgt 180
ggcgtttctg tttccgtgca aacatctggc gagataaggg gcctatatag tttcgccaca 240
gccacctcgc agggcccccc tctccggttc ccgccagcaa cgacacgaca gaacaaccaa 300
aacttgggtg gaaaaaccgg tgcttgaacc gtaagttgga taacgtcatt cggtttcgag 360
gggcaaaatt aagacttctg aattgggcca ttatattata cacttttcca a 411

<210> 422

<211> 689

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (650)..(689)

<223> Area matching *Drosophila* EST AI518422.

<400> 422

gtggaaacga tttctcacga aggtaagatc ggcttgaact tgaacgggga tttcgggtggc 60
taaggcagcc acgcggtttt acagtcactg ggggtcgagg tctgtttgga tgacccagc 120
ctacctatgg gtcacactat tggagggata tatctggact caagcgttgc tcacagaggt 180
cctatggcca ctaccgccac taccaattag tcccgccagt gtcctcatgt tccgcaacaa 240
ctgggacgct caaagatccc gatgaaaacg cgtttttccg cctggcaaatt agtttttatt 300
taactcgcac gcaatttgca ccttttact actttatttt gacgtaacag tgcagaacag 360
ctgctgcgaa cagctgttta gggttgcaac gtgcgcggtg acgcaaggca gccggctaaa 420
acgtagcact agaagtgtgc aacgtaaggc gacaaagtct gcaaccttaa aacggtagtt 480
atttacggat gctgacatta ttttaaaagt agttacacca tttttattgc tcttttttga 540
attaacattt ttacatctat tttgtgctt acttacgttt ttctataaac atatcgatag 600
cacaagctgt ttctcttgc gcatctctaa tcacgtttac gtaaatttca gaaggagcag 660
caacaaggat gtctagaaat ttgggttttt 689

<210> 423

<211> 959

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (27)..(689)

<223> Area matching *Drosophila* EST AI535025.

<400> 423

ccctgcgcgt ttcgattcga ttggttcttg aaatggtaaa atgcggctgg gccgtcgaaa 60
aaattgagaa aaataaatcg cgctcgagtgt gggacgcgaa cggaatcgct gtgaaaatac 120
cgagttaaat gtgcgtgata gaaactttcc tccgaaaagg atctgcaatc gaaacggaag 180
ggaaaacgca gagcaagaca tccttgccca cgcaggatag ctgtgtgaag aagacgcgac 240
gataggccaa gagggagggg gagcacaac aggataagca gtggcagaag aagaagcaga 300
aggcggagcc gcatctgccc gcagtcaaaa caagagaggg aagtgcaca aaagcgagat 360
taaagtgcac tcagctgggg gaaatgtgaa atgtgaacga tgttgcaacg tcgcgctgct 420
tgcatcgcca agtaaaagca gagtcagaag aaaagcaaaa ccaaagcaaa gccagaacaa 480
acaaaatata caaagtgaga gaggagagaa agagagcggc agtggttggt gtatctgtgt 540
gtagtgcggt cgcggtgtgc cttgtgtgtg tgcgtgttac ttgtctcaca acaaattatc 600
gtttaatttg cttcgatttt gcgacaacaa caagctgtgc gaaaggggat gtcctttcca 660
ccaccaccac tatcaccacc ccctgctccc taaggtcata ggccaccagc cgagaggtga 720
gtaaatacaag ttgtttgaat ttgtttaccc aaaactcttt tgcacctaac gataacaaac 780
tgatgagttg acctcgctga aagccgcgta ggaaacgaat gccaaattta accaaaataa 840
taaaacacgt ttgccaacgc cagcagcggc gacacaacag caacaacca tgtccaatta 900
aagttgcagc agggaaaaaa aagaaaaaaa atccggctgc cggctgctgc aattcagag 959

<210> 424

<211> 598

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (8)..(536)

<223> Area matching Drosophila EST AA950826.

<400> 424

attcgaggca agcgtagcga tgcgcaaaga acaagcataa gcgaagaaga taaagatata 60
gattaaaatt totgctacaa aaataaatat atatgtaacg catattgtaa atgttctaag 120
ttaagtgaca taaatcaaata atttgtgtaa agtttaatat ttaataacgc gtcgaagtag 180
aacgagtgag gctacagaag agcacacact aaagtgggtg acttggcgag cgcaaataac 240
ggaaatcaaa ttcgaaataa acgctgcgca atagacgggtg gtgtacataa gagtttaaca 300
aaatccgaat cagaatcagt tgaaagtgtg atttttttga gcctttgtct ggtaagtga 360
gagaaagctt taagcgggaat tacatctata tatatatata taaatatata aatacgaagc 420
cagcccgtag ccatttttga aaggggattt taaaaaacac acacacacac atatataac 480
acagctgaga acacatccac atataacccc aaataaaatc cgaagaaaag agcataaaaa 540
aaacgcaaaa caaaccaatt tcgcaacttt ttaagtgaac cttccaatca ggcacttt 598

<210> 425

<211> 517

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (48)..(150)

<223> Area matching Drosophila EST AA949934. This EST
has sequence similarity to mammalian Casein kinase
genes.

<400> 425

tttgcgccgg agctcacttg atttttgata gcttggcgcg gcagttgtca ttccgtctcc 60
tctccgccg tatcattgtt tttgcaatcg cagctctctc gcaaatctgc gctgcgggtg 120
tgcagtacat atacttgtga gaacttgtgg tgtgttatac gcgttaatcg ctttatcgct 180
gtgacgttga ataaattgtg tttgctccag tttccttttg aaataaattt caatgcagtg 240
cagccacggt ttttattcgc tttgctgtgt gtgtgtgtta aaagttggac aaaaaaatg 300
gcctggaaca taacagaaaa gagttgtggc tgtcaaactg ttgctaaaca cctcttatct 360

caatcttttt tgacttgaca gtctgcccac aactggaaaa ttatctatcc tctcttctcg 420
ctctgttggtg tatgtgtgtg tttgtgtat cttctacttt tttgagtcag ctggctgtgc 480
tttacttttt catctcctgc acagctttaa cgagttt 517

<210> 426

<211> 582

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (411)..(582)

<223> Area matching *Drosophila* EST AI109292.

<400> 426

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ggaaccgtgg agcttacgtt ttgctttttt catcatagcc caaacagctg acgaatttta 120
actttactaa agtcttaaat ttttaactaa gccagggatt ataaatattt ttctgatata 180
tctgtaaaaa cttttttgaa aatcatttat tctgtaaata ttttcaaaat ctatctttta 240
taaattaatc aattacaagc tctttttcct ctttcagcta attttttgct gtacctgcac 300
cattggttca gaatactatg cgatctatcg ataacaacga tggcgagggt gaacaagttc 360
aagttcaaac agctgattcg atttgttttt aattttcatg tgatataacg aaacccaaaac 420
aagtgaagcg ggcgaaagaa cacatccaag atggaccagc acagcccaat gttgtggcga 480
cctctgcttc tgctgcgcgg cctctacctc agtcaacgcc accagatgag ccactacgac 540
gcactgggat caagccgtca gtgcacgcag aacgaagatc ag 582

<210> 427

<211> 709

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(279)

<223> Area matching *Drosophila* EST AA202259 (inverted).

This EST forms a 1693bp EST contig with AA391736
and AA820861.

<400> 427

```
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taaccctttc catataaacc tgatttaatc tttgattatt gtgctctcgc tgggggatta 120
ttgctgccgt tcgttggtgc tggctttgct atttttgaaa attccactaa attatccggt 180
gtgccgtccg ctgctctcc gccgttcttg tagttgttgc tattgtgcgt ttttgggcag 240
gtaaaacagt tcatttgcct agggttgcca catcggtggg cgttccccag gaccacctgg 300
aatgcacata aaatgttaag ttttattgcc ctttttacag ttctccaca tttacgactg 360
ccattgagtc gtaaaacacg tgaacaggta gcgatctatt caaggccaca gctgtttagg 420
aggttggcaa ccctggcggg caggagattt caaaacttcc agtggatatg ttctaactca 480
aggaattttt atagccgatt tgtttgaata aatgtacaat gtacataatg tctgcggcag 540
acgctgttaa ttataaatac aactgcggcc gcaagggaag tcatcaattt aaaaagctgc 600
tctgcattaa ttggtatcta atacctcttt tgctggtgag ctttggcaat tttccgttcc 660
aatcaaacia ttatataaaa gtgttcttcg agggacttat gaaaccgac 709
```

<210> 428

<211> 666

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (131)..(647)

<223> Area matching *Drosophila* EST AA142065. This EST
has sequence similarity to succinate semi aldehyde
dehydrogenase genes.

<400> 428

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ggatggcgat agtctgccca gaggtggaga aaaatcgatt actcccgat atcgatgtct 60
ctatgatcgg tttcttgtca atttaaagcg attgggttaa ggtcccaatt aatcgaaagg 120
tgaggcgggc tattttaaaa aagggaatt atccattaac tttaggtaga ctttgtgcac 180
atttattaat atagcggcgt gttattctac aattagacaa caataaacca atcgattct 240
agtggaagac agcgtatgaa agcagtgggg gtgatccctc catcggaatt cagtcgtact 300
```

tgaggttgcc catgcaaag tacttgatgt ccacatagtc gtcaatgccg tgtttggaac 360
 cctcccgtcc gacaccggac tccttgacgc caccaaacgg agcctctgct gcggagatga 420
 tgccttcggt gacgccgacc atgccaacct ccagtcgctt ggccacccgg aacacctgct 480
 gcagattctc gctgtagaag taaccggcca ggcctctcct ggtgtcggtt gccttcttta 540
 ccgcttcttc ttcgtctcgg aaccggtatg atggagacca ctggaccaa gacctcttcg 600
 agtagagtgc gccgaagggt gcacatctgt gacaattgtg ggtgcgtaga aaagggatcc 660
 cttgtc 666

<210> 429

<211> 559

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (76)..(559)

<223> Area matching *Drosophila* EST AA536402.

<400> 429

cgctcgggta taaatgaaga gctatttctt tagcccagct cagtaggttt tttttgttgt 60
 tccgtgcggg tgctcatttc gcgtaatatt agtgtaaatt cccatagctc ctagtgttga 120
 ccagattgtg aacgttgtgc cagacgtctg ttaattagca tatagcacia cgaatatata 180
 taccaaaaac ccggcaaaat tacaactcat ctccgacgca gtagccagtt ctttgttact 240
 gctgctcgcg caaataacgg taaatgtgga taacgggtgga taaatcactg ctgacctcga 300
 cctagacaac aaatttgtac atagctatgt acattgtata aaccgaaagc gacaaaccga 360
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 gacagggggg agtggagcgg agaaatcgag tgaatcagtg ccgcaacgta acggtaaccc 480
 ccgatcccgg ccaccttaga ccagtcccat ccaaagtatg aaccgcccag aggaagggtg 540
 tgcgcccaaa gaatccttc 559

<210> 430

<211> 599

<212> DNA

<213> *Drosophila melanogaster*

<400> 430

ctcgatgttc gacgacgctc agattcagat tcagtttctt ttcaccttcc gtcggttgta 60
gatcgtgccc agcggaagca acggatacca agtcccagac acacaggcac caaatgcctt 120
ggaaaatatt ttgaaaaat tccaagtcac aatcgatagc gactaatgcg ttcgagccag 180
attaattagc cagaggtgaa aagtgcattg cgcggctaca gatactgatt ttgttttaaa 240
aatcgcacac ccaaaaccag ttaaaaaaaaa aaacacaagc gaaatatata ttttcgagtg 300
ccccagtgcc agtgcaaaaa taataaataa agctatcgta aaataaatca aattttgtgc 360
aacgcgagaa tacacaaaag atatattcga ataaatacaa ctaataatat cgtgtcgtcg 420
ttgcgtcgcc cgttgacaaa agtgcaataa tcatatattt attacaacca attacatatt 480
ggtaatcaaa agtaataaaa tcgcaaatca aggcgaaata tttgcatgta catagcataa 540
gtgcggttgg aaaaatccaa aattgcaaga gttacgaaaa ccaaacgaa aactggaaa 599

<210> 431

<211> 606

<212> DNA

<213> *Drosophila melanogaster*

<400> 431

gggcacacgt atgcatgtgt gtgtgtgtgt gtgtgatttg tgcacaggta gaggtgaacc 60
gtatctgtgt gcgtagcagt cccttaggta agcaaagaaa atgtgcccac cttaggtgaa 120
caggtagacc gctgctcaca tgccggttgt tgttcttgtt gctcttggtt ttgctgctgc 180
tggttaaggcc gctcatgttg ctgttgtagc ctgcgatgtt gctagctgct gttattgttg 240
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gttgcccatg ttgctactga tacaactgtt actcgattg gttgaatcac cactgttgct 360
cccactgctg ctgtttcggt tgctacattg tagcttctgc taatgatgtt aactcttgct 420
tatgttgcat ttgtatgtta tggtatgtta tggatgatgc atctacaaaa gtgctgctta 480
tggtgcagtt gtctttgcta attgagatat tgtagcttat gctggtcatt atgttgctgt 540
aacaacactg ctggtattaa agataatggt gtgcattaag gtaaggttct tctgcatggt 600
ggtgtt 606

<210> 432

<211> 169

<212> DNA

<213> *Drosophila melanogaster*

<400> 432

gtctagacca cataaacgcg tatcgatggc gacgaaatgt gtacatcgca catgaacgaa 60
cggggcgagt gagtatgtac agtttaagag agcgaggcaa tatgaaatat aaacaaataa 120
ttaactgaca tatccgtatg cttatcgcg c aacaaaccgc agcagcagc 169

<210> 433

<211> 585

<212> DNA

<213> *Drosophila melanogaster*

<400> 433

gtacacagca taacataatt tgctttctct cgcactccca ctcttacctg ctgagagcaa 60
cagccctgct gtctcgctca ttgcactcg ccagttgcct tctcgctccc ccagccaccc 120
actctcccgt tcggccgctt tcaccgcctg catttgctgc gcgcctggta ttcggttcgg 180
ccaaaaccgc gttcgcttgt atgcgagtgg attattgttt ttgtttcgaa cgcgagtaaa 240
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gtgccgcata gccatacagg ctgacttcca taaatgggac atgcggaaaag aactactatt 480
atacaatata aattataaat ataaatacat acaatgtatt ttaatgttgt atagaatatc 540
ttgatattaa agataagatg caaaaattaa aataataatt tataa 585

<210> 434

<211> 849

<212> DNA

<213> *Drosophila melanogaster*

<400> 434

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ccctccccct cctgttacca tcccttgggt cgtttgggtg gttcgttggt gctatcaaac 180
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aaattagatt taattcatgt ttttgctct cttcaacagg tccagtacat tacactgagc 420

aaatgtgaag aaaattcaca tattgtattc agcgatagaa ttatttttat atttagttcc 480
 gtctatctct tcctacttct cacgtagaca agtttttaaa aaatttgccg agcattttgc 540
 aatatttggt ttctgttttt ttctgcgccca atatttttag cacctcttca atttttctct 600
 gtcgctgccca ttttttggtt gttttcctac ttaacgccac gagctgtttt tctcagataa 660
 aattcatagt gttggatgga ggtgggggtg gggggggggg tggggcatcc tggtgagtgc 720
 aacattgttg cctcgtttga agtggctgtt taaccactg atggcccaga aggctaaaag 780
 tgcataatgg aaagatttat cttagactt gttatgactt ttaaaggcat tttcatagca 840
 aacgaattc 849

<210> 435

<211> 585

<212> DNA

<213> *Drosophila melanogaster*

<400> 435

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 aaaattaatt ttaattcaat tatgaatgct cagaattata atgaggaaat cttcttggtt 240
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 tcccgaataa attagcgcgt gtgcctcgaa atattttaaa tcgctaactg gcgtgtgtgt 480
 gaataataat aataataata ataataataa taataataat aataaccata aataggaaa 540
 ggtacatttc caaagcaatt tacgctgccg cgggtataat tagaa 585

<210> 436

<211> 505

<212> DNA

<213> *Drosophila melanogaster*

<400> 436

acgcagacga cgaactcctc atgtgaccga gtaataaaat agcgacgttg cgcacaatgt 60
 aaataaaaagt aaagtgtgaa ggcagctggt caaaggaggg gaaaaagaat aacaaaaagc 120
 gaaaaagcaa accaaggcca cataacataa cataaaataa taataaaaat gccggcgcgt 180

ttaagcggct gatttctgtg cccttctatc cgccatctct gcattcttctt ttcgtttccc 240
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 tgcaagctct catatgtttt tccgcgctct gctttccgcc gcttttcccc ccgttttaat 480
 atgtattttg ataatactac cccaa 505

<210> 437

<211> 581

<212> DNA

<213> *Drosophila melanogaster*

<400> 437

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 ttacgtttac gtttcacaca agctaaaaac taagagaaga gcgcattctcg taagaaatag 120
 agtccacaag tgtctacaaa tttccagttg gcaatgcctt tgctggatgt aaagtgggtg 180
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 tgaaattttg caaaaaaaaa aaatggggaa taaatatata aattataatt tagcaaaaaa 360
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 ccacaaaccc taattgattg caccatggta taatggcatt agtgagctat accaaaacga 480
 gcaactttcg aaatccatca gtactggtga aaacaacaaa ccgaaagaaa tgagtcaagt 540
 actacgcatg ctttactggc ttcccatttt gctgctgctg c 581

<210> 438

<211> 637

<212> DNA

<213> *Drosophila melanogaster*

<400> 438

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accatatttt ccttatttct cgtgtaaaaat gaatatatgt tttttacagt ttctctaaat 360
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 ttggtttggg aaatttatca gctggtagcc gcgctggtaa aggtaacagc gcttgcgacg 540
 gacattctct aacacagccg ggaaataaac atccagaata atttgagtgg gcttcacac 600
 tggcaggcaa ataaccatca agaaaaaagg atttaaa 637

<210> 439

<211> 563

<212> DNA

<213> *Drosophila melanogaster*

<400> 439

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 ttgatcatta aaatcaatca gattaatgct cgctaataaa atgtaatcag caattatcaa 180
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 atgggtgtgt gcttgagcat gcgggcgcac ttgtgccacg tacacaaaaa cacaatcatg 540
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<210> 440

<211> 662

<212> DNA

<213> *Drosophila melanogaster*

<400> 440

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 agcatgtaag ttactaaact caatataaca atgtgcagtt acgctatcac gtaaaaaacgc 240
 aacaaactca acataacccc actttcgata gtaaaaaacta taactataaa gttatgagca 300

taaattaata ggtagcagtt aattttctct ttctcccat attcgcatth ttcgteacgc 360
 acttttttcc cttgcacgaa tatttatcgt cgctttgctt tgtcttttcg ctacaatcgt 420
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 agataacatt gctttaatgg cttcgtatac tttagagtta gaaaggactt caaatgaat 660
 tc 662

<210> 441

<211> 496

<212> DNA

<213> *Drosophila melanogaster*

<400> 441

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 gaaacgttaa ggcataaaaa caagcgggtg taagacagtt tgccgttgta attggccaga 180
 aagcaaattc tgtagctaga tagttagata gttagtgaac acttaactgt tgagataacc 240
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 gcttgatgat cgattaagcg ttttcacacc tttcccagtc acgtcgcatt cgcaggttat 420
 ctgtatggat atgggtacat gcatatgaag catacgacat ggtgcccctt tccccgctgg 480
 gttatttata aaaagt 496

<210> 442

<211> 559

<212> DNA

<213> *Drosophila melanogaster*

<400> 442

gtgacacgta tgtgtgtgcc gaaaaacagt tgtttttctt gctcgccaaa gaattttctac 60
 caaagtttcc cccctcatat gcatttccac accatgtttg ttggcccaac tattatcgcc 120
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aatttttcca tttcaatttt tacttagttt ttgcaaccag gtttttggcc aggcgcattg 360
aaccaccttc actttacagt ggagattgcc tataaacgaa aacatttcat gacttcagaa 420
gtactacatt tttttaattt ttggctttta ttatcaataa tttgcatata aaatagaaat 480
tttcaatgaa aatgtgacta ttaggtagaa tttacttccg gttggaacaa tacctattgg 540
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<210> 443

<211> 397

<212> DNA

<213> *Drosophila melanogaster*

<400> 443

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aaatccagtt tggttactc gaaaattatg cgaatatctg ggatgtaaag agcttaaagc 360
ctgaaaaaaaa tgaaactttt ccattaccca tgaattc 397

<210> 444

<211> 470

<212> DNA

<213> *Drosophila melanogaster*

<400> 444

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tgagacacct agggatcaag gtctagaata cataactggt tacgtccttt ttgttctaga 180
aatctctagt ttagtgaccg caaacattac ttttttgcag gaccatttta tgaacgggtca 240
cattaaaaaaaa tggttagtga taaccacaaa atggcgaaga tacagactgt caagtccgtg 300
gggacaatcg ataaagggtat cgatgatttt tttttgcaaa attaccaatcc ttgaaatgta 360
cctttattag gtactatata tcgtatacac attgtaccaa taaagtacag caatatgatt 420
aaactttttt ttttataaaa tacttggttt gccaaaggcg ttgcactttg 470

<210> 445

<211> 182

<212> DNA

<213> *Drosophila melanogaster*

<400> 445

ctctatgcct cgtttgctga gacagcagca acagacagcg gaacagaact gaacagaaca 60
caactgaacc gaactgaaca gaaaccaaca cacaacaaca taacacgaca aaacataaag 120
aaaccgaaca caaaacccca gcagaaaagg caaaaagct gaaaagagt cgctgagaat 180
tc 182

<210> 446

<211> 370

<212> DNA

<213> *Drosophila melanogaster*

<400> 446

attcagcgct tctctttggt gagagctttc agaatgaaga gaagtaatgt taagagaatg 60
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ctgctgcaca tttctaaaac aaaaatataa aaataaagat ataaaatata taaaataaaa 180
aataaaaaat ttctaaaata ataaaataat aatgaaatga ttttaattctt tacgaaactg 240
ttgtcagcag tattattaca ttattattga taaagggtta gtttcttcag catattatcc 300
acctcactcg tagacatgga aaacacatgg ataattcctg ggaaatgcc gtgtcacgta 360
gaagacatat 370

<210> 447

<211> 435

<212> DNA

<213> *Drosophila melanogaster*

<400> 447

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gtgttgctag ccgaatgttg ggactcaaaa gataatggcc ttgctatagc tgggcggcaa 180
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tcagcaccta cctgatccca cggattccac aatgattgta cacacctcag tgggttccca 300
 agctcgtcgg cggaatgacg tctcccttcg acggcattgc ctgcttctgg ctgtcactag 360
 tctggattca actgggtatc atcaatgccg gcttgagtt cctcaaggat ttcgtacccc 420
 ttcagctggg gccgg 435

<210> 448

<211> 235

<212> DNA

<213> *Drosophila melanogaster*

<400> 448

acgtgaacca accataaaac agcgggctat cgaactgggt ccagccgaac agtgctggat 60
 aatgcaacat atatcgcaac gcgatgggtt taaatttaat gttatgattt ttatattaaa 120
 aaataaatat ttttttacac cagttattat gccaaatctt ttaaatgtat acaaattagt 180
 aatatttaag gaacagaaac cattgttaac tattttactt gtcaaagccg aattc 235

<210> 449

<211> 328

<212> DNA

<213> *Drosophila melanogaster*

<400> 449

tgtagacca ctggaagacg tacatatgcg aagacggggg caaaacaaac ggcggcgaac 60
 agagggagat acatgtatgt aaaaaaaaaa aaaggaaagg caaataatac tgtttatcaa 120
 gtgatgaaaa gcatttaaaa tgtcgagtat gccagggtatt gtgtttaaat gcatgccctt 180
 cgtcgcattt cggttggaat gcacctgata ttggtaagga gaatgttcaa aagacataag 240
 ctgaatgctg ttaataattt taaaaatatt taagcaataa atgcatatat tgcataatgg 300
 cattaaaaca aaaggcaata cagaattc 328

<210> 450

<211> 110

<212> DNA

<213> *Drosophila melanogaster*

<400> 450

ggtcaaccgc tctgggcccc gttttaattg ttcgggctgt ctgacaaatt tcagtttcgg 60
tttcagtgac tgtccttgcg gcaagctgaa gctgatttcc ttgcgaattc 110

<210> 451

<211> 472

<212> DNA

<213> *Drosophila melanogaster*

<400> 451

agccaggcga ccagccaaag cttccatttt cctcttcccc tttttcggcg agagagcgag 60
cttttccgcc tagcacagtg ggccaaaatg tattcctcct gccagctcac ttccagtcgg 120
tcttcacgct caccgatggc actttcgaac ttcccgaac atgtggagtc tctttgatat 180
cctgctctct taaggcaagc atttaatggc catctgttgg catccttacg aagccacaac 240
tctttgcccc gctttgcaga actcaacact tgccaatagt gctattttgt accactcaaa 300
agggtaaact acagcgttta ttcttttggg tggatattat attctccttt aagcaaacaat 360
ttacacattc gttgtatggt ggtgctaaat tattaagtgg agatactgga atactctctt 420
actaccatgc ggcacattta ttagctttaa tgggttggtt tctgacagtt tt 472

<210> 452

<211> 790

<212> DNA

<213> *Drosophila melanogaster*

<400> 452

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cagcagcagc agcagcaaca gcaacatcaa cgcagcggca gcaacatcac cgcaacagca 120
acagcttcga gtcgcgtgtg tgcgttcattg tgaggttgtg ttggcaactt cgttgcgtgt 180
gtaacaggcg cccagatttt ccgagagagc tgaaaaagaa catttccaca tgcggagtgg 240
ggtggagtgt tcccatttgt ggatgttggg tttgcggaat tttaataggt taagctgtaa 300
gcggtgtgaa gagagggggg cgagaggagt gttgtttag agaggaggca agggggcggtg 360
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ccggtgtagt tgccttataa acgagcctaa aaatgcgaga taaagagcgc ttcgcacgaa 480
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ctttaccatc agctcaaatt cttttgcgca ttctacgac gttgatgtcg ctgcctgttt 660

ccggtgtcac ttccttattt agttgttcac gtttgtttgt tgttttgtgc tgttgggtgg 720
 gatttcgctg gatttcgtcc ttgtaggctc aaccaattt aacagccatc agaaagtggg 780
 cagcgaattc 790

<210> 453

<211> 404

<212> DNA

<213> *Drosophila melanogaster*

<400> 453

tatgagctca tccagcactg ccgacgtcac cccccccgc gttccattta ttattttcat 60
 gacgcggcca agaaagacgc tggaagagcg aaacaagctt ttcgtgtttt ttctattcct 120
 tttgttcogt ttgttttttg gggaggatta catcaagttg gagctgccac atagcgcaac 180
 aaaatgccgg gacagtcagc tggtagcacc tgctgtatc gataaatcga tagttcctgt 240
 tttaaagccc tgtcgacggg acgtaacaaa atattagacg tcagtggcag tggatttcga 300
 ggattttaaa atgctttccg tcaatttctt caacatcacc ccaatgtgtc tgcgcgactt 360
 ttggtatgac tcgtcaagcg cgccggcctt tatagtccgc caaa 404

<210> 454

<211> 563

<212> DNA

<213> *Drosophila melanogaster*

<400> 454

gcggcgcgga aagcagctgc tgctctctcg cgctcttttg ggccataaac atcttacctg 60
 ttacctacca aaccaacttt ccaccgaaac atgcggcaaa tcgcatgatg caagacgcct 120
 caaacatttc gctagccaaa gaagtttgag aagtttacga ttgtgtgcca aaaataaagc 180
 acgtgcggtc gctaagaga gagtcgccgc aatctcttaa gttagtttct ctttcgcctt 240
 agtcattgac cttttggttg ggtcctaaat atgtgcgcat tttgtcgaaa tcttttagcca 300
 ctttgttgtc actgactaat cctatgtgcc aaaagacatt agctcaatga tttgtttagg 360
 cctttaattg cacctgattt aacggccttg tgggacaaat actgcaagtg aaacttgcca 420
 caaactattt gtgtgcacaa taattgtaac aagggttaa atgtcacattgt ggtaacacgg 480
 aataaaaagc tttcgatagg agagatgacc gtaaactaaa tacatacaat aatatcgctg 540
 atgcaatagc taatatatga tat 563

<210> 455

<211> 518

<212> DNA

<213> *Drosophila melanogaster*

<400> 455

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cctcggggccc ggtggttgtc tgtctttgtc ccccgctcaa tccgtcgact tatcgggtcga 60
gtgtagtttta tatgccc aaa agttgtcaac tgtcaaatca cgaaagagaa ggagaagagc 120
cacatacccg agtcgtaatc gaaaagaaaa tcgagaaaaac aaattggaat acttttcgaa 180
acgagtcgcy tgtcaacgta aatactttat atgtttgcaa agtgcgtgtg tccatataca 240
aatgggtgaa tcggtgcact gaaagaaaat gtatatcttc tagttatgtc tgaaattaac 300
gtgctatttc agatcataga tggtccttat aaacatgtta ctcatTTTgc atacttagaa 360
gattgtatat tttttggtcg gtgcacctgc ggcagcctta aatcgcaatc ggaatgcaca 420
tttaaagcaa aatcgacttt taaatccggg ctcgTTaatt atcacgccta gctggcaaac 480
caaaactaac attcaagtcg agaaatccac gaatcatt 518
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<210> 456

<211> 324

<212> DNA

<213> *Drosophila melanogaster*

<400> 456

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ctagggatgt aagaatacat cgatgtatcg agaatcgatg taccgtgccc ataattttcg 60
atgttttttg ttgatatcga tgctttgctg aaccagctgt ttaattatac accgttcaca 120
caaccgcttt ttggttccat gtgaattatt taaatcgttt tagatttaaa taaaagtttt 180
tgtgtgtggt cttttttatt tcttttactc ctattttcag tcagtttctt cttattatca 240
tatatcatcg tatatttatt tatttgtata tgctgatact tatcattgaa tgaatcatat 300
cttaaagctt ataaatgaaa aaat 324
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<210> 457

<211> 325

<212> DNA

<213> *Drosophila melanogaster*

<400> 457

gtcgttatgg gttattatgt gatgtacaac gtgtaagtgt gcgtgcctca agcacttgac 60
 ctcgccatca atgatcgag aaggtgggtc ggtaaattg gtgaccaga tgcagtggaa 120
 gcaatcagga agagaaagga tttgtctccg gaacaaagca aatttttgat gacgtgccta 180
 ttggcgaagt caaccgcga cgcaccac ccactcaaag aaattggggc aatcaaggca 240
 tatgtagtgc ccataacacg gttaccaatc acttatcacc ttcccgagct acagttttca 300
 ttgcattgaa gttcctcggc agcat 325

<210> 458

<211> 524

<212> DNA

<213> *Drosophila melanogaster*

<400> 458

gtgcagagag aacaaaagag agtgcgagaa agagcgagag agacgtcgtg tttttgggta 60
 cagctgttaa cgaaactccc acgctgccgc ctctgttgct gcgctgctac tgcgctgccg 120
 gcacgctgt tttgttgac atttttgtgc ggcttcttc gatttttgtt gctgtcatcg 180
 gttttttaaa aaatggggtc gaacttcttt tagctaaaaa cgaacagttt ggcaccccaa 240
 ggatcacctg tttctaaact gaattgaatt attataagtc gctaaataaa cgatattttg 300
 gattctaggt tatgattaaa aaatgaaata agtaaaaatt aatgcaaata attaaagttg 360
 ctcggtatca atcctatgta attgggtggt accataaagc attttgggtc cttatgcata 420
 acgcaaactc ataacttga atggaaagt taattactta ttattccaat actcgtcatg 480
 tatctgattt agagatatct tatcttttta atacttaaat attt 524

<210> 459

<211> 571

<212> DNA

<213> *Drosophila melanogaster*

<400> 459

cgtggggtga caaagagagt gcccagaggga gagagtaaac gagtgcgaga gagagagaga 60
 gagagagaga gagagaggag tccgcgagaa agcgccacga agtatgctct tgttttgtgc 120
 tctcattttc accttttgcg ttgtctcatc ttaacttttc acttgtgttt gtgttgccag 180
 gcgagctttt ttcttaagaa ggagaaagga gaaacgagaa ttaagcgaag gtaaagagat 240
 ggaaaaggag aagggttttg taagaagaag aatttcgatt acaaattggct aatttgtgaa 300
 ggaaattaac cttagtttta agaagtataa gtaggtttga tctaattata attattatc 360

tgttatttta ttttatcaaa ttatttcaat ggtaatgtga catgaccact gtgacattct 420
 tataccatat acttttatat atttttcatt tttttttcac acttatatag attatgagag 480
 ctgactatta ttttaaccat tgctggtgaa gccacaaaat tggcatggta actttcatct 540
 tcataaccac attatccagc ttaattgtgc c 571

<210> 460

<211> 455

<212> DNA

<213> *Drosophila melanogaster*

<400> 460

ggtcacactc agccagcagc atggtcacac ctggcgatgg cagtttggag atatategat 60
 tgtggttctt aggcgatact ttcttggcgc cagcttaaaa aatttaaate ttttaatttaa 120
 aaaatttcca ggcaaatgca ctagttttta taggcaacta agcggaatct aaagccattt 180
 aactgccaat ttgtatacca tatgtattgg actgcaatga atttagtagc aaataaacia 240
 catatgtaag gttattaata caaaattgtt tactttatat acctcgctaa tgcggaactt 300
 tttttgggtc catgttgctt ccaaggtttt agggtcactt aaaatttact taaatgaaag 360
 atttttcaca gtaatggggg agatttgctt tcagaaagcg tcgaactcct tcttttctaa 420
 gggcttaaag aaatgtgtcc cgagaagggg cgatt 455

<210> 461

<211> 106

<212> DNA

<213> *Drosophila melanogaster*

<400> 461

ccttgaacca atctacaata tcttcacnat cataatgac atccctttta acgcatcacc 60
 cgatttcaaa gcaaatacag aaataaactc aggcagatc ggtttg 106

<210> 462

<211> 51

<212> DNA

<213> *Drosophila melanogaster*

<400> 462

ctccagatac tttttgaaca ctgaagaaaa cgcgcagttg tgggtgaatt c

51

<210> 463

<211> 79

<212> DNA

<213> *Drosophila melanogaster*

<400> 463

cgtgggcggc accagaatac gagagagaga gcaattccag cgcattccagg cacatagttc 60
cgttagctca gttgaattc 79

<210> 464

<211> 470

<212> DNA

<213> *Drosophila melanogaster*

<400> 464

gctgtgtgcg cttcttttga attccctttg ttttcgtact gcctgtcggc cacttgagcg 60
gcgtatgcta catgctatat gctaaatagg caaacacatt tttgtaacaa ttctcgaaag 120
tcgtccggtg aatgtgtggc atctatagga gctgtctaag tgggccattg gccattcgt 180
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gattgaacca taacagatac tcgtagtcag ttgcgcgagc gggagtttct tcgggatcca 360
ttaatggatt tgggactata aatacacttg cgccgtggta tctatctggg gaatcgtttg 420
atatttccat ataaatagcc ctagcatcgc actattgaca ttttgcaccg 470

<210> 465

<211> 507

<212> DNA

<213> *Drosophila melanogaster*

<400> 465

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gaccggagg acgaaggctc tctcgaaatt atcttcaatg tgaagattct tctttctgaa 120
tgttagctaa aatatgtttg gaaactggcc agtagagatt gcaatggctc tggttaagga 180

taccattagt agaacatcag cacagtagaa acctggagtt tctgttgga atttacgtgc 240
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 ttttttacta ttttgtgaaa aaataaactt atcacacctg tgttcaaggg aaataattaa 360
 tatatttatt ggtattgtag aaaggaaaat ttagtggtga aagaaatgcc aagtgggata 420
 tccccaattt ggtaagtatg gtacatatat actggaatag taagggtag ggaactctaa 480
 tccggatgtc caaagctttc cttaggg 507

<210> 466

<211> 260

<212> DNA

<213> *Drosophila melanogaster*

<400> 466

atctacacga tgcctaattg caagtgtgga aagtaaggga ctgttttagac aatgccataa 60
 attaacctgc aaatcgtgac aaatcgggac atcggaaatc gaatatatct tgaaatcact 120
 ggaaacattg aattgaaaca aaatatgcat aaatttaaca aaaaaaaaaa tgcgcaaggt 180
 gcctatgccg gggggcatcc ttgatccaat gagaattact tttagaactt tacgaaatat 240
 gaaatgaccc ttaattaatc 260

<210> 467

<211> 534

<212> DNA

<213> *Drosophila melanogaster*

<400> 467

gtcccacgga agctttaaca gtggagcctc gtgttttgct ctctcgctct caaactgttt 60
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 gagatcattg ggtaaaaatc tgtagataa aatggtgacg gagcattaaa tgctgaagat 180
 gattttatgc agtaactttt aaattaaaca gagttattac gttatgttct gaatgggggt 240
 ttgaatgcgt tagatgtaaa ctgtgatgtg ttaataaaaa caaattccaa tgtgttttcc 300
 ctaaaatatt tagtaatatt ttgaaaaatt cttcaatata tcttaaactc gtttttcgca 360
 aattgcctat tgacgttcca ctgaaatatg ttttctctcg agtgagataa ctcccttaa 420
 attcgtagta aaaatgtcga acattaacag aaattaatca tatgggtcat gaagttgatg 480
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<210> 468

<211> 615

<212> DNA

<213> *Drosophila melanogaster*

<400> 468

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ctgcaaagta tgctacgaac aagaagtttg cttgaggata atcttaaaaa acatttatgt 60
tcatccttta aaatgtcaaa cgatttgagg actctagaga tttcgggaac accctgttat 120
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gtactgtgct tcgctctaca agagattcca gtgacacatg acgaaacaga aaaccgaaca 600
cagcacgttt atacg 615
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<210> 469

<211> 27

<212> DNA

<213> *Drosophila melanogaster*

<400> 469

gttcgggttg agttagagca tgaattc

27

<210> 470

<211> 551

<212> DNA

<213> *Drosophila melanogaster*

<400> 470

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ggcgaacgca gtgcatgtga agagtaccgc tataaaagtt tcgccatcag ctctcccgt 60
cgctcaccgt gttatatgag tccaacaccc aaaaaaggga ataaagagag ccaagcagca 120
gcgtcttttg cagcgccagt gccgaaaaac gttgcaaaaa cgagcgaatg aaatcaaaca 180
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actcgcagtc gaaattgttg ttctgcactt gattgtatta attgtttttt tatggtattt 240
gtttttttctt ccttgcgttt cgtgtgaatt tgtctggctt ttcctttccg gctctcactt 300
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ggggtgtgct ctcaaagggc gccaaaatga gctgcattta aaatttcgga atattgctac 480
cataaacgtg gcttccaatg ggcccgagtc ccattacggt catttcgtgc gtgcaacgaa 540
accagtgtga a 551

<210> 471

<211> 465

<212> DNA

<213> *Drosophila melanogaster*

<400> 471

ggccgagcca cgacgacacg aagcgaaaca cgaatggcaa acgaagccga agttgcgagc 60
gagagagaga gaatgggaga aaagtgcgaa agagagtgtg taacggagca actacacagc 120
aagaaaataa atgtgtctag gctagagctt tggatgaat accaatgat aaaagattta 180
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tgacccttaa ttggaactac ttttcccca gtgtgtgggc cggcagagag ggagagcaca 300
aagcaaaatg caacggaagc aactcatcgt ggcacaatgg gcagactttg tccgagggct 360
ctccaccggc acctcacccc actacacaac tgcgccccct ccaccctcct cttcgacaag 420
ccgaagtttt tgccgtgaca cttcattttt attttccgac cttgg 465

<210> 472

<211> 215

<212> DNA

<213> *Drosophila melanogaster*

<400> 472

ttttgagatc gaaacatatg tatcaatcga gcggccgtgc gtgctgctga agtcgaagaa 60
aaaatcacgg gaaatcacgc cacttcggtt aaaacagccg gcaaaatata atgagttaat 120
atgtgttttt ttccgttgtg tttggcggat aagaaaatcg cggcatgagg gatgctgaag 180
tgattgagtg cggcgcacta atgtgcagcg aattc 215

<210> 473

<211> 412

<212> DNA

<213> *Drosophila melanogaster*

<400> 473

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gtggggaata ttaatagatt cacgtcggct atgaacagaa ataggtgccc aaatatatac 60
gtattacatt ttaggcgaag atagcgtggg cttacgatgt tttccaaata tacatatata 120
ttcccctata aatcttatct aaatcaccta ctctgcttcc attatatgct atcattcaat 180
ctctaaaggt ttaatcctta cagctgataa gtacagttta attggaggcg taagtataca 240
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atccttcgac tatttaaact accgcgatca aacacaaaca cgaagacctc aagtggtcga 360
ggctgccggt ttggctatct ctggcacttc atgcacttca atctatgaca cg          412
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<210> 474

<211> 559

<212> DNA

<213> *Drosophila melanogaster*

<400> 474

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ggcgaatgct aaacaaaatg agagagcgga atgaaagctg tctcttgagg agcattttcc 60
agcactgcta gagcttttca agagcaccac aagattttta agcggaaagc ttttcaaaga 120
tgtaactgcc tttttagaaa cgtaaaacaa aacattctgc aggacgtaca aaatgtatgt 180
atttaataag acaaagagtc tattatttat gatattctata atataaaaca aatgatgtta 240
caatcaaatt aaaaatattt tattttacttt cgtttttatat tttaagccaa ataataataa 300
aagtaattaa aatgtagata ttaaaataaa aatttaaadc gattcggtgc acacttttgg 360
taaaatgtag aaaccttcat atggatttcc attaattcct ttcgatactt tttaacactg 420
gctgatagct tacagccaaa ctgggttcaag caaggaaccg aacctcaaca cttttttaag 480
ctcccacttg gtgactttga aatagtaaac atgggttttta tcagctaata tcagatogtg 540
ccaatctatc aattaccca          559
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<210> 475

<211> 474

<212> DNA

<213> *Drosophila melanogaster*

<400> 475

ggccactcgc tcgctgtctc tttctctctc cctcacggat actcgcgatt ttccgcgact 60
ttgaaattcc gtatacgtcc gttccggttcg tcggtcgaag ctattctgag cggtagcgcg 120
cttttgaaca catcggaata gttgaaaatt ttgagattta tttatagaga gaacgggcag 180
tgttttgato tctttgctga tttccaaagg tctctttgaa tataattaat caatgggtta 240
atcagcccta tagtggattt cttattgaaa aataataatt aaaattcaat cactatgtaa 300
ttaaatgtat ttttacaatt tatgagataa aaattgggtg tacaggttca taccatattt 360
ctaactcata aattattatt cgaataaacg cacctcaaaa tagtttttga aaaagcccg 420
taaaaacatt gacttcaatt cggctattac tattagccaa gtttacacca tggg 474

<210> 476

<211> 849

<212> DNA

<213> *Drosophila melanogaster*

<400> 476

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gtgtgtctaa aaatagacac aaatattgaa gttgattttt atacggccat cgtcagatac 120
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aacattgttg cctcgtttga agtggctgtt taaccactg atggcccaga aggctaaaag 780
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<210> 477

<211> 157

<212> DNA

<213> Drosophila melanogaster

<400> 477

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ttttgatagc tacgcagctt cttgcgtccc agaattc 157

<210> 478

<211> 94

<212> DNA

<213> Drosophila melanogaster

<400> 478

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tatataaata ttttctatgt gtgcgtctga attc 94

<210> 479

<211> 485

<212> DNA

<213> Drosophila melanogaster

<400> 479

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aaatgtattt gaaataattt ttgtgcacgc cattcgagac ttccataaat acaaagagga 480
atggg 485

<210> 480

<211> 1145

<212> DNA

<213> *Drosophila melanogaster*

<400> 480

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<210> 481

<211> 232

<212> DNA

<213> *Drosophila melanogaster*

<400> 481

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taataagcat aatgagaaca tggcataata cgagacttaa gccacatgat gtactatgta 180

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232

<210> 482

<211> 522

<212> DNA

<213> *Drosophila melanogaster*

<400> 482

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agaattgaaa acagaatcgc atcaaataca ttatacttca cagttgaatg acgagaaatc 180
agaaaaaaat attccccgc ctttctaag aaatcaaaat cacaagttta taagtgccaa 240
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ttaatctatt ctatatctat gtgtaatcga atcgaaatgg gcagtcgaac aaattgataa 420
aatggcagct aaagccggag aagctacaaa taaatggatt aagcccagca gggtgagtta 480
tcaaaagcga cgccgcatta cggtagcccc acaaatgaaa ta 522

<210> 483

<211> 325

<212> DNA

<213> *Drosophila melanogaster*

<400> 483

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ggattggatc ggattgtaat cgcaggcggg acagagggcc gcagcaaaag aatcggatcat 180
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tcaacggaaa catttgtgat tccaagcggg gtggatttga ccggtgctat agaaacgggg 300
gttaaaacta atgattttta atttg 325

<210> 484

<211> 426

<212> DNA

<213> *Drosophila melanogaster*

<400> 484

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ctggtataat tctactttta aatgagagct ttgttttaga gttcgaatcg attgttttat 180
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gtggtgaagg cttcacatta aaatctctat tgatccgtta actatcttaa attactatct 300
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aaattatttg gttggtatgt atgggccgcc cggggccggc gtgcaaatca ttttctgcat 420
cattaa 426

<210> 485

<211> 527

<212> DNA

<213> *Drosophila melanogaster*

<400> 485

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ccaacaactg acaccacccc ttcagtctgg cgattccacg ttcagtcgcc tggattttgc 120
tacttttggt gttgtcgctc tgcttgctgt ttgtttttca cgtcttgccg caacgccagc 180
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taaatttagt ataagtacaa acaataatag agatctctct attaagcgga caacataagt 420
cgtgtattta atactattag acttacgtcc aaagaagcta taagcgcctc actattgtgg 480
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<210> 486

<211> 504

<212> DNA

<213> *Drosophila melanogaster*

<400> 486

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aaactactgg agtgtggcac agaaagtgta aaagtatgca taacatatta aatataaatt 180
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 gcacaagaaa gagagacaca ccaccgtgat acggtttgtt gtggaacgca aaggggtatt 360
 cgatcgtttg tggagcgcac tgcgtttgtt tgtggttcgc aattgtctta gcccgcgaga 420
 atatttatta ttaatttatg gcattttatt atgtaccgcg ttgttggtta ataagcaatg 480
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<210> 487

<211> 584

<212> DNA

<213> *Drosophila melanogaster*

<400> 487

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 tattaatagc gcagcgccac tccgcggctg tgttagtgcg ccagagtgcg aaagtaacag 480
 taaaaaacta aatattaatt cgcgttgatt ccgattcgta ttgcaagttg ttcaaaaccg 540
 agtgctagtg atatttgcaa aaaattaaca tattttccgc tggc 584

<210> 488

<211> 439

<212> DNA

<213> *Drosophila melanogaster*

<400> 488

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 atttgcacaa aaaatgttga atcagttcga ttttcaatg aacactcacc cattaatata 120
 ccattgtagg aggggggtata ttgatttccg tcagaagctt gcaacgggga agggaaacgt 180
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aagttatctg gataagtcaa tcaaagtggt gtttctactg caggaagtat gtatataata 360
agtatatcgg acatgtacat cggaatatta tgacaaaaaa gtactttcat tatatataat 420
tcattttagt tttttgacc 439

<210> 489

<211> 118

<212> DNA

<213> *Drosophila melanogaster*

<400> 489

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<210> 490

<211> 352

<212> DNA

<213> *Drosophila melanogaster*

<400> 490

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tgcgactgcy atgtgcgctg ctacacacgc tacaatgca tacagcatac agtggcagaa 240
aacagtttgg cacgggttat aaatacgtat ttattagtaa aataaataag ttgctcagtt 300
ctttagacga aactatggat tttattttta tattgaatag gatgagaatt cc 352

<210> 491

<211> 333

<212> DNA

<213> *Drosophila melanogaster*

<400> 491

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ggctaaatag ctaggacatt tttacagtct atctctttgt gaaaaccttt ttatcaaggt 300
ctttaaaaag taagtgcatt taagcccgaa ttc 333

<210> 492

<211> 91

<212> DNA

<213> *Drosophila melanogaster*

<400> 492

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tcgtacaaat accgaagaca atattgaatt c 91

<210> 493

<211> 426

<212> DNA

<213> *Drosophila melanogaster*

<400> 493

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cactatcagc aactgctctc atgtatattt ttatcattaa tggatcattg gtttccgctt 420
aatttg 426

<210> 494

<211> 548

<212> DNA

<213> *Drosophila melanogaster*

<400> 494

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 gcatataa 548

<210> 495

<211> 120

<212> DNA

<213> *Drosophila melanogaster*

<400> 495

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 cggctatatg gggaaaaata acaaatacat ttccgtaatt atatggttcc gaaagaattc 120

<210> 496

<211> 408

<212> DNA

<213> *Drosophila melanogaster*

<400> 496

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<210> 497

<211> 559

<212> DNA

<213> *Drosophila melanogaster*

<400> 497

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gtcctaacta tttggttcc 559
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<210> 498

<211> 592

<212> DNA

<213> *Drosophila melanogaster*

<400> 498

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acaaattagt caattcgttt aataattggt ttggatacgt ctacaatggt gcatggttat 540
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<210> 499

<211> 108

<212> DNA

<213> *Drosophila melanogaster*

<400> 499

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<210> 500

<211> 284

<212> DNA

<213> *Drosophila melanogaster*

<400> 500

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gatgtgtctt actacagtcc aacttgctta ctaaaaccaa tggtcagtat agaaaaaggt 240
gactcaggac caaataggaa ataattatag tttaaactga attc 284

<210> 501

<211> 455

<212> DNA

<213> *Drosophila melanogaster*

<400> 501

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<210> 502

<211> 522

<212> DNA

<213> *Drosophila melanogaster*

<400> 502

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ggtgagtttc actcgcaagg aaagataagc tgaataacat aa 522

<210> 503

<211> 676

<212> DNA

<213> *Drosophila melanogaster*

<400> 503

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ttcattggct ttgagg 676

<210> 504

<211> 541

<212> DNA

<213> *Drosophila melanogaster*

<400> 504

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<210> 505

<211> 59

<212> DNA

<213> *Drosophila melanogaster*

<400> 505

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<210> 506

<211> 288

<212> DNA

<213> *Drosophila melanogaster*

<400> 506

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accaactgaa tggcatgtat tctgaatacg cagtaaaacg aatcgatact ggagaatggg 180
gttatgcac cctctagtac gtgtggcgt cgtttttcaa tttgttgctg ccggggaagg 240
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<210> 507

<211> 234

<212> DNA

<213> *Drosophila melanogaster*

<400> 507

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gttaaaaaat agatacaaaa atgtccgaat tgcaggtgaa ctgaatctac gtcaaatacg 180
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<210> 508

<211> 31

<212> DNA

<213> *Drosophila melanogaster*

<400> 508

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<210> 509

<211> 892

<212> DNA

<213> *Drosophila melanogaster*

<400> 509

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<210> 510

<211> 53

<212> DNA

<213> *Drosophila melanogaster*

<400> 510

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<210> 511

<211> 197

<212> DNA

<213> *Drosophila melanogaster*

<400> 511

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<210> 512

<211> 305

<212> DNA

<213> *Drosophila melanogaster*

<400> 512

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catttcgttt gtttacagtt tttcgttttt gcgccatggg aaggctgtat tcggattctc 180

tttaagcaat gaattttaaca aaaaatttagc tagccagtga agcatatctc tttaattcta 240
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atata 305

<210> 513

<211> 387

<212> DNA

<213> *Drosophila melanogaster*

<400> 513

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ttcgattttc acttggtttt ttaaaagcct tctcttatca gcaatcgggt cttaatagct 180
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tgtcaaatta aaatttttga tgagagcaaa tctgtcttca agttttatca taaaaatgaa 300
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<210> 514

<211> 530

<212> DNA

<213> *Drosophila melanogaster*

<400> 514

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aagaggcaag ttcttttggg gtatttacga ctaagcaacc acattgggtt tggccagcgt 180
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ataaacgggt ttcgttggcc aaaatgcgtc atcgccataa agccttgccg aagtcaatag 480
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<210> 515

<211> 516

<212> DNA

<213> *Drosophila melanogaster*

<400> 515

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tgcgctcctt ttcgactttt tagcaattac ggcgtagcgt aattggagag aggtgtaaat 180
tcacaattta gcaactgcagt cgttgtgcca cttgaagtcg tgagtgcagt tcgataatct 240
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gattgcgata ccattcgatt cgattgtagg aaatgaaagc acttaaaatt atatagatag 360
atacttgtat cttctccagc agaagcgtgc ctttacttga tatgcgtgac aagcaaacac 420
cattaccctt taaatgtcag actgcaatga attttggatg tattaccgcg attctggcct 480
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<210> 516

<211> 583

<212> DNA

<213> *Drosophila melanogaster*

<400> 516

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gtaacgttga gttccgcgtc cgtgcgttct gccttccaat agaaagtctg ggtgtgaatt 120
taccaagatt ccagtgcgaa aatcaactca cattgctcgg tgatccgtgc ggcggtataa 180
ttgcagccgg aattgcataa gttgcggcga gcgaaagaga gtgcacggat ttacagttat 240
aaagggccgg cagcgggtggg gcggcgacgg cagagcacgc agaagaagaa gagacggcag 300
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<210> 517

<211> 437

<212> DNA

<213> *Drosophila melanogaster*

<400> 517

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tccgggggtgg ctgcccctgg ccccaagcgc cccggagaat cgctggcatc tgcaacggcc 180
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tccttcggca cttcctt 437

<210> 518

<211> 442

<212> DNA

<213> *Drosophila melanogaster*

<400> 518

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aatttctctt taagctgttc cttctaaagg acacaagaaa ctaatatgtt tatgaaataa 120
gaaacttaac cgtgtatgtg ttttccaatt ttgcgtgaac aaataaaaga gctcaagcat 180
tttatcggtt gagtaatttt agataaaaat ttattaatat tttttaatgt tttcaatttg 240
ccatagacaa ctttttttcc aataaaattc ggtaataata ataacaccat gcctgcaatt 300
tttatataaa ttttttagtag cacgctctta gtttaatat taggtcaata aaataattat 360
ccttattggt ttttttttta atttgcatat tggttggtga ccagctgtta agaagaagag 420
agggagagag aaaaagagaa cc 442

<210> 519

<211> 536

<212> DNA

<213> *Drosophila melanogaster*

<400> 519

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ttaaacaag cagctgcatt tcaaaacttg ccaatgtaag tgaagtaact gctagaagct 180
 cctacaaaca agttttccat attccacaat atgcatttag catacgccat gtagttaatt 240
 acgtatacga cgcgagaaca aaacgaactt gaatgttctg cggcaaggcg agcggataga 300
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<210> 520

<211> 469

<212> DNA

<213> *Drosophila melanogaster*

<400> 520

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 cgtgcgcacg ctctttggag tctaccgct ctttcagtcc ctctttccac tctctcgatc 180
 ccagaggtgc ccaaaacata agttgaaact tatttaagta cggcttgaaa tatttaaatcg 240
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 tattcaagtt acgcgggttaa ttaaaaacat taatagaagg gtttttcttt ttgaaattaa 420
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<210> 521

<211> 417

<212> DNA

<213> *Drosophila melanogaster*

<400> 521

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 aatattaatt ataaaaatatt caaaataatc acacagcata taatattttg ttacataact 120
 attttaagtt ataaacatat atttctgtta tatttaaata gtattgttta tactcgactg 180
 ttttaagtgt atatcagcga tttgtaccac tgtgccgtgc tccacttget cccgctccca 240
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 ttctactact acgatgccgc gcccttctgt tttcattcaa aatttcatta aaggatgcac 360

acatgcacac ctccctcccc cagacacaca cacaaacgca ctggtctgtt gaattgc 417

<210> 522

<211> 543

<212> DNA

<213> *Drosophila melanogaster*

<400> 522

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tattttgcta cgctcttttt gtgtttactt atcatgaacc atgcttggtta tgcaataaaa 120
attatttatt agaaagtatt actatagtat tgataaaaac tcaagtaaca accaaatatt 180
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tgtctcataa atgttcagag cgttccgctt cgctagttgg gcacaaactt agcggttgcca 480
gtgggtccta caaatagact ttagggcggc acggtgttcc caattgacga attataaaca 540
aaa 543

<210> 523

<211> 510

<212> DNA

<213> *Drosophila melanogaster*

<400> 523

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cggtctcggt gcctggtcgg tgccttgggg ccagcgtag tcatcgatc catcatcatc 120
atgagcctta gccgccttat gccgctccc ctgaattgac cgaattaaag ctctgggatt 180
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aagaccagga gaaattgcca cagtcaaac aattagacag acgggccaga ctctgtctt 300
caacttggtt ccgcggcgga taaaagttgg tgtcttatgc tgggaaaagt aaaaagtgtc 360
taattaaatg cttgtccaga ctggctttgg aaaatacaag gtgcttcaat gcaaacaat 420
ctgtacgaag ctgaaatacc cttagacat actattaaat ttaaattttt caagcttgta 480
gcgcattttt caagctttcg aaatgaattc 510

<210> 524

<211> 527

<212> DNA

<213> *Drosophila melanogaster*

<400> 524

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ataaagtatc caatccaaga aaatgagggt atgcgaatgt agtaattaga ttctaagttc 180
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tgggctgtgc tgccgcattg ctgctaactg cggctttcca cttttaaact caaaataata 480
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<210> 525

<211> 91

<212> DNA

<213> *Drosophila melanogaster*

<400> 525

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agagagatgc taaatttagt tcaatgaatt c 91

<210> 526

<211> 417

<212> DNA

<213> *Drosophila melanogaster*

<400> 526

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gtgctatttta ttgaaacaag ttaagtgggc tgtaaatggt tacaattggg gaattaaaaa 360
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<210> 527

<211> 578

<212> DNA

<213> *Drosophila melanogaster*

<400> 527

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caaaagttaa attgacaggc ccccgagcc cctaaaatat tttttttaa ctagaactga 540
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<210> 528

<211> 169

<212> DNA

<213> *Drosophila melanogaster*

<400> 528

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gttggattcg aaacaagacg accatgatgc atacacaaga ctcaaagacg gagttttttt 120
tttcaatttg gcaaggcaac tgcaatagtc tattccttga caagtgaac 169

<210> 529

<211> 348

<212> DNA

<213> *Drosophila melanogaster*

<400> 529

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aactactgat attattaatg cttctagtgc tatcgatata atagcgaata caccacctt 300
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<210> 530

<211> 463

<212> DNA

<213> *Drosophila melanogaster*

<400> 530

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catcttttca caaagtttcc atttattgca cctcgcagcg aacgagggtta tattgttttg 120
acggaactaa gcagatttaa ccacaagtat caattagggt gaggtttact aatgattttt 180
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tgaaaagggt atccattcat tatttaccat cgggtgctctc ctgattgcta agtatattat 420
agtcgggatc gtgccccttc ctacttggtc attgtttcct ttt 463

<210> 531

<211> 150

<212> DNA

<213> *Drosophila melanogaster*

<400> 531

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acagcagcaa catcagcgcc aacgattggt acacagcgcg aaaatcgggg gtgccttcaa 120
agcaattcgt ttcacaggg aggtgaattc 150

<210> 532

<211> 439

<212> DNA

<213> *Drosophila melanogaster*

<400> 532

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actatgatat ttccactgcg tcatttgata ttgatgtat tgtgattcaa agcttgatc 180
aattgcctgt tcaattatgt atgttatatt ttttagtagg aggggtaaat ataatgaagc 240
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aattgtgcct catttcctac tcaaattttc tcttaagcta caagggtatt gtaatgaaca 360
gaaaagctca aacattcttt cggttaaaaa taaattacag gcctcataat ttaataccga 420
caattaatat ttatttaaa 439
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<210> 533

<211> 521

<212> DNA

<213> *Drosophila melanogaster*

<400> 533

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gtacccatca aacacacgaa aatattattg ttactgtgta acgctttaaa attaatttat 180
ttttatttgc aaacataagt cgcaataaaa tctgtttaga aattaactta aattttaata 240
ataataaaaa ttggaatgaa taatatacta aagtaaggag tgcctaacia attagcaaag 300
aaaataaaaa atttaaatgt agcctaaata taaaaacat cggcacagtt agtacgctgc 360
aaaagtaatt tagcaacaac attcagatgc aaccagttcg ggtttcttgg cttcctcgct 420
ccattttcac gtgccttttg tttttgtgcg ataatcaca aagttttctg aaaacgaaac 480
cactgatagc gccacaaagt cccccaaca caaaccacca c 521
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<210> 534

<211> 511

<212> DNA

<213> *Drosophila melanogaster*

<400> 534

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aagacaacaa caagtgcgat cggaagacgg cagcttttca ggagcaaac atacaggta 420
agatatgcag actaatccca tctaattgg aaacacacac tattttattcg gggttttttt 480
attaatacca agctgaattg ttacatttaa c 511

<210> 535

<211> 461

<212> DNA

<213> *Drosophila melanogaster*

<400> 535

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gagaggacgt aatgagttag ctatttaagt ttatgcgaat aataagatat taccaaaaac 420
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<210> 536

<211> 383

<212> DNA

<213> *Drosophila melanogaster*

<400> 536

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gcgctctctt tgctcttttt gagagcgcc aagtatctgt gcgctgggtg gcgtgcgaaa 180

agtatctgtg tgcgctggaa aaagtagcaa acgaggcggc acgacgacaa cacgaacggc 240
 aacaacggca ataatgatta tcattataag tgggctggcg ctccggctgt gtgtggcact 300
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<210> 537

<211> 544

<212> DNA

<213> *Drosophila melanogaster*

<400> 537

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 gaggtactgt atcggtaaaa tttttgctaa ggaaataaaa ttacttggaataaacttgaa 480
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<210> 538

<211> 530

<212> DNA

<213> *Drosophila melanogaster*

<400> 538

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<210> 539

<211> 507

<212> DNA

<213> *Drosophila melanogaster*

<400> 539

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agtttcgagc taaaaactag aaattacact gttaaattta aaacttacta ccaccagtt 180
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gaacaacaaa gggggtcaca aggcgtaaat ttagttttaa ctatcccata tttcaatttg 420
gctttcacia tcttatcgcg gccacgggtg taatctgata aaatcccagc cccagcaaaa 480
tagtaccgga aaatcacttg ccctaac 507

<210> 540

<211> 577

<212> DNA

<213> *Drosophila melanogaster*

<400> 540

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ttctcatoga tccagcattg atcttgccat tttcatgaat cggttggcat tagtcaccgt 240
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caagcaaaat gaaacattca atatnnnna tgtttcaaag gttttctata ttttatattt 480
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<210> 541

<211> 513

<212> DNA

<213> *Drosophila melanogaster*

<400> 541

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tgttgatacc attttcttta aggttattgc agtgcaatgt cctcaattgt cggtcgcctt 180
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cccttcgctg gcacaaaatg tgaaatgtga aaggatttcc cgttttattg tcgtgggtcc 360
gattccggag ttcaatattg gtttattttg ttgacttctg atttgctcgc atttgtgggt 420
tatttgccag tgtgggaaca cattaaatat ggtagctgg aaatcaaagg ttatctggat 480
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<210> 542

<211> 302

<212> DNA

<213> *Drosophila melanogaster*

<400> 542

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tttttttttt tgggcagtca aattgaggaa acattaaaag tcgcgccaca tcaggcactt 120
tttgttcggc aaagctttgt ttcggacacg ctgagtattt ccatcgcaac gggtgaccac 180
tgtggcagac cccccacaaa aattcgtaac cgcaaccaaa tctgcaaaac catttgcaaa 240
ttaagcgca taacgatgtg tgggcagata gaagagaaat gtaggataaa tgggtgaagg 300
tg 302
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<210> 543

<211> 611

<212> DNA

<213> *Drosophila melanogaster*

<400> 543

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tttgaaggaa caaggacggc aatcatatga aaaccggaaa gctttcagct gaaagcactc 120
acatgcacgc acaccgcgt ttagcgcacc gctcgtgcgg cgagcttttg agagcgacat 180
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aaagaattgc aaatttaaaa ggaaaagaag aaagacgaat ttaaataattc acaagatata 360
attatacttt ttcaaaagaa tgggcctcta agttatattt aagttactta tctaagacct 420
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atcgtcta at aaaagcttgg attcgatatt tgttttccaa tgccaggaag attgttaa at 540
tttgaagttg aaaccgcact ttttaattgt caaattcaca ttgcattatt tgggttttcat 600
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<210> 544

<211> 82

<212> DNA

<213> *Drosophila melanogaster*

<400> 544

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tatatgctaa ttttattcca at 82

<210> 545

<211> 858

<212> DNA

<213> *Drosophila melanogaster*

<400> 545

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tggtgctctt ccttctctca atatcgtttc cttgagcgtt tcttgagggtg tgacgtcacg 180
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tctgagctgt ccgagtggta ttggtgcacc aataagaatc ggccagtggg tccagtgcct 480
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 aaattataat gaccaagtag gcgacaagaa ggattggatg ggtgggtgtt ggggtggccg 720
 atgtagacgt agacgatgat tatataacag ttttctgtga ttctcctcat tccgatcgaa 780
 tcccttcttg aagcaggctt aattaaaac ttttggcatt cacttggaca aaattaccta 840
 ctttaagaca ttcttca 858

<210> 546

<211> 277

<212> DNA

<213> *Drosophila melanogaster*

<400> 546

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 atgaaccaac ctttcatat taaaattagt ttttctccc ctgccaaagc cgattattgg 120
 gaagcgaana gagttcgatc cgagacaaaa aaaatgaatg ctgacaactt agtatttggg 180
 gaatctggaa atgggatctg tttgattccc cgtttgtgtg attccaagcc cgtttatgac 240
 ccctgccttc cttcatggaa tctatttcaa ataattt 277

<210> 547

<211> 370

<212> DNA

<213> *Drosophila melanogaster*

<400> 547

ggcgtttttg aaaattgaaa aaatagagag ctttagtagg tggcaaaaaa gcgataatca 60
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 agttaaattt ttgcttagac tttgctctta aatttctttt aacaaaattg gtaaaccacat 180
 tgaggacatc tgaaaataat aattaaacaa attgcaactt ttttcaacaa agttcgaaat 240
 actttcttga aaatagctaa aaacattggg ctatccgatt atttctgcct ctccaaagcg 300
 gtaaaccatc gttaggcgtc catcactatt cacagatggg cgggatattt aattttgaac 360
 gcatgattat 370

<210> 548

<211> 539

<212> DNA

<213> *Drosophila melanogaster*

<400> 548

gacgtgcctg tacccatcac acacctacaa acgtatacgt catacacaca cacacacgca 60
cacatgaaga ggcagacaga caagcaactc tgggctcccc cctccctaaa cctctcccct 120
cccagccaca tactgccgca cttgcaacgg gaatgttggt ggtattgctc gcactgctca 180
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aatttttggc taattgttcg tcattgggca aaaatgaaat gctgaggaat ttgctttata 480
aaaacactta aatttatagt tattagccac tgaatttgta ttgcagtcgt taagaattc 539

<210> 549

<211> 449

<212> DNA

<213> *Drosophila melanogaster*

<400> 549

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catggtaaaa aataaaataa tttataataa atgttttaaa tataataaca aatattttga 120
gttaatactt tacatttata tttaatcaag gtaagctaag atatttgaga tttatttagt 180
ttttaccaag ctgcaaatta tattacacct tatacttttt tttaatgacc agtghtaattt 240
cacttggcac gttttaaagt attttgtacc gttacggata cggtcatatt ataaacaata 300
aaatctcgat ggactcattt agccgtacaa aatataaaca aattaatacc aaaaagacat 360
aatagtcgct tttgaagtat atcaaacttt tatcaaacca tgagctgcaa ctacgcggat 420
ggattgtcag cctacgacaa caagggaat 449

<210> 550

<211> 85

<212> DNA

<213> *Drosophila melanogaster*

<400> 550

gactggcgta attaaaacgg ctcccgcgct tattcgcgcc cgaaagagag cgacaggtag 60
agagaaatgc aaaatctagt tcgga 85

<210> 551

<211> 485

<212> DNA

<213> *Drosophila melanogaster*

<400> 551

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cgagcaacga atatacatg acggacatgt cccatgcagc agtgggacca tgcgcgacta 120
tcgcttgatt ccgatggcac gaaatgggtca ccctggaccg ccttccttg cttatttttc 180
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ccgacattga gtaacttgat tgacttaaatt ttatttctag gttgtcaaga acattatttt 420
taatcaataa ggtattttcta aacaattatc tgcaccttga aacaccctac atttttcgtt 480
ttggc 485

<210> 552

<211> 314

<212> DNA

<213> *Drosophila melanogaster*

<400> 552

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agagagagag agagcacgag agcgaggctc tcccagagca aaaacttggt ttcaacggcg 120
ctttgaagag gagcataaat atgcgcaaaa aagcacagaa taagaagcag gcaaaatgaa 180
ttaatagaca atcaagccaa acgatgcgtc tgaattaata aaagaaatac cataaaaaag 240
ggaaagagaa agagggagaa aaacccttga gttgaaggaa gggtataaag gttggaagcc 300
gcgggcaggg gggc 314

<210> 553

<211> 515

<212> DNA

<213> *Drosophila melanogaster*

<400> 553

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actgagatac gtcacgacgc agaattttca tgaatgaatc gcgaccggca cttttgttaa 120
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aataccgatt ttaagaaagg tatctggctg gttcc 515

<210> 554

<211> 357

<212> DNA

<213> *Drosophila melanogaster*

<400> 554

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aaaagcaaca agcgtgtggg aaggggaaat cgaaagggga agtaaagagt atgtgtgggt 120
gtgtgtgtgt gcgtgaaata tggaaattga aatgcaatt aatcgtgaat taatggcaag 180
ccatagaaat cgctcaatgg cttaaagtgc aagagaaaag tgagcttttt gttattgttg 240
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tttcgttttc gcaacaaca taagccatca agcgaagtgc tgaaatagtc aatttac 357

<210> 555

<211> 619

<212> DNA

<213> *Drosophila melanogaster*

<400> 555

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<210> 556

<211> 295

<212> DNA

<213> *Drosophila melanogaster*

<400> 556

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<210> 557

<211> 203

<212> DNA

<213> *Drosophila melanogaster*

<400> 557

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 gggatcaata ttcgggtcaa cacaaaaatc caattggaac taattaaaat tataatattt 180
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<210> 558

<211> 202

<212> DNA

<213> *Drosophila melanogaster*

<400> 558

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aatcggttggg aatgtcactc cagtaataca ctgcacgttt ttcactactg ttccacttgt 120
ttttactccc tgtgaatggc acgtctaacc gttgtcgata tcgcaaaagc atgctatggc 180
agccgcacaa ccaactgaat tc 202

<210> 559

<211> 311

<212> DNA

<213> *Drosophila melanogaster*

<400> 559

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cgatcatctat gggtttttct ttgctttata ccgactttgc cctgcgtata ccccttttta 120
acagcgaagt gaactggaag gaaattaaaa atatattgtg ctgtgtgtta tactaacagt 180
aactactaat tgctaccgtt tttaaattata cactaaaaaa ttgttttggt tttttgggat 240
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aatttaataa a 311

<210> 560

<211> 511

<212> DNA

<213> *Drosophila melanogaster*

<400> 560

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aaaccagtcg cgtgtttatt aataaccaa atatgcacac aaccgcccac gaaattggtc 120
aaaataacaa acagtgaat aaaagatata ggaacttcag gttgattgga tattaattcg 180
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ttgaaaacgt gcattctatta ttatatgttt ttagaccaga aagtttaa at aaatttgggt 420
aattaaacat acttgcaaaa catttaagtt ttgctccact tttttatagt ctttttatgg 480
cattaaaatt tcctactttt aatttcgaat t 511

<210> 561

<211> 354

<212> DNA

<213> *Drosophila melanogaster*

<400> 561

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tgaagatgat gatgatgcaa ggattcgaca tccaatcatt tgcataatgta tacacacacg 180
cactcactcg cacacacact cacacagcct ccaaagtgc tgcgcgagag gagagaaact 240
gaatttttca ctgcgccctcc ggcgaaagtc cggcggcaga tttgttggtg ggccaagaag 300
actccaatat atattttgcg gggcgctttg gtttttgggg cttttcttaa ccca 354

<210> 562

<211> 505

<212> DNA

<213> *Drosophila melanogaster*

<400> 562

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aattgccaaa gtaatattaa gaatattaca actgactatt tggcctccga gtaactttta 120
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agcgcggaac gttattaaat aaacaattta ccttaaaaga cctcaacaag gtgaagtgtg 240
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taaataacaa ttaaatatgc atattttatt ataagcttgg gtcatagttc ttgaatttac 480
tgtcaacttt tttcgaatgc taatt 505

<210> 563

<211> 406

<212> DNA

<213> *Drosophila melanogaster*

<400> 563

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gcgctcagtt gaaaatctct ccaaggagtt gcgaaaaaaa aaactttgaa aacattgttt 120
tggaatgtcc acttggtcgg cttttgtgtg ttgaaataaa ataatagtta tctgcgaata 180
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aaaatggaaa ctacaattgt tactacaaca actacaaccg agttgaaatg cactatgcgc 300
ggcagtaaaa agaaagatgt taagctgcgt tccaaactct aaaaatctga cgttttcaat 360
tcagttagaa caaacaattg gctaaactac tccatggcca attaat 406

<210> 564

<211> 368

<212> DNA

<213> *Drosophila melanogaster*

<400> 564

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caattaggat aggctattac aatttataaa aattataaaa ccgttaaagt ttttaagtgc 120
ttaaagtaaa tgtctataat aatgcttaga ttatttttta cccattctat tgttggaact 180
aattgataat actttgaaaa atcaaaattt aagatgagta ataagtagta agtagtttag 240
cgatagaaga ttaattttta gaaaaataaa taccttacct taatccattg cttattccca 300
atctattgac ccaggtgtt ttagcactca ctcacacaca cacgttcaca aaaaatgggc 360
agaagggt 368

<210> 565

<211> 278

<212> DNA

<213> *Drosophila melanogaster*

<400> 565

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cgctgttttt tctcttcggc gctggtacgg tcataccgcg aattgtactc tctgagattc 180

gagttcgaaa gtacgttttag catatgcagc aaccaactaa gagataaaat tcgaaatcaa 240
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<210> 566

<211> 290

<212> DNA

<213> *Drosophila melanogaster*

<400> 566

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aaaaaaaaaca aggttcgggt tcagatttgg gtcttggggt cgggatctcc ggatctgaat 180
cgagtcgcat cattcccgggt gtccgggaat agccaagagc caatcaggcc atttgccatc 240
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<210> 567

<211> 739

<212> DNA

<213> *Drosophila melanogaster*

<400> 567

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<210> 568

<211> 766

<212> DNA

<213> *Drosophila melanogaster*

<400> 568

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<210> 569

<211> 700

<212> DNA

<213> *Drosophila melanogaster*

<400> 569

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 gttgttggtg ctacaatatt tctgtttgca cttgtcggct ttgtttttgt tgtttatccc 660
 attctatcac tctctggcat tctctagaag cagcggtcag 700

<210> 570

<211> 484

<212> DNA

<213> *Drosophila melanogaster*

<400> 570

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 tttcgtaaag gcagcacact ccgcacaaac aacatgcgaa catatacaga cagactgcaa 180
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 cccttttcaa tttttttcaa ttgtacagcc aatatatttt ttatgatttg ccctggaggc 360
 ggcaactctg ttcggggata cgggcacata catagaaacc agcgagttgg ccaaatacaca 420
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<210> 571

<211> 497

<212> DNA

<213> *Drosophila melanogaster*

<400> 571

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 atattaacgt ctttctatgt aagttgaagt atattttatt aagttgcaga gagacaaatt 240
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 agccggacaa tccaaaatgt ctgtggaaac acaagaatgt attaatgatc ttgaaaccat 480
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<210> 572

<211> 373

<212> DNA

<213> *Drosophila melanogaster*

<400> 572

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<210> 573

<211> 1306

<212> DNA

<213> *Drosophila melanogaster*

<400> 573

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aacactgcca actcagtcga cgacgagtcg tcgctgttgt tgcgttggtt gttgccgcca 240
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 1200
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<210> 574

<211> 603

<212> DNA

<213> *Drosophila melanogaster*

<400> 574

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 aaaagttgca catcaaaatt caagttgtta atttaaaaaa cattacaact aaagacatca 240
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 acacatgcaa gcaaccacca ctttgccttg acttgtgcgc gagggacga gacaagcata 540
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<210> 575

<211> 392

<212> DNA

<213> *Drosophila melanogaster*

<400> 575

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<210> 576

<211> 375

<212> DNA

<213> *Drosophila melanogaster*

<400> 576

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aaaatatect atcccccttct caaaaaataa ccaaacgctc tccaatttat tcgaattaag 360
ggtccaattt ttgga 375

<210> 577

<211> 322

<212> DNA

<213> *Drosophila melanogaster*

<400> 577

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taactataac atacaaaaaa aaaaagcaaa gaaaaatcaa atcaaatact actactcgaa 120
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aaagtttgag caatttttta cgcaagccag gaaggaatcc gtatatttta taatcaattc 300
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<210> 578

<211> 262

<212> DNA

<213> *Drosophila melanogaster*

<400> 578

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ccactccac tttggcttgc atcttccct gcattgtgat gcactggctc tgcattttcc 240
aggggcggat ctggaggcta gt 262

<210> 579

<211> 783

<212> DNA

<213> *Drosophila melanogaster*

<400> 579

cactggctca ggtgaatgat gccacggtga acttgttcat cggttcacta gttcgcgcgc 60
cgagtgttat tgtttgttt gccgtcgtcc tcgcatttcg tctttgttaa tttcctcaaa 120
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gaaaaattaa atgttcttac tttggttttt tcaacatata ttatcataaa cttgtagctt 720
aataatacaa aatgtagcta aatctttaac tcgttatccg tgatgttaag gaatgttgaa 780
ttc 783

<210> 580

<211> 316

<212> DNA

<213> *Drosophila melanogaster*

<400> 580

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ttttaagcc ttcttttaggg caggggtgtgt gtgttcgagt gcgtgtgtgt gtgtgtgtgt 120
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<210> 581

<211> 511

<212> DNA

<213> *Drosophila melanogaster*

<400> 581

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gcgtactcac ttcagttggc atcggacgtt cgtcgtgcga gggatcgatc gcggttgtgg 120
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<210> 582

<211> 168

<212> DNA

<213> *Drosophila melanogaster*

<400> 582

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tctcggaatc tcacacaaca cagcgatcgt gcctctcttt ctggtcgtgt tccacogtct 120
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<210> 583

<211> 490

<212> DNA

<213> *Drosophila melanogaster*

<400> 583

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caaacttttag ggctaaaggg aagttacatt ctatttaaca aaattgaaaa atattgaatt 480
tttggcgcca 490

<210> 584

<211> 409

<212> DNA

<213> *Drosophila melanogaster*

<400> 584

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<210> 585

<211> 705

<212> DNA

<213> *Drosophila melanogaster*

<400> 585

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<210> 586

<211> 424

<212> DNA

<213> *Drosophila melanogaster*

<400> 586

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agaaccggtt tgctcttatt agctcgctgt tgggcgcacg tgttagatac tttaccgtt 360
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taaa 424

<210> 587

<211> 230

<212> DNA

<213> Drosophila melanogaster

<400> 587

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gtcagagtga aagagggtttt caccttgatg cctgatgccg ttacacacgg cgtatggggcg 180
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<210> 588

<211> 480

<212> DNA

<213> Drosophila melanogaster

<400> 588

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aaacaagtgt ttacgattac ataaagtcgc gttccgctgt cagcaaactt gctctcggtt 180
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<210> 589

<211> 294

<212> DNA

<213> Drosophila melanogaster

<400> 589

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gcgtttcaaa tccgcgccga ttgtttcgct tattgtcatg ctcgatttaa ccgcttagag 240
ttgcggcagt acggaaaaat acacatataa ttcacaaaag ttatgccaaa ctaa 294

<210> 590

<211> 460

<212> DNA

<213> *Drosophila melanogaster*

<400> 590

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tctggctgcc gtcgaacgtt gtcgtcgttc ggttgaatcg aatcgaaaag cgcagctcgc 120
caaaaagcca ggccaaaatc tcaaagccac ggctcagtga aacagttatc agaaattttc 180
gaaaaatcgc gtaaaaagtt ttcgaaaaaa aaaataataa ttaaaaacat aagcaagcaa 240
ccgatttcaa gtggcaaaaa taacaaatta gaaaaaaaaa acgcaaaca aacacagcac 300
atTTTTTgga ttaagtgcc catagttcct gttagcagca gcaacacaca ccaaccactt 360
ggattactat aaacaacagt attatcactt aaaactagca caaaaattgc aaaattttct 420
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<210> 591

<211> 485

<212> DNA

<213> *Drosophila melanogaster*

<400> 591

gcccgtccgt tttttttcgg ttctgttttcg ccgcagtcga aattcgtcgt cgtcgccgtc 60
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agctaccctg ctatatatac cactatatat aatatccgtc tatatgtgct accatatcga 180
aatcggttct atttatcggc acacacaaat aatcacattc ggatggccaa cgtaatttga 240
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gagctcatta tttctgccta attagcatac aaatcgtaga gagaggctct aagtcggctg 360
taaagtgtta taaacaaaat aaaaatatgt ttcttccatt gggaaaaatg agtggttgatt 420
gctaateggt aattccttag caatttatag tgcaataaac ataaatcgtg accagtgaca 480
tagtt 485

<210> 592

<211> 300

<212> DNA

<213> *Drosophila melanogaster*

<400> 592

gtatcgctt ttaaagtgcc aaaaatggag agagaccgaa gagagagaga gagagagcga 60
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gaaatgattt taaatatttg tggctcatgc attttaattg gcatttgcaa acgtgtgtgg 180
cctacaaatt gaagtacttt ctatacggat taaaataaet attttgtgtc attgcgttgg 240
cgtgtaaatt aatttaaatg agcttcgctg gggattttat aatcaacatg aatcgaattc 300

<210> 593

<211> 184

<212> DNA

<213> *Drosophila melanogaster*

<400> 593

cgctggatcg tatagtgggt agagatgggg aaaacatcga tgggtgctgag gggatcgata 60
tatcgattgc gtttttgact actgtcgatg attgcaggcg ttagtgcctt ttggccgggt 120
gtgctttcac cctctctagg tttacccggt cgctgttaac cgttacaggc gctcttttta 180
tttt 184

<210> 594

<211> 866

<212> DNA

<213> *Drosophila melanogaster*

<400> 594

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tcggctgctc tctctgtttg ttatcagtgg cgtgcgctct tttatcaa at tggaaagggg 180
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tctgtgctat acattttata cactaaaggc atgaggaaca gcttaaagcc tgaaagtttt 600

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 cgtgctaaat agtttctata agttgctttg tgtgtttacc aagtgatttt tgcgattaag 780
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<210> 595

<211> 352

<212> DNA

<213> *Drosophila melanogaster*

<400> 595

gtattacact atcggaagat ggcatgatt gcgcttcgtc ccactcgag cagcgctgat 60
 agtcggattc caccgaacat ttacgctaa attaataaaa tttattaaaa ttcatttctt 120
 gttaaattga agaattctaa aaaatacttt tcagtttaaat ttaaattaaa taacctatct 180
 aaagaccaca atcaggcatg ttccggtaat agtaatatct tttcgattac gatttggcaa 240
 aatctttcga cttcggtttt aggtgctcgg gttttcgctg aatttttgcg atcggaatgt 300
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<210> 596

<211> 846

<212> DNA

<213> *Drosophila melanogaster*

<400> 596

gggttagtga gtgagagccg ccgaaaacaa ttaaactaaa tttttgtgat atttgaccgg 60
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 atttgtttgt gctttccacc actgaaagtg tcatttaagt ggcattttca cagtcgctgc 180
 gttttatttt acttctctcc cttttgtcgc cgattgttta ctccacgat acacaaacac 240
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 tgttgccgtg cgttgttttc atgtctgtgt gccacaatcc ttatcaccac aaacaaaagc 840
 gaattc 846

<210> 597

<211> 443

<212> DNA

<213> *Drosophila melanogaster*

<400> 597

gtctggggca gcacaactag ttatttattt ctgctgacgg atgtggatca tctgccacaa 60
 cctatcataa gtcggctgca aaggccccag atcgggaata gtaaccacaa aagtattata 120
 gtactacgga acctctacct cccctctgca ccccgctccg caattacttc atgcccttgg 180
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 ctcttgcctt cttataacct tttatagggt atcatggcaa tttaatgttt ttacgccaac 360
 tacgataata gctttttattc agtcttagac taaattgggt tacccttgat atctaacata 420
 gtttatcaat tocaatagtt cca 443

<210> 598

<211> 402

<212> DNA

<213> *Drosophila melanogaster*

<400> 598

tttcggacta ttgagtgatt tccctctctt cggggaaatt cgagatggag agtaaagcga 60
 aggaaaatgc aagggttggg gtagctggga aggcttttga tgggcgcggg tttgttggat 120
 gggttttatg gctacaccaa gacacttaat tgggaaaaag cttcaataaa atgttgcatt 180
 aagccattgt agctacgaga tcttaagccg agcaattgta atttgagaca ttttatttca 240
 attatTTTTa tttggcattg atattacaat ttcgaaaaat tttaaactat gtatgaacac 300
 tacggggaaa ttaagttata tatattccca tattgggaaa tataattagg ctttaggtta 360
 ttatctttct tttatagtta aagactttgt taattagcaa ta 402

<210> 599

<211> 513

<212> DNA

<213> *Drosophila melanogaster*

<400> 599

gtttgaagta aagttgagaa aataactaaga aaatctagat aagcagtgct ccaatatgaa 60
cagtaatcag taaattagtg aagaatgcga tatgaaatag tacagatata gtacgcgagt 120
atccactgta catggcgata aggcagtttt ttgaaaaccc cctccaaatt gaagttcaca 180
ttctttgttg ttactcgttt ttcggcttca ccttcatttt gttttatcca aattgcgctct 240
taaaaatgat ggaaaaacat atctatgcat gtgctgggtg tgcgtgctg tgtgtgtgtg 300
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gggcggccaa taaagccaga gtgcgaggcg caagcaacaa caagcacacg cgggtgcagtg 420
ggaaacacgt tttccgcttt ttgttgtggt ttttcatgcc cttatcaccc gttatgcgaa 480
atgctgcgtt aaccgaaaaa cccaattacg aat 513

<210> 600

<211> 600

<212> DNA

<213> *Drosophila melanogaster*

<400> 600

atcgaactaa tgggggggatt caaaattata tagagctgta aaacaggagc cagctaataa 60
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aataagccat caaagtcagc attatttgca gtgtttgccg accacttccc cgataagcca 180
tacatataga gttacgtaac tggagatcgg cgactcgagt ggccgggctt tggctttata 240
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cttcagatgt gaaattgcta gatttctaga atcgatcaga ttttcccat tcataaactg 360
ggtctgcgac tgtggctaata cagcgcaata ctgattgatc gattggaagt gccattggac 420
aatttataga gcgatccata aatcataatc gactgggtatt tattgtgcgc tattcgcaac 480
tactcgagcc cagcttttag ggtttccggt ccagctggaa gatctttgtg gggacgcaag 540
gcttctggga aaccgagacc ccaagaaaaa gatcacatga tagaaccccc ccatatgatt 600

<210> 601

<211> 571

<212> DNA

<213> *Drosophila melanogaster*

<400> 601

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ctctgtggca ttatagagaa aacaaccccg agttacatac agcatcctcc cgactccgaa 60
ccttggagat cctggcacat cctgctcctt ggaaccttgg ctacaagcac tgatttgtca 120
acttttgaaa atgtcgaagt gttgtcgtgt tgttttcggg ggtggctttt ctaatggcaa 180
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tgtttggtct tttggcaaag ttgaaaatgt tccgttaaca gttaaatttg cacttttata 420
ccgctgggcc aaaaggaaaa agaaacctg ccccttgata ctgccacca agtttgttgt 480
tgtgtgtgaa tgtgttgggt ggggtggaaa atgccgtgtg tgtgtgtgtg tgtgaaatag 540
gcgcccctcg cccccacaac caaaacaaaa t 571
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<210> 602

<211> 475

<212> DNA

<213> *Drosophila melanogaster*

<400> 602

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gtgtggagcc aagaatacaa aaggagagag cccggagaga ggtgtaagta gtgtgcgctc 60
cgcgaagagg cgcacaaaaa ggaagtaact aaaaataaca aacatctcgt ttgggttgt 120
aaggtggaat gaactcagaa cccgcgatgg agaagatgcc gaaaaggaga cgccgaggag 180
acaaaccaga caccagaga tccatgcccc aaaactgatt gaactacagt gatcacttgg 240
ttagaggcac cctaatacatt aacacgcctg gcacacacga ttgaaaatga agtcaccact 300
ttaaaataac atatatactc atttaaactc tcccatttac cccaatgtgt tctaaatacc 360
tacagtctct gttaatacat gtttaccata aatcccgcca gattctcgga attaaagtgc 420
tttgccaata tttttttgaa ccatttaaaa agatattaac ccaactgtta tgggc 475
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<210> 603

<211> 371

<212> DNA

<213> *Drosophila melanogaster*

<400> 603

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caaactctat atacttttta gacttgccgg aaatgcgaaa ctttaaagtt ggagctgcgg 120
gtagaagcgg taagatcctt gcacgaaatt gataaacagc attgcatcag caattagggtt 180
tcggtgttgt ttaagttctg ggaatcgaac aagataacca caatattttac ttatttatcc 240
aactttttgc tctctctcac gttgttcaat aataatctcc acccgctcaa cagcaggtaa 300
atacgtccaa agttctacaa ctttctactg atgaaattca ctttaacacg gaaaccggta 360
tgtttttgc a 371

<210> 604

<211> 488

<212> DNA

<213> *Drosophila melanogaster*

<400> 604

aaccagacca ttgcctatcc gcgctcatte accgactgct tcatcatgtg cattggcatt 60
ggcttggttg ccagatttca ccagctctat agaagaatcg ctgctgttca taggaaagta 120
atgcccgcgg tcttttggac agaggttcgg gagcactatc tggcattgaa gcgtctgggtt 180
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ttcatttgc tccaattggt caacagcttt aagtgagttg agaaatgact tctttacaca 300
gcttagatat attatgtata tttttttttt agaaatatag gtgttggtgact ttctggtgat 360
gtttggcttt ttggtactcc ttaggattcg ctgtagttcg cactttactc actattttcg 420
tggtttcttc cataaacgaa tacaacgaaa gatgtcacag ccctgcggga tgtgcctcca 480
gagcttgg 488

<210> 605

<211> 500

<212> DNA

<213> *Drosophila melanogaster*

<400> 605

atctgtacaa tcaatttcat gaaggtacaa tcgatatttt ttataaatcg attattataa 60
gttaagaaat taaaatattg attaaaaaat ttaaaattta tctatattaa caatttattt 120
gtttaataaa taaaatgtat ttttaatcgt taatttttta ccaaggaaag ttttttaatt 180
taatttttct gtttacgata cgcactctaa tttgcagcat ttttgactaa aaaaaactta 240

aaaccttatt tcatagtgc aaaatgattc atcgagtat ctgtaatctg tatctttctt 300
 ttcacttctt gagattaacc attattaata atcacataat ataaaccact tttaattcaa 360
 gtaagttgtc agttcctgca ccccgattt taaatgttaa cgcataagcc cggggcatta 420
 aaaacaggtt tggcagggct tgcgcggtc cattgcaaaa aaaattcccc gccacagagt 480
 ttttcgcta ccaattaact 500

<210> 606

<211> 387

<212> DNA

<213> *Drosophila melanogaster*

<400> 606

gccacatag tgtgttgcc gtgaatccag ttttcttttg cgacatcgtt tataaagaaa 60
 tcccaaagcg gcgaggtaaa aaacagaaac atcaaagca gagtaacaat tgggggtgatg 120
 attcatttca tccgaaactc aaatcgtttt cgagacttat caaagcacgt taaaattgat 180
 ctaaattgggt atacaaattt cacacatata tttttgttta gaaaactgca tttaaaacgt 240
 gtaaagttgc agcatatttg tttctctgtg tggagcgcgg taggtgcgag ataaggtgat 300
 tcgaaagcac gttcaccact cgcacgggggt ctgttttttc ttccagcaac ctctagaaga 360
 aatccccact agaataatac tagtttt 387

<210> 607

<211> 322

<212> DNA

<213> *Drosophila melanogaster*

<400> 607

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 ctccggcggt tcgcccactt cgaccattt cgctggcccg atcgccgat ggcttggcat 180
 gaattagcac cttttttgga ctttcttttt gtccggtctt gacgcatttt taatgaattt 240
 accatggcca aataactttt actaggctgc gtgtctacgg gttattcgaa tccaactcac 300
 ttctaaggcc ctgccacttt ga 322

<210> 608

<211> 590

<212> DNA

<213> *Drosophila melanogaster*

<400> 608

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ggccaggcca aaaatacagt ggtcgtcgag taaataagcc accgattcag aatttccatt 60
tgtcaataaa gccagcaac aacaaccag tatagcccat atatcactgg gtctggaaca 120
tacataaata tttttatata gtttatggat ccccagctc agctgtgtgg aggtgtaaga 180
aacaaaaagg cgaaacgca aataaaaaac agtaaccaat ttcgcaaaa gctcgccaag 240
ctgacagaac ggcaaaattg gaagagagta aagagcgaaa cgctgacgtc gagcagcttg 300
ttttaacttt tgtttaaaat ttaaattgct aatgaattga tgatgtcttc tggttctaag 360
aacatactaa gggggaaaaa gacgtgttat agggatatgg caatagaggg gagcaactta 420
taattaagag cttagcttgg cagtaaagcc ccacatgaag aaaaaatttc ttaaaaagt 480
taactttttt ttttaaatac aagaaacagt ttatcttacg cttacttgaa ataaatctaa 540
atttttgaac tttttttgac tcctttacaa tgagaaacat gactaccctt 590
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<210> 609

<211> 416

<212> DNA

<213> *Drosophila melanogaster*

<400> 609

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ggtaaagggtg tgcgactttg tctttgcctc tctctctcgc acaccgctc ttctgtatgg 60
ctgtgtatgt gtgtgtgtgc tgcagcaggc gggctttttg tttttttttt togcgacctg 120
ttgttgctcg cttgataatg gcaggctttg ttgttgctgc tgctgctgct gctatcagct 180
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ttgttgctta ttggtataaa tgttggtgta attatcacta ttgttgcggt tacttctact 360
aaagttgctc ttgttgaaag ttctcgtcgg tgtaccgttt ggcgttggtg taacta 416
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<210> 610

<211> 504

<212> DNA

<213> *Drosophila melanogaster*

<400> 610

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 gcctctgctg gcggaaaact cctgggtcaa aggagccaa aacaaccgtc gacggatgac 420
 gacttttccg actaacaacg gacgcgcatt ttcccaccgt ttccgaggcaa gagcgcattg 480
 aaatttgtgc gacgccagcg caag 504

<210> 611

<211> 879

<212> DNA

<213> *Drosophila melanogaster*

<400> 611

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 aaggaaacga catcaaagat gggctaagcg cgttttcaaa gtataccgca taaaatattt 120
 ttagagggca aacattttga acatttaaac attttactac attagaatgc ataaattgat 180
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 taagtgttcc cactgctcaa aaacctttac ccagaattc 879

<210> 612

<211> 443

<212> DNA

<213> *Drosophila melanogaster*

<400> 612

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eggagcattg atttgctgtc ttgattttg cttatgacct gaggtgctct cttacatata 120
tataaacgcc atcatccagg cagacagtag gcgagtgtaa gcgagagaga aagagcatgc 180
gacacacata cgcacacaca ttgacacctg gcgcaggagt cgcggcttgc ggcactttca 240
aataaattaa aaaatagcaa caaaaccaac agggagagag gcgaatagag cagtaagcct 300
ttccccagct tctctgctca gtagtaacat tagtaagagc aacaaaaaca gggacaagag 360
agcaaaaata catgcctacc ttaacccaat taaaatacca tattatttaa caaaagaaat 420
tgtgttattt gcaagcaacc cca 443

<210> 613

<211> 231

<212> DNA

<213> *Drosophila melanogaster*

<400> 613

ctgctgccga ttctgagttc tcgatttctca gttcgattct cagacgttgg cgaaccgaga 60
accggtgacg tagtacgttg ccgtccgccca ttattacaac gtcggctgcc acacgcaaaa 120
ttggacatac cagctaacca aaaataacca acgccaaactg cagctcggat gcgaagtgtg 180
cttgccaaaa gtcaaacgat aacgaaaata acgcaggacc ataaaattcc c 231

<210> 614

<211> 473

<212> DNA

<213> *Drosophila melanogaster*

<400> 614

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cgacaacaac aaagtgtagc gctgccgccc gcactttctc cgcagttctc gccatttctc 120
cgctctactt tctccgctcc tctctccact caataatgtg ccaactgttg agtttctctc 180
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cctctcgcctc tctcgccggc atcgaaggct gcttacaggt ttttatagta cttcggcttt 420
gccgaccaca gccaaatttg ccggcgcaatg gttggcttct gcgttggttc cgg 473

<210> 615

<211> 188

<212> DNA

<213> *Drosophila melanogaster*

<400> 615

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tggataaaga gagatccgca tactcttggt gtagttgttg ttgttggtgc tttgccggct 120
ggcttgcaat taacgctgac gtcgacttcc acacacccct taacccttgt gtgccggcga 180
atgcagtt 188

<210> 616

<211> 439

<212> DNA

<213> *Drosophila melanogaster*

<400> 616

tgcgatagta tccgactctc tcccgaagc cgtgctctta gtgaaacttt cacgctcttt 60
gggggtttcga gaagtgaatg taagttgatt gtcgtaagcc ggctttgacg tcgttttgag 120
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aaggaaaaca agtttcttcc gacgctatgg gctgcgtcga cgtcagcgtt gcggcaacat 240
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gaatgcacga tggaatagga cgggggggtg tacccegcct tgcaaccaga cccgactttg 360
gctgctgccg cttggtaaca ttcgctccgt tgatcttgct aacttgacca agttatttga 420
actatgcaca tgttgcaga 439

<210> 617

<211> 144

<212> DNA

<213> *Drosophila melanogaster*

<400> 617

tgtggtaaga gagtatgagc gtcgaacaga aagacaattt aagagagcgc agatcgact 60
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tagtgctcag acacctaagt atac 144

<210> 618

<211> 410

<212> DNA

<213> *Drosophila melanogaster*

<400> 618

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caaattgaaa tcacaatgag ttgaggactt ctgaagtcgc actggcaggc acataaattt 180
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tttttatgtg gcccaggagg cagtgcagcag tgcacataaa aataaatgga aaagcgcaag 300
aacattctgc ctgctcgtga ttaaaaatat attttgaaat tctgctaaaa tcgattgcat 360
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<210> 619

<211> 531

<212> DNA

<213> *Drosophila melanogaster*

<400> 619

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actggctgga atatttcatt ttcacgacta gcagtaaaac ctaccctacc tgtgaacagc 180
tattccaaac attaattcct attttcaact gttatttaag tgaaatatat ggcataatgca 240
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tatacacgga atttgaagca attttataaa ttaaagcaaa atcacatttt tatgttttaga 420
taatgaaaag gtatttttact gatctgagtg aaacattatt aatattattc aatatcaact 480
aagttttcac tgtattacca tttgtcacia aatttcatta cactttgcta a 531

<210> 620

<211> 583

<212> DNA

<213> *Drosophila melanogaster*

<400> 620

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cagttgcttt cttctaaaat tcttttcgca gcttcttctt cccgtgtgac actcgattgc 180
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ggatcgcagt cttagccgaa ggagccaatt ttcgtatttg aatttgagat gatgcactga 300
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gctatgttga ttaaataaac tgtttgcaat tattcgcttt taattttcga atgttattta 480
atagctacta caccaattct tgataactag acttatgaat taatgaataa caagttgaaa 540
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<210> 621

<211> 462

<212> DNA

<213> *Drosophila melanogaster*

<400> 621

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ttacatttcc gatttctagt cattcttctg gacaattatc aaaatagaac cttgcaagcc 300
tttgtaaaca aacaaaattg tggttctacg ctttttaatg attcatttct gatttaacag 360
cctggcaatg acaagattta acagcagtac ggtaccgaag ggataaagcg acgtcagatg 420
ttgggaaact aactgaaatg gaatttctta ttgcttacat tt 462
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<210> 622

<211> 145

<212> DNA

<213> *Drosophila melanogaster*

<400> 622

gttcgaattg acagtgggtg ttggtgaact agatcgcgga ctcgaagttc gggaaactttt 60
tagtgtgttaa gcttgccagt aatgaattga agtatttaaat aactttattt tgaatgaagg 120
gtttgaacat aaaaaatatc ttcgg 145

<210> 623

<211> 518

<212> DNA

<213> *Drosophila melanogaster*

<400> 623

ggctggcgat tggtgtcgct gctaactggg atactggaat aaatcataat gcattttacgc 60
accgttgctc ctcaattttc gagtctgtgt gcatgtgtgc atgtgggtgt tgtgtgtgcg 120
tggtgtgtgt aacctttggc aaaggaaaaa tcaatagcaa cagacgtaga catttgtttg 180
ccgctgttta tgtgcagccc tcgcattgtc cttcgcccc aaaacaaaga gccacccttg 240
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tctgctaccg gcattccaat ccgccatttc cattgccc 518

<210> 624

<211> 249

<212> DNA

<213> *Drosophila melanogaster*

<400> 624

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tttactacga ataccgttca ttcgcttcgc ttggcttcga ctgactttcc gatgatgacg 180
ccggcgaacg ttgattatga agatcatcat cgccgttctg tgggttatcc gagggtaggt 240
atatatttt 249

<210> 625

<211> 534

<212> DNA

<213> *Drosophila melanogaster*

<400> 625

gtgggcactg ggtactgagt gctcggctct gggttctctg ggccactctg ctctggcaca 60
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acccactttt cgggtattcgc actgagaccc aactgctact acccacagaa agtggacaac 180
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caaaagttag cccaaaagaa aaggataaat cctgttgctt cccaaaaacg aaaaccgcag 480
ttttaagcca aaagtgtcca aatccctggg taaataacta ttttgcccag ctga 534

<210> 626

<211> 557

<212> DNA

<213> *Drosophila melanogaster*

<400> 626

ggctcaataa atataccatt tactcgttga gtgaatcggc attcccgtta ctctgtagcgt 60
aagcgggtat actaaccgac agacttttga atgactaacc gaaacaaaga ggttttcgaa 120
cgtatctgca tcctagtata atcgggtgacg agtgagtctt cttgccgaaa atatctcatt 180
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taaattttcc gaccggacag ccgcagcctg gttctgcgtg agttcaacaa tctctaaatg 480
gtcgttgcaa tgtaatgtgc tgcaggcact gcgaatcggc cttttccctg gcgcaagcac 540
atTTTTTTTga atgactt 557

<210> 627

<211> 397

<212> DNA

<213> Drosophila melanogaster

<400> 627

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ggaagggagt gagctggggg ggttttgccc aacaattttt catttctccg gccaagacat 180
gtgcatgtat gtatgtccgg agtatttgga ttccgggtgag caatgagtga cgaaagatgc 240
cctgtcgagg tcaccagctg tgcgtgtact ttccacggcc acagttttgg agtgtcgaag 300
cactgttttc atattaggtg gggccttcct catgtggcag gtgcagcagg tgctcgctg 360
cctttcacta aacaaaagcc gaagagccaa ctgagtt 397

<210> 628

<211> 408

<212> DNA

<213> Drosophila melanogaster

<400> 628

gcgtggccga tgtattttac gatgtttttt tcgtaacgat taaatatgga acttctgggt 60
aattacagct aatcttcaat caatatattt catttgttaa ttaccaatg gaataaaacg 120
atgtcgctt ctcacctcca tcctcgttct ttggcggatg cttcgactat gagctactaa 180
tttctcgga tgaggcaacc gcaaatggaa gagcgtcctg ttgcacatgc attaaccatg 240
gcatcacgac attatgctaa cttacacaca cactcagtgc tgcaccgat acgagaatgt 300
ccatacatat gtacatacat actatgcaca tatacaggca caggagctc atcaagtctt 360
ccggtttgtc gaggatgttc acattgttta tgctccggaa taaatgaa 408

<210> 629

<211> 566

<212> DNA

<213> Drosophila melanogaster

<400> 629

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tggtttttaa ttttttttaa tttttgcccg caaacctgca actgtcacia caggcgacgc 120
caagaaaaat gatggggcag cgggggctgc ggtgggtgat ttgcaaaact attgggttgg 180
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cgcatttccg gcgccactca acagactaca gccatataaa caccaagcaa acatcaataa 300
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 aaaattactt aaacattggt tattacacaa taaaatagaa aaataatggt tataaaacct 420
 tactcaaata acttacaaat ttataaccaa atttccataa caaaatacac aatagattaa 480
 actgtaaaaa tataatttga ataattctca aacatttcat tacaagaatt tttaatttta 540
 taatccttaa acagggtttg aaacta 566

<210> 630

<211> 570

<212> DNA

<213> *Drosophila melanogaster*

<400> 630

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 agcgacgtta cgctgcggg gtattttgtg gtccctgatt tctatgctcc ttgatcagcc 120
 agccgaaggg tatgatgttc cagaagagca cttagtttca tatctttgta caatatataa 180
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 acaattttag ttattaaaat tgtgcaattt aagtttatta gttaaaaacc tctctcgaat 480
 gatgttcttt tgctttctaa atactgttga taagctataa ataatgttga atagctatta 540
 ataatgtcgt ggctatatta aattatataa 570

<210> 631

<211> 579

<212> DNA

<213> *Drosophila melanogaster*

<400> 631

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 aatcgcggtga tcgagatttt gttggttaatt tatgggccga acctggtgga atttgcaagt 180
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aagccagacg cccagttcac agaaatgttg ttttatatat cccgaaaaat agaatcacgt 480
tcacctattc ctgataacat cgccagatcg ttcaccaggg cgttttgaat aatgaacgct 540
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<210> 632

<211> 511

<212> DNA

<213> *Drosophila melanogaster*

<400> 632

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ggacaaggga cttgtccgtt atttcattga gacagcccag aaagtgcgcc taagtccttc 180
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atgtgtttgt cattgtttgt ctttcccggg tcgaaggacc tgctctgttg aagccttgaa 420
aaattttcca ccccgggaga agcacgttca gatagggatc ttccgaattt tgggtttttg 480
gctcggttta cgcattttac tggaattcgt c 511

<210> 633

<211> 505

<212> DNA

<213> *Drosophila melanogaster*

<400> 633

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ttgtgtattc gtctgttgac ggggaaaggg gaatgtgcgg attacctgcg cacctggatc 120
ttcgggtgcat tgccagcagt tgcagatcga ggctaggtag ctccaaacag agtgcacata 180
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tacttggtat cgattaggcg ctaaataatta caattttaat cggacattaa attcatgggt 360
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tatgaaatac tttttattgg gaattaagtt gatttaaatt atactttatt aaatttgtat 480
attccttattg gaaatcggca taatt 505

<210> 634

<211> 262

<212> DNA

<213> *Drosophila melanogaster*

<400> 634

ccatgggtag tttgaagtac tacgcggtaa aagccgaaaa tcggaaaatc cagagggcaa 60
gaacatacaa aactgcaagg caacgaacgc actaacacag cgacatccag acagacacgc 120
actcgcacgc acacacatcc acaccgaga ggtttgcagt tttggtatct cggatttcag 180
cagttgttac catcgttttg tagtaactac catgaccact gggaaagctt tcccctttcc 240
cccctgggcc ggggaaggag gt 262

<210> 635

<211> 210

<212> DNA

<213> *Drosophila melanogaster*

<400> 635

tgccgagggt aagccgaaga gccagggtat gcgtgctcac tttccagagt tgtattaggg 60
ttgcagtagc tgccctgtga aagaggataa aatttgaatt ttaatgcaa cagagaacgg 120
ataaataatg aaatcgtctt atttactttt ggcacccttt tgaagcgtcc ccttttatat 180
tttgaccag ttttgcacat aaacagttat 210

<210> 636

<211> 317

<212> DNA

<213> *Drosophila melanogaster*

<400> 636

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accgtattac cgccaataat tataacgac ttgtttagaa agaaaaataa aataattaat 120
taattaaata cgataattta tggaggtggt cgattttcaa gtcattcaac atttcttata 180

tgatcaacat gaactacagc cegttcatta aatatgggta aaatataaac tccacattcc 240
ttttacaaca attactttgc atattttattg ataatttacc tactgaaaca caacactatc 300
taatcgtoct tcaagcc 317

<210> 637

<211> 170

<212> DNA

<213> *Drosophila melanogaster*

<400> 637

ggtataacct aagggaaatc cgactctgct tcagaactaa taacagatca agtcctaaca 60
taaaaacgat caaaaccgat tgattatctt tgcacactcc attataacat ggctcttttt 120
agacataaat atcggtgact tcagaattag ctctgtattg gactttcata 170

<210> 638

<211> 433

<212> DNA

<213> *Drosophila melanogaster*

<400> 638

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taattaagga tttttgtgtt tgaattcacg cccactaaaa cacgacccat ttaaatacac 360
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ttaatgtatt gca 433

<210> 639

<211> 606

<212> DNA

<213> *Drosophila melanogaster*

<400> 639

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 acctgggtccc aggccactca gttcatggca gcggccatgg cggctgctgg gccgagggga 540
 aaacgggaat ctccacaggc gatgccgggt ggtgggctga tccggcggtc tggaagggat 600
 gtgggc 606

<210> 640

<211> 375

<212> DNA

<213> *Drosophila melanogaster*

<400> 640

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 ccctgttget gttgctatct ccctccagtgc cgcctgcact ttgcatgcga atgctttgtt 120
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 gtttattttg gcccgctgcg agtaaagtgg caggggcagg tggagaaggg gttggggttag 360
 ccaggggggt gatgg 375

<210> 641

<211> 435

<212> DNA

<213> *Drosophila melanogaster*

<400> 641

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gaatcccaaa aagtactaat ccagctgaaa aacaaccatc ttaaccggcc atgtccaaaa 240
aaagtgttag ccaagtgttt tgaataacgt agttgggtga aatgcttaaa aaaaataagc 300
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ggctgcccga gtgaaaattt ccagcttaaa aatagtacta gatttgagct tgaaagaaaa 420
cccttgaatt tcctt 435

<210> 642

<211> 790

<212> DNA

<213> *Drosophila melanogaster*

<400> 642

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cacacacgca cacacaccag gccgtgcgac acacatagac atgggcagga gcagataaac 180
gccatgtttt tcaaategct gccaggcgca ttcctttcca ttttgttcca ctttgctgcc 240
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tcaatgcat tctgcagact gccatttttt agcataccca ttacaattta ttttaatttt 720
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<210> 643

<211> 565

<212> DNA

<213> *Drosophila melanogaster*

<400> 643

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agattcccac attttggcga agccaagaaa agcggcgagt actcgcgatt ttcccacgcc 120

aatccaatta acattgatta gttgattttg cgctcgctgt cctggaggaa atttgcattt 180
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acaataaatt aaggacatcg agcaggaggc caaaaaatgt gttgcatact ttggggcaat 540
aaaaggggga tttcattatg aatgc 565

<210> 644

<211> 511

<212> DNA

<213> *Drosophila melanogaster*

<400> 644

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aaaaaaatca ctccgaagac cacgggcacc ctgtaagcaa aatatgaagg ggcttctgaa 120
atgcgattta gttaattggt aaaaacaatt ctaattcggt agtcactata tgacgtttat 180
ttaaaacaat aaagtaacca aacattttatt aaccttttaa attttaatat aatctatggt 240
atatgttgat attgcaagat tgtgctggag tattgaacaa tttctgcac aacaagtctt 300
aaatgtgcaa gtgctacaaa aaattttttc ctgttaattt aattgttact gctaatttaa 360
gttagttacc atattagttg ggaattgctt atgttatatt atccgaagtc aagtggagcg 420
caaatgataa tcttatcagt tgcgcacatcg cgcctatgcg tatgatgcc agtgtgacac 480
ttggtggtat ttaattagca aacggaagaa a 511

<210> 645

<211> 558

<212> DNA

<213> *Drosophila melanogaster*

<400> 645

ctccggccca aagcggaat gaatggatcg gatcgaatag accgatgacg ataggttcgc 60
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ctttttctgg aactgtggg aaaaagacat acccttacca tattttttatt attgattgga 180
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 atctaaactg ctgccgaagt atgtatggat gttacataaa ggacaccaa ttacacctgc 480
 ctaagtttta ataaaaaggg tagttcaagt atcttaccac tggcatactt tcgcgttctt 540
 tcatgaagat gaattggg 558

<210> 646

<211> 572

<212> DNA

<213> *Drosophila melanogaster*

<400> 646

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 acgcgcgttt tcatacttgt attagcacac ttgcacttta ttctagcttc aatattgctg 180
 cgttaagttg atoctatatc ctacacctac atttgaaaag tattcttaca ctttaatctg 240
 aaggaatggg agatttccga cctgtataga aattttggat aatattcttg aacgcgcctc 300
 aaaagtcaat ataacgtttt attatttgta aacttggtca agctgtatta tggaactttc 360
 catcgattat tctgtgatgc agatgcgata gaagactatc aattctgaca ccacgtcttc 420
 gaggtgctaa gagatagatt gagaatcagt ttgaatatag tataacatat ctgtagggtg 480
 ctatatatcc tcttaataac taaacacaca aggcaggagt ggactctttg attattgtac 540
 tttccgggtc agcttagcat tcgactgact tc 572

<210> 647

<211> 507

<212> DNA

<213> *Drosophila melanogaster*

<400> 647.

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 gcaaaagtat taagcacaca cacactgccg gtgcgcacgg acacacacag cacactcccc 120
 caccaacaca ctagagcaag tgcgtgtaca tagagggttt gtgtgggggca catatgtgcc 180
 cgcacgatgt cgatactggc tcacattggt agtattttaa aagcgacgaa cggccccgagc 240
 tcgaaagcac gactgaaaac cttaattgat taagcgaatt tgttctatca agctaattca 300

attgctcggc cagttgactg aatgatccac tgcaagcgca gcctttatgt aatcggaatc 360
 agtgaaaaaa gcgaaacacg gcggccgcca aaggaatacg actccaggac ccgagtcaaa 420
 tcgaatttgt ttgtggcgcc tatttacgtt aaagtaaaaa tcttggtgct tggggcaccc 480
 gcttctcgaa cccttccac tcaaagg 507

<210> 648

<211> 26

<212> DNA

<213> Drosophila melanogaster

<400> 648

gccatgacga ttcgaatgtc gaattc

26

<210> 649

<211> 412

<212> DNA

<213> Drosophila melanogaster

<400> 649

gcttgcgcca aaacttcgac tgcaaccgtg ggcacgcgg gagctatcga tccatcgata 60
 cgatcgctga aagataggcg tcacacattc ctatcgatta tacttagcaa agactcgac 120
 cgtaatgcac agtgaggcga aatgttttct tttacttata gtatagttat acaattaata 180
 ataattttta taatttttga actaaatcat aagcgccgcg ggggtgttctt ttattcgctc 240
 tcaggcacgt catccaatac aaattttctaa ctacagggtt ttaaaccctc tatataaatt 300
 ttttgaaaag gttccttagc cagcactgag gtactacact ggccagggga ctttcgttac 360
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<210> 650

<211> 492

<212> DNA

<213> Drosophila melanogaster

<400> 650

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taaacaaaaa gcagatcaca ggagggaaaaa tgtataaata gcgcccccaa gtcccaagcg 180
 tgacgctata tatccctccc tttccctttc ccattccctt cgggccatcc ctctcctttg 240
 gtatttttatt tttaaatttt tgcagtcggt gatgttggtg tttttgtttt tgtttgggtg 300
 aagtcattgtc gttgacaata tcaaggccag cccacctacc aaacctaatg tcctttgcac 360
 agtaagaaaa agggattttt tataattatc cataaaacga aaggtcacga aaaaaatatt 420
 gaaaagagct atcctttaca tcctataatg ctaaagctaa aggtgaattt agggttttta 480
 gngcgacttt aa 492

<210> 651

<211> 582

<212> DNA

<213> *Drosophila melanogaster*

<400> 651

gtttcgctgt ttgtcgtaat cactgcgttt gcttttcggt ctcccgtttt cgtctttttc 60
 gaccaacaaa aggcgaaaac aacaacagca aatacaaact gtttgccctt gttctttttt 120
 ttattttttg cacaaccgca tttcgggttt gcagcaaaat taagaaaaaa tctctagtgc 180
 acttttaaga aagaaaattc cgtttaattt tagcatttta tgttttagcaa ttttaatata 240
 agtcaatctg aacagcgctt gaaaaattcc caaattagtc aaatcattgc taaaagcgat 300
 attatcaagt cacgattata gttatgtagg ttcattcaacc tggacaaaaa tttgcccaatt 360
 taattggcta aaatctatca agatgggtgg tttaaagata catttttagtt acttatcaat 420
 atttttagaa gtaaataaccg gggttaaatg tttcgtggaa aactagaaat ttaccccaca 480
 tcattggcta taattttatt atagcgggtg tatattttta atagagcttt atttaagtct 540
 ttttggttct ttgataagcg tttaggataa tgagtaaata ga 582

<210> 652

<211> 528

<212> DNA

<213> *Drosophila melanogaster*

<400> 652

gatccgacca tgagaaattc tgcaattcca tttagttttt aacgtatgct tactttacct 60
 ctctgccttt gctataaaga attcgcaact gggatcaggt tttatgggta tcgtcttgat 120
 agatgcgacg ttaagtttgc caagtttagac tcgtatatca gcaactagtt ggtaaact 180
 catcaciaag ttgatttgaa aatattttta gctgtaagtt tgttcattgc gcatacgccg 240

tggttaacatg tggttaggtac acccacatta cgcattcgca ccgtttgctc atagagctgg 300
 ggctttgata gataagaatc gggcccgaaa caatgtcatt agtccagtta acgtggcctg 360
 actaaacaag ctaatttccc agttaccaa tgctggcaat tttcggtcag ttattttgaa 420
 tggagtccaa tcatccgagc attaaacaat gtggcctctg caaagttaa ctttattttc 480
 atgattagga gctctcagt cccagtgtga gttattttaa taaccata 528

<210> 653

<211> 446

<212> DNA

<213> *Drosophila melanogaster*

<400> 653

agcgggcctg tatttttaga gttaccagag tatgttagga aaataacgaa attaacgact 60
 accgatatct tatgcgactg atgtgtgctt tcgattatct ttattaaagc ttttgtccgc 120
 catatttgaa tttaaaaaat agagggaag cttgcaatta aaatgtttga ctgaagcagt 180
 ctgttccatt tttcaataat gccttattta ttcgacgttt tttttccaat acacttgaaa 240
 gatatcggac agttttgcat tttggtatct taaacaagat tacaacagag cgaacttttt 300
 atgagcggag ttactagaat ttaaactctg caagcatcgt ttttccggaa taaaaataaa 360
 tgttttctaa gaaagttatt cggcataaca taattgggta agcccaattg attcttttct 420
 attggtcttg gtaatagtgt aaaaag 446

<210> 654

<211> 403

<212> DNA

<213> *Drosophila melanogaster*

<400> 654

gtcgggctga tgacgcacgc ttcacctaatt tgaaattcga cacttctaatt tggaatttga 60
 atcaaccgga agttgcagcg cagttaatgc tggtgttcgc cttaccagg cgcgcagtt 120
 ggcggctctga cgatttgtgt gccaacagca aagatcttac atagtttcaa aatgtttatt 180
 tgttttagttt ctaatctgta ttttaataatt aaaaaaagg ttaaagaatt tgtgctttat 240
 tttattagta gaaagggttt tggtttctgt aaatttttaa tttttcatat tttcgtacga 300
 tcgccgagct ccaactcgcat atatattatg tgcccggtgg acccccttaa tacattctct 360
 gttcaataaa tattattacc tattgcccta ttttggttac aca 403

<210> 655

<211> 525

<212> DNA

<213> *Drosophila melanogaster*

<400> 655

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ggccagcccc cgcgcccccc ttttgctatc tcgcttgctc gcatggacaa aatcaacaca 60
agttcacaca catacaggca cacggatgtg aactcacaat gacaaccact tcgtcaccag 120
caaataaaaa agtgctggcc ttaaataaat tgcgttttat gtaattccac tacattcgta 180
cgttacgaaa acaagcacta ttcattattac acggtataca ttattacttc atatcgagtc 240
caaattgcta ggcaggaaag gtcttaaatt ttacgccttt atggggagtt taccttgggg 300
ttcgacctga caaagaagtg tgggccgcgg cgagactgtg agaaattacc aagtgggtgt 360
ctgttatctt aatcccaaatt actctagaaa catttggtat actagaattt ggagatttaa 420
gcatattata aaatatattt atttatattt actaaaaatg cttcttaata ttcgaaaaca 480
ggtttttttaa tagccaaagt aaaggactgg gatttttttaa taaag 525
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<210> 656

<211> 589

<212> DNA

<213> *Drosophila melanogaster*

<400> 656

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cacaggcgaa tgtcggaatg ataacagtca gtgagagagg ggggaaacac gacctcctcc 60
tctctcgttg aaggattgca aaaagcgaga gggagaggaa gacagataaa agatagaaaa 120
aatcaaccta cgagatagct cgaccaaaaa taaaagacaa accaacacga agcgaagaaa 180
aagcagcgag acgaaatgag agcgaaaatg aaaacacaca caaaaatggc aaaaacgaag 240
agcagccaag caagcagcgg aagaatgtgg aacatacatt tttgtcgta agacggcgga 300
aaagagtggg cttgagaatt gagaattggg gaagaatggc cggtttgggg gaataccttt 360
cggctttgat tgtgtgcgtt gcgcgaccgc cctccccgtc catacaagta cgatagtgtt 420
gtgttggtgc gttgttgctt gaaggttgcc agtttattta tttttggcgc ccatctcgct 480
ttggccatt gattttgcac tgcttgccctg ccttctcact cgcccacttg ccacaccagc 540
acttgtttcc cttttcaaca attctacat cttgaaaccc tataaatcc 589
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<210> 657

<211> 528

<212> DNA

<213> *Drosophila melanogaster*

<400> 657

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ctcctgtgac gctgcgatcat cataatcagc gtttgtcgat tcatcaaaga aaccgccgcc 60
ggttgctctc tccactctct ctctctcttt tcttccattc aaggataccg aaagagagag 120
atcgagagag tgccccctct ccttcacact tccctcatgg gtttcttatg taaatcattt 180
aaagggaaat tgttgcacaa ctttaacgag ttgattggag ggggaggggt gaggctaact 240
gcttgtgggt tttcccggcg taaccctcat tcccccaacc cactcgccca ctttggcagc 300
tgtcaattag agcttacagg gagaaaaaat gaaaaccgga agcttcatta tggtaagttg 360
gcccttccac aaggctcttc gccccaacag gctgttggga aaatgagatt aggggtgggtgg 420
gggggtaaag tgggggggacc cagcttttat gggcctggta attgatgcc aagctgccaa 480
ccatatgctg atggaatggg ggccgttggg cgctgcagaa agaaaggg 528
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<210> 658

<211> 776

<212> DNA

<213> *Drosophila melanogaster*

<400> 658

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ggtaggagat acgaatcgga tttgaagtgc tctaactgat ttgaaattcg tatttggatt 60
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tattttattta tgttgaactc gcggtattggg tttgtttata tggacatctg gcggtggcct 180
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attgcaaagt ctcataaata tttcaagagc aagttttttc gtcttcatct cgttcccgtt 540
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gttgaaagag aaatgtatca tgaggttcat ggactttgat gtgccagtct gtcacctgag 660
tcccactgct cagtgatgaa aaagttcttt tgagtgtttt atgtatgttc cataaacacg 720
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<210> 659

<211> 756

<212> DNA

<213> *Drosophila melanogaster*

<400> 659

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caacatactc aattggattg gatgatgtgg atggagaaaa ataaggggcg gtcattgtac 120
catacaatgc tataatttta tatattcgcc caaagttggg actacgcaat acacagtatt 180
cgtctacgct taaattaagc gatgactaca tacatatagc atccaaaata taccagttta 240
gcagattcga aggtcatttt atgtgtcatc ctaccatcaa tagagagctt tataatgttc 300
taaataaatt taattgtttt cgagaggaaa aatgctatta tattattgtg aatcctataa 360
acgagtagtt tgctaaaaca agtaaaacac agtttaaaat ataatttctt aacagtattt 420
tttaccgtgc attcgcataa acagatgacg cgtcagtttt ctgggggtata tacacataca 480
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aattccggac tatggagcat tagcttcttt gtggaacatc cgtgccacgg aagtgggcct 660
catgccgtgg ttttcaactc gcagaaaagg acagaaaata agtcgaaagg caacacatta 720
ccattgccat agaacggact tgaaatgcgt tgagga 756
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<210> 660

<211> 630

<212> DNA

<213> *Drosophila melanogaster*

<400> 660

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cgccgaccag actctcggac aaccagtgat gatctagcgg atgcggttgc gtcctcacia 60
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gatgagaagc gcgtagaaga accatcgaac tctcgagcgc atcaactcaa cgctcaatgg 480
catacgtgta ataaattcag agctctacaa attattggat aattaaaact gttctattgc 540
gtgctaaata gacataccat aaatcacaaa tttgtgcgat atgcatatcc caaatgtcaa 600
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cttgcttcgt ggtgtgaagc cataaatata

630

<210> 661

<211> 162

<212> DNA

<213> *Drosophila melanogaster*

<400> 661

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aagttaaatt aaaaaaaga acaacaagaa gtggagttgt acacaggaaa aaatgatatc 120
aagtgccttt tcttctaata tatgtttatc ttttgaaaaa gc 162

<210> 662

<211> 509

<212> DNA

<213> *Drosophila melanogaster*

<400> 662

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gttcactgtg tgtagctagt ggtacacaat gaaaatgcaa tcgaagtagg caataaatc 120
gatgagtaca tatacatgtt tcttgcagct ttagcatact actttattac tttgtgttaa 180
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taaaactggtt tcggactgca ttctttgggc cacgttattg gcgctgcgct agctgctgct 420
gctgctgctt ctgctagttt gagcaggctc agcgcaagtc gcctggctga aagcgaaatg 480
atcatatgcg gtgcaatttc tatgaattc 509

<210> 663

<211> 182

<212> DNA

<213> *Drosophila melanogaster*

<400> 663

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gcgcgctccc gttgectctc ctcacagcag ccgccttcga acgcccgcgc tgcctgcttt 120
attttcgcgc cgctgctgat aaaataaaga acaatattaa tttaagttaa aaatacgaat 180
tc 182

<210> 664

<211> 528

<212> DNA

<213> *Drosophila melanogaster*

<400> 664

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ccacgcgaaa gaggtagatc tcttatttca ttcacatttc aacgttcgaa ccgtgtgttt 120
gtgtgtgtct cctgcagtga cgccggtgaa gacgtcgaat gagcagaggt ggtggcaccg 180
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agtttaagat ggtttacata actgatacat aaaacaaaact ttgcatggaa accagagaag 480
aacagagggtg gcgcccgaatg cagggcccca gagagagcag agccgcag 528

<210> 665

<211> 633

<212> DNA

<213> *Drosophila melanogaster*

<400> 665

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aagaagtttg agaagttctt agttaaatat tttatgatth tctgaaaggc ttttcctttg 120
taattacttt cagagcccta taaactataa ataccactca atgtggtacc cccacacca 180
ggaactagca actttcatag atcgaaaatg cccgcaaacc cgactgtcaa aacaggcaaa 240
caaattgtgc aaataagtcg gggaaatggt atttatgccc gtaagatttt ccgtgattaa 300
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tctatatata cccagcacca gcccacccc cagccagaaa gcaaatcaac ttcacatcac 540

tttcaaatcg agcaaagcca aagtcaaatc caactgaacc tctgctcttc cactttttct 600
cttttaatca aaaagaagtc gatgcttctg act 633

<210> 666

<211> 460

<212> DNA

<213> *Drosophila melanogaster*

<400> 666

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tataactacaa acgaattatt cgtgaatatt aaacctatct acgcagaacc aaaactacag 120
taacaaaata tcatttgttt ttagagaaat gtttaaattt ttcctatctt catcacagaaa 180
taaagtataa ttgttagaat taaattttat tttctgtatt taaatcttat gctgaagtat 240
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attgaactaa aaatgtaaaa ctatttcttt ttaaatttta acattaaatg gtcttacaac 360
aaaaaaatat gtggaacata accgtgaatt ggtttaatat aaaatttata ttttaataag 420
gtggaataag gcaagatgct aagcccttta agtgccaggg 460

<210> 667

<211> 443

<212> DNA

<213> *Drosophila melanogaster*

<400> 667

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ggtactctcc cacatcggca tcctgcaatc tctttggctc agcatccttg taagctgttg 120
tcggagcaat ctgggcatgg ggcaactgaa aggaaagcaa ctttccatt caggagcgcg 180
caagccgcag gaatcgcgag cgcagacaat tcagttcggc tttaacgtaa tggacggaag 240
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acttgggaag atacaataga acgccgacca gtgggtgtgta tattaagggt tggaatgctt 360
accaatgggg aattaagtgg caaaaatatt gcaactacga cctaaacgca agggcagtta 420
ataacttcgc cagcttttgg cca 443

<210> 668

<211> 524

<212> DNA

<213> *Drosophila melanogaster*

<400> 668

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actgagagca tatttgtgca ccagagggct gcataacaac attctctttg tccattcggt 60
atacttcgta ttcagaatac atgtcattca gttgggcccg ttctttttgc gttcacttcg 120
tatatatctg gcgatcgaaa tgaactaact gaatgtgttc aaagaatgaa tgaagccaat 180
gaattttcaa tagtaattca gagtgcttaa aattcttcat gttgtcattg agtaaaatga 240
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tggatagtct tttggtcata gatatcatta ttctgaccaa gattggaact tttcaaggta 480
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<210> 669

<211> 537

<212> DNA

<213> *Drosophila melanogaster*

<400> 669

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cgcggacgaa tcgcgagcc agagaagcgg taaattcgaa ataaccgttt ggaaagagca 60
acatgatgag gttctttatt cgtttttagt aaaatggtag aaagtgaata tgtgatttaa 120
ttgataacca gcatgggcgc cgtcagtgtt aattgcgttc cgaattgctc tttcgaaaac 180
gcagacacaa atgcacacac acaaagtagc ggcaccaca cgatcgcaat ggcaaaagtg 240
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ctggcgcccc atgcataaaa atgtacaatt tggcgctctt tgcacttgct accgtcggtg 360
gaaaagcaaa aaaacctacc aaccaacaac aataggaaca taaactgaaa caaaaagaaa 420
accatttttg cttcgcgctt tttgtttttg tttggaccgc cgctcacgca ctttcgcgct 480
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<210> 670

<211> 459

<212> DNA

<213> *Drosophila melanogaster*

<400> 670

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gattaccagg taaacacaca ctaaagttaa gacctaatg gctgataaga tagctttcaa 180
ttggcaagat cgccttttca attaaccatt ttatcttgga aatgacagta ttatccgtta 240
tgaaatttta tctacttcac atgaagccta atatcatgtt taaatgtctt cattcaattc 300
atcagcttat ttacaatga ttaactgata aagatattat aaattaataa tcttgtttcc 360
aaaccacgt ggggatgtaa gcaaaccag ttccgagcga aaccaattt tacctgggtt 420
ctattccggt ttttgggcca tattcttcgt attggcaaa 459

<210> 671

<211> 371

<212> DNA

<213> *Drosophila melanogaster*

<400> 671

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aaaaacacat acacacaact ggactggacc tggccaaatt gaatgaccta cattcaaaaa 180
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ggtaggccag cgctttggaa acgagatgct atagtcacgg gaccgtccac cagatatgcg 300
cagcgggtaca tcacgcgcac gcaccatata agctaagagt tttggacaag tcaactgaaat 360
gtacagaaaa c 371

<210> 672

<211> 551

<212> DNA

<213> *Drosophila melanogaster*

<400> 672

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cccaaaaata tctcgtgcgt tgtgttaacc ttagacagac agctgtattt atttttaagt 180
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gttacagtgc tgcaaactaa gctatttcca agccaaatct ggcaactcat aaaagaaggt 360
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 agaaattaaa attaaaccta tatgcctagt tttgggggta aaaagggtatg gttaatttta 480
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 tggtgccaac g 551

<210> 673

<211> 382

<212> DNA

<213> *Drosophila melanogaster*

<400> 673

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 aaaattagac ttttagcaaa ctgtacaaaa cagcagggtt gtcacacgt gtcacaatat 120
 agtgtcagaa gaatcaaaag ttgtagcaaa caaatccga cgaatatttt atcactatcg 180
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 aaaacctgtg acgccgctgc tatttctatg attagtcaaa gcaactaaga atactacgaa 360
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<210> 674

<211> 515

<212> DNA

<213> *Drosophila melanogaster*

<400> 674

gagtggccac aactgaaagc aaatgtagtg agagggttga gagagagttg catcgaagag 60
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 tcgcgcccat tgtttttcct ctttgggcat cgccgacaaa gaatttacta aagattttta 180
 aaagcattta atatgatttt aaattagatt tatctgttta tattgtttgt aaaaaaggaa 240
 gactaattac caaatttatt acataaatta ttgcaagttt agacttttat atagacatca 300
 tctcttcgat agtctgctag acttactgaa ttagtaata aagtaaactg caccataaaa 360
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 agtggagaga gaaacctggc ttaaaagaga agaaa 515

<210> 675

<211> 513

<212> DNA

<213> *Drosophila melanogaster*

<400> 675

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tgtcggtttc ataggactag ataatagaca attggagttg taaaaacttt cataaattgt 180
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actaaaaatg gttacatttg ttaataaatg aaatcaagag ttagttatat gtagatagag 300
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tatttttgaa agccccttag aaatggtttg ttggattggg ggataagaag aaaccagaaa 420
cacagtcagt atcttttttag ccaggaaaca tgacgcgagc cagcaaagcc gcagaaataa 480
gaagccagaa cttgacagcc accgaggaaa ata 513

<210> 676

<211> 549

<212> DNA

<213> *Drosophila melanogaster*

<400> 676

acctgtagca taagcatcgt atgatacatt caccgcttca gtcaatcaca gttttgttcc 60
caatacaaac atgcgcatcg cggccaccaa agtcaaacac tgctggcggtt ttacttataa 120
acagaaactt ttggctccttc gatgccggtc ggccgcatat ctcttttgat ttctgataat 180
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gtttttgatt tgtccaagca ttaagtagtt cgttttgccg acctgcaaga caattatatg 360
ccttccatga ggaacaagat tggggaaaac cctgacgacg actttgctcc atatgaggag 420
aaacattact ctacatggtc attctaccgt agaattacgg caagggtag accaaatgga 480
ccccgaccgg tattcaactc aaataccgc agagaaccag gtgggttgag cgaattaact 540
ttccaactt 549

<210> 677

<211> 339

<212> DNA

<213> *Drosophila melanogaster*

<400> 677

ggccgcggtg agaaaacacg gacggcacac agttgcataa ctttgagggtt atgtgtgcgc 60
ccagtggaat ttactaatta aatgcgagaa attgtgaatt atcgctcagc atctgtgcgt 120
agaatttagt gagttctttt atttgcagtt tcaaaggcta tcccttcatt gtataacacc 180
tgctttcagg tctgtggtgt gtgtctttga ggtagaacc ggcgaaagct ttccagtagg 240
gcgttgaaaa atgagagggg tgcggggtaa tacaaattga caataattga cattgtttat 300
aaaactatag ttggtaatat cgggccacca acaactatg 339

<210> 678

<211> 582

<212> DNA

<213> *Drosophila melanogaster*

<400> 678

tgctggccgt gcttcttctt cttctctctc cactcagtca attgctggtg ctgacgttgt 60
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cccactatct atgctagaga agtgtttggg attgtattta ttggcaatag attataaaaa 180
atatcgcttt aactggcggt attccccgta ctaatagtag tatcgatag gactactacg 240
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ttatacaggc caaatagata gattgagtag tggtattaca gatgttttga acatagggtct 360
gcctgggttta cattgtttat caaaatttaa taaggaaagg atcaaagaat atgggtcaca 420
ttattatgta attaaaaagt tctcaactca aaaccagggt cataggattt caactatgct 480
atgcaatagc taacgtataa aatgccagcc tatggcctat ttggcgactg ctttggtagt 540
agtatcgcta gtgggcatgt tttccaggcg ctctgcgcc aa 582

<210> 679

<211> 323

<212> DNA

<213> *Drosophila melanogaster*

<400> 679

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 aggtttccgc aatcatgagc ttctccttga tggcccgatc agatggcgac gagaacaaga 120
 cgaacaacgt ctactacatg cgacgttttc tctcagcccc actattttaat cacatgggtgg 180
 gtactgagcg cgtgtcgtcc gaggatacga tattggccat gatgcgaacc cattacaacg 240
 tggaacatca gatccccgaa acagagcccc cgttgaagct gcacaaacag atcgactttc 300
 ccgctgacct acgcctcgaa ttc 323

<210> 680

<211> 521

<212> DNA

<213> *Drosophila melanogaster*

<400> 680

acacaaacgt acatacgtat cgtaagctca cagtaacttg tgcaaaaacc acaacctata 60
 aagtggcaac gtgttgcaag acagttgtcg atttgtagtg gggaaagaggt tccgtcaagt 120
 tggacgggaa gaattatggt caaacaggtc actgatacgc gatggaacca cagaaacata 180
 caaatcttcag atcagtctac acaaactggt gtaaaactac aacttagata tgatcaaaca 240
 agaaacaccc ttacattggt gatatacag acgaccatat cggccatttg gtagctgtgt 300
 tgtaatcttt cgaccgctgt agtgagtcga ttgccttcac agagtcaaata ataataaat 360
 tttcacagcg acgtacatat gagtctgtta gtatgtcatg aatgtggaag ataacatatt 420
 aagaaaatta aaacgaatca acacattaat ccaatgtata ccttccatct tataatatca 480
 aatgaaatat gggtcacaca atacatatat ttatccaagt a 521

<210> 681

<211> 722

<212> DNA

<213> *Drosophila melanogaster*

<400> 681

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 agttggcact gaacatctga ttggatcccc aggtgaagtg tgcgaggcaa cggcacgatg 120
 ctgctcgttt ggcgcccgtg agcgacgctt gcggttagagg agcacagata taggggtccgt 180
 agcacgaaat tcaccttcgc gcgcttttca caatcttttc ggtattttaat ttaaaccatcg 240
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 cttcaattag gaaatatctt tatattctcg taaatgattt cagttccaca aagtgtttcg 360

atttcaaaaa taatttgcac aatattgatt ataattaa gattatgtat tttctttttt 420
 aatattttgt ttttatgcct taacacacaa tttttacagt aattatcttc ctatgatgtg 480
 acgtcacgtc ataccatac acacacgttc tccattcgtg gacaccaaca caagcgaaga 540
 gtacattcac gtttttcatt caaacattac tcgaacagcc ttcttagttc gacgccactc 600
 tgcgaaaaag tgcgaaatac agagaaaatt gccctaggcg cctattttta acttgttatt 660
 gccgcagaaa tgtattccaa attaaaaggg ggattccatc aaaaattaag tcggtaaaaat 720
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<210> 682

<211> 860

<212> DNA

<213> *Drosophila melanogaster*

<400> 682

ccagaaacag aaactgagtt tcttgctaaa actcagttgg aagccgaagc gagttcgtgt 60
 atccgatgga tactttcgtc ggtggtggat tttctgcggg gggtgactgc gtgttcgacg 120
 aacattgccg cgactgttgc aacatgttgc ggcagcagag agaggtgcc acaaatttcg 180
 gtttgcaccc ccgagcataa aaacgtgcaa tttgatccag gattcttcaa cctgtaggat 240
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 aataaataat attccatata gcctagtttt tgtgtccac caataataat tcattttctg 600
 ttgaacgcct tggtttgaaa actaaataa caaacaaca tattatttgg cataattaag 660
 cgatagtcta aatcaacgca atttatgttc agaaacataa tatgctaaaa agttcactgt 720
 caaaaccaa aatggtagta caccattaaa accgaccaa ggaccgttc catgttatga 780
 tgaggtttca agtgtcaaga ctgttaaggg aatagtttca attcgaagcc ttagggatga 840
 atcatttcca tggggaacct 860

<210> 683

<211> 570

<212> DNA

<213> *Drosophila melanogaster*

<400> 683

agctgtactt cagtagacat ttttgttcga aactgggttt caagtacgac gcttacgtcg 60
ctgtcgacgt cctcgttggc gatttatgcg ttgggttttg agttgctcca agttttgctg 120
gctgttgcaa ctttcgtcct attttgtttt gttttatttt taatgtgatt tatgcatgtt 180
cctcaatgtg tgagtgtgca aaaatacttg aacgaaatta ttgcagcttc tttttttcgt 240
acatttattt ttgtggattt tattgttggt gttgtcgcga gcgttgacag tcgcagcctt 300
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gatcgactg agtactaaat ccccgccatc ctactcaaa ggcctctcca tgctgttctg 480
cctccgtgac tgcataaatt tagtttgagc aaacgcgata gataagatag caagcaaaca 540
gaccgcagca atcgaccgaa ccgtcagatc 570

<210> 684

<211> 485

<212> DNA

<213> *Drosophila melanogaster*

<400> 684

caccaggata ataatcactc tcaactgaga gcaactgaga gaggaagct ctaatgggaa 60
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tatecttcgt gcttgatgga cgcaacgttt aattcgcgct tgttctgtaa aacaaagaaa 180
accaaaaaag taattttcaa tcgcatgaaa ctcatgttta ttgaactccg tttgttttcc 240
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ctaggtaaaa tacatcctcc gaaatcgtgg ttgttgcat ggcgcttttg tgtaacatcc 480
cgagt 485

<210> 685

<211> 22

<212> DNA

<213> *Drosophila melanogaster*

<400> 685

ctccggccac acggatgaat tc

<210> 686

<211> 378

<212> DNA

<213> *Drosophila melanogaster*

<400> 686

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tccctcccca ctgaatcctt ttgccacctc ctgcgcactc ctgtttctgc ttccttcttt 120
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cgtgcttttg tgctgctgcc tgttttgtat gaaaagtga ttaaggcgaa tttagcgcgc 360
gtcgggctca cgttccaa 378

<210> 687

<211> 504

<212> DNA

<213> *Drosophila melanogaster*

<400> 687

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acagttgaat gaacccaagc atttattaaa aaaaagaaaa acaaaaactaa ataaaagcta 180
tcacatacaa taacaaacag aaagagcatg caagataaac gaaaaaagct acagttgagg 240
ataatgctgt agttgtactt ggatacagtt gggaaaagca gatggagaca agaaaatgat 300
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ctaaaatgta tttaaaatgt tttagcttgc tttgaaatgg agtttaacct gtgtattata 480
ttatacagtt gttcatttga attc 504

<210> 688

<211> 427

<212> DNA

<213> *Drosophila melanogaster*

<400> 688

aatgagtgag tgccgtacga taggtgggcg gtgagcaatt gcacaggaag tgcccaacag 60
agaaagagag agagagggac agcgagagag attgctacag agcgggagag agcctggcaa 120
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gtttatt 427

<210> 689

<211> 157

<212> DNA

<213> *Drosophila melanogaster*

<400> 689

gtctgcactt tcatggcgga aactcgaaag cgaaacaatg ccataaatac aacaaacaca 60
cacacacaca ctacggtcg ccgaaactaa aatagataaa caaattcggga aaggaacaag 120
gaaaaacttt tacagaatgc gagtgcagag ggaattc 157

<210> 690

<211> 408

<212> DNA

<213> *Drosophila melanogaster*

<400> 690

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gagaagagaa agactgtaag cgatttacta tgatctctat aaaatatacg tatacttgga 120
gtttgagcaa tttaagactc caattatatt cgatatttgt taatatatct ttaaaatgtc 180
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agcgccaata ttgatgttcc tctctctctt catattgctc gctctttccc acccttttgt 360
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<210> 691

<211> 455

<212> DNA

<213> *Drosophila melanogaster*

<400> 691

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gatacattcc catgtattgc aggcacccgg aagttaacag atacatatta attgcacttg 240
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gttatgttcc acttttgact tcttaaaccg cgccaatttt gtaaattaag agttattctg 360
aacggaagca aaagctggat ttccaaaaaa tcagaaacca attgatcgat ctttcattta 420
gaagcaatta cagcgttact tttccaaatt gaaat 455
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<210> 692

<211> 686

<212> DNA

<213> *Drosophila melanogaster*

<400> 692

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gagtgttaaca gggagagaga gtgaaaggag agagagcggc agaaaggcag ggaacgaggg 120
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aacgttattt cacattatc agaaaaaaaa tggttatatta agtaatggga ataaatttag 480
gaaaccttta gagttaaaaa tgtcattccc cttatgtcga tacaatgcag tatacccgctc 540
tgctctatta taccgggtat aaaaaccacg ccaccaaaagc gaatgagaaa aattacttca 600
accaacggaa ctacactgaa ccaaaagaac agcgaaagga agacgaacag gcttggttgg 660
gcacggccaa gtgatgaatg gaatgg 686
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<210> 693

<211> 927

<212> DNA

<213> *Drosophila melanogaster*

<400> 693

ttggagccca tctaataattt ctaacacatt tgatattccg aacgggtgcc gcaaacgcca 60
gttccgttgg cgcacgcgtc atgggagccg cagatccgaa togttaaatt tagcccgcca 120
gtcgccgcct tggagcgtgc tgaggcgctt gggaaagatg gtgactcaat tggattttcc 180
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tatectaaaa tggttaattt gaaatccatt taagcagtaa aatttttaag ttagcaccgc 840
gcttaactaa cttcattaat tactttcagc gaacgggtta aaggtaccac ttaattagta 900
aacatggatc atccgttggc tggaaaa 927

<210> 694

<211> 355

<212> DNA

<213> *Drosophila melanogaster*

<400> 694

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ctgacagtaa ttgtgtggtc tctgcttcac accacattc gccagggccg cgagaatcat 120
gaggagcata cgaaaatcgc tcagccggga ttttccatgc ggttttagagc ggttttatgg 180
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atgtgtgaaa ttccgtgacg gataacggaa gtgtggaatt acttaaaaag tcaagggtgca 300
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<210> 695

<211> 201

<212> DNA

<213> *Drosophila melanogaster*

<400> 695

ctccgcgctt tctgcatttt cctctgccac cgccgatgtc tctgtcgacg tctctgccga 60
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ttccattct cagcgtgcac tgataaaaat aaatataccg aaaaatccca cttctcata 180
ttaatatatt ctttcgaatt c 201

<210> 696

<211> 114

<212> DNA

<213> *Drosophila melanogaster*

<400> 696

gtctgtcagc tttgtgtcgc ttcattggcg cttgactcgc cgccgggcttt atttgccata 60
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<210> 697

<211> 696

<212> DNA

<213> *Drosophila melanogaster*

<400> 697

aatcaatcgc aaggggtgcc caaaaacaaa caaaagtacg aaaatagagt gccgcagacc 60
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ccaggcgggc tcccaccac aatcagtcgg ggaacacgtg ctccaaaata tcaacaaaag 180
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ttaacaaaat atttactgtt cgaaagaggg gttttttgcg aatcgatgat tagttgacgt 480
gttattatga gaaaaacata aaagattata ggacattatt tttttaaaaa tgttgcaaaa 540

atgatttaaa gtttgcgatt tccttggtaa atacatgaaa gcgtatacag gtattactat 600
 taccaaatta taacgattta atatgcatat ccttattatt aatggctctt gaaataccct 660
 aatgtaaaac tatttaagca atgaatacat tattaa 696

<210> 698

<211> 786

<212> DNA

<213> *Drosophila melanogaster*

<400> 698

tcttgccaa acaacgcgag cagctgatgt cgcattggtg gaaaatgagg gtggcgcgag 60
 tggaagttgc catatcgctg cgatcacaag cagcaaatat ggaagattaa gcggaaaacg 120
 aaagacaaaa taattacaat caaacaaccg aattataaaa agaaaatggt ttgtcctccg 180
 agttcgttta aatatgctta tctacgtatc aattaaaaaa accgtagaaa gaaattcacg 240
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 gtgtacacac ttttcttgtc gatgtttgaa gcgccattga aatgatcatt tgaatgtttt 360
 caaattacca catcattaca ataaattaaa ttgcttatta ttgattttt actgggaaat 420
 ccgtgcaaat ggaattacaa ttcagctgga atcgtcaaac ttacaacata aacttattgt 480
 tcttttcgga caaatgcttc gaggagcgtc tggcgtcaag gaagagcgag tgcacatcct 540
 cgatatcatc cttgctgacg tggttgcgtc cgttcacctt gcacatctga tgagccgggg 600
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 atgcgtttctc ctccagctgc agtccctcgg tctgggcgag caacttgatt atctgctcca 720
 tgtcggcagt ggagtagagt agtgtgcgga tgatcagcaa acgatcgagc agatctagcg 780
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<210> 699

<211> 574

<212> DNA

<213> *Drosophila melanogaster*

<400> 699

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 aatgcataaa atacttgtag gcaaataata tccgaaacta ttataaaatc tatgctcaag 180
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gacacacaac ttctatctgc agtcatttca cactttattc caccacacca cacaagtaat 420
attcaagttc ctttgaccgc agtcttgaac ttttcccttc acctcccaca aattaggcag 480
cttgaaagcc aaaaggcgtt gattgatttg aataaggttt cagtaaggcc cgagaaaagg 540
tgcaatgat ggaaaaagtg acgcccgaag gttt 574

<210> 700

<211> 621

<212> DNA

<213> *Drosophila melanogaster*

<400> 700

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gagggcgctg ttgttgtaga gagattttcg gcttccagca tcgcaacgca acgctctgca 120
aaaaggggtgg agtccatttt tcaattccaa tgatccacaa aaaaggcagc ctgtctgcca 180
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caatgcaaat acttatgttt tattaaatcg ttatgccaat taaggcaatc gtcgtctctc 300
tcaatcttcg ttctttcatt tttttcgcag tgtaaaagag tcagcagcag cagaagaaga 360
agaagcaaca gcaatgcaat tatgcagcct gcgtgtgccg aagtgtggag tgtatccaca 420
cccttgacaca agaagttcca gagagagaga gcgagagcgg gagaattgca ctggaaccga 480
gtgagcaaca acaaagggcc gtccactggt gtgttggtta aatgccataa ttgccgggtt 540
attaattaaa acaaaggcag ctataaaacg taaaaaatc aaaaacgaga acaaaaaact 600
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<210> 701

<211> 366

<212> DNA

<213> *Drosophila melanogaster*

<400> 701

gtctgtactg actgtaccca tattatttgc gcgccaagct atcaagttat caagccgtca 60
acttttatct gccaacgacg gagaggcctc tttggcgaac taacttaatc tacaacggag 120
catacaaaca cacatatgta catatataga tttgtatata tacggttaca gggtacgttt 180
acgggggcatt cgaagtacaa ttacgggttg tggacacacg gtcgtagaag cagctaagca 240

aactgaaagc tgaggcccct cgagaacatt tggcgatagt cacattctat atacatacat 300
 atatacaatt ggacagctgg atttagataa ggacctaatt aaatgccatt atggttccaa 360
 aataat 366

<210> 702

<211> 469

<212> DNA

<213> *Drosophila melanogaster*

<400> 702

cttcaggctg atcgctggac gagtttagtt cgcctagcca cgcatttgtc acacacacgc 60
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 atagcttttg cctcagattt tgctgtagct tcaggtagc atacagctgg ccatggctgc 180
 ctcacgacca tgcctactaa gcatcatgac gaaatcaaata cacaacacac ccccgttcga 240
 tgccgacttt aattgaaaaa tcgggatttt cgccccagtc ggatcattta cattcgactt 300
 tgtttgactg cgaaatccta tatctagatg ctttgtcatt cattctatac cgccaggcat 360
 gttgacctgg gtcgcgccgc gtaaacattt tcaaatttgc caaacatatt tataaaatcg 420
 acccatgggtt atggttcccc ataatcgaat cgatctcgca cgagaattc 469

<210> 703

<211> 963

<212> DNA

<213> *Drosophila melanogaster*

<400> 703

ggctcgcta cgtcactttg tcgtgtgtgt gcttagacta gcgttgccat gtcgcgcgaa 60
 ttacgaagac aggaacaata aataaatagc agttaataa atagtagaaa atgccatata 120
 aaatatatgg gaattgactt taaattacat ttttgagttt tcaaaataaa aactaaattt 180
 taaatactta aattataaaa aaattaatta aaaaatgaaa tagtttccac atttcttgaa 240
 gaatatactg ttaacagcag ttaacgaagt gtaagcagaa ggaacaagta caatgttatg 300
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 aacaattata aaaagtcata ttgctcggtt tttttttttt ttttttcgga taaagttttt 960
 tct 963

<210> 704

<211> 431

<212> DNA

<213> *Drosophila melanogaster*

<400> 704

atctgtggtt cagctgctgg tgtttggtga ctccgttcgt cattgattgg actccccctt 60
 ctttctacca acacactctc tctctctctc tctaattgta cgtcactttc ccacgggtgc 120
 acgtgtgttt gtaggggctt tgaatggctt aaaacgccta cgaaagcagg gattgtgttt 180
 gtcacggtgt cattgcttgt taaatttatg caagagtctt ccctaatttg ctggatttgc 240
 ttacacgttt gaattttgca aatacttcta aagagctcca taccctaacg acattcattc 300
 ccgttggaat ctgttttttt ggctagtttt gctcgcattt tgacccccctt ttatttagct 360
 gtgtggcaact tttcagatga ctcacagat atggctacga gtaaatggga ataaaagagg 420
 gcaatattgc g 431

<210> 705

<211> 754

<212> DNA

<213> *Drosophila melanogaster*

<400> 705

ggtcacacta aatcattggc atcttagctt tttttttttt ttttgatgca cgcgtgtatg 60
 ctgtgtattt tttttttttt gctattttta aaatggattt cgagagcaaa tactgcacca 120
 gtcaagtaaa tggcactatt accataacta cgcgcaaagt ccttgatgaa aatctaaaat 180
 ccttactgga tgaggggaaag ggcgagggtga gtgtctagt aaccatctag tctcaaaagt 240
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tgcgctataa gattgatttt tcgggaaatt ctgcgggcta cgcctacttg caatatatca 420
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 cttagaccat ggcaagtgtg ccaggagatg ttgaagatac atccctttac catcgttcga 660
 gtctacgagt atcaattaga ccagttcttc tatatatttg agtaccgcaa caacgactcg 720
 gcccgcgaagt gcccatcagg agagtaagga attc 754

<210> 706

<211> 156

<212> DNA

<213> *Drosophila melanogaster*

<400> 706

tctgtacaaa aaaatgttca gccatttttg attcaattaa ttcattgtcg cgttgccagt 60
 gcgacggcat ttcgagggt gttacgcacg gccgtggaaa cgtaagcagc tgaggtcaca 120
 ctaaacacgc gatctggcaa taccacaatt gaattc 156

<210> 707

<211> 989

<212> DNA

<213> *Drosophila melanogaster*

<400> 707

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 taaaccacaca cgtagaaaaa ttttagtgga tcatgaaaat caatttagga taacattctc 120
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caatgggatt tctttgaagc gcagtcgcaa ctgtgaagtt tctaccaacg agagcgaatg 720
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 tgtaaaaatc tggataatca ttacatttt 989

<210> 708

<211> 183

<212> DNA

<213> *Drosophila melanogaster*

<400> 708

gtatgactct tatcacttgc actccgtgac gtcgacgatg acgtcgcggg ggcattcccta 60
 tgattccatt tcttttttca tgtttttctc ttcttttttt aatggactat atattcacgt 120
 ggccccagca aatccacaat tcagtctgat tcccaactct gagacaagcg gacgtacaag 180
 tgg 183

<210> 709

<211> 304

<212> DNA

<213> *Drosophila melanogaster*

<400> 709

gattggatta ttcactaatg gtagtatcga taggtcgatt gtcacaatac cgatgcttca 60
 gtttcgatat cgactgtttt tagtatggct gtattttgtc agtattttta cgттаататс 120
 таатааттгт tagtatacaa tttcaaagac cgcgatattc aaaattgttt tcaagttatt 180
 ctcatTTTTTA tttaaaaata ataaaatcgt tttttcactt tgtttacaaa tgaattttat 240
 gtatgttctt tttctacaac aattagattc ataactgatg atattttggtt ttgctttcac 300
 atag 304

<210> 710

<211> 855

<212> DNA

<213> *Drosophila melanogaster*

<400> 710

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<210> 711

<211> 825

<212> DNA

<213> *Drosophila melanogaster*

<400> 711

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agccaagcag agacctacc cctcctcctc cctactccta gcgggtccact caactaaacc 120
tcgtacaccc gtgcactcca accccccacc actccccgcc tatgtacaat ggcataagat 180
ataagatatg cgcattttctt ataatgtcga accgaaacgt ggcgaaataa atgtttgttt 240
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gtgggctgcc agaagaaaag gtgggtagat taagggttta aagtgttat taatcttttc 540
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aaagaaagta tttagttaag tctttatctg caaggctgat aacaaactaa tatgcaaata 780
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<210> 712

<211> 798

<212> DNA

<213> *Drosophila melanogaster*

<400> 712

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ttgtgtgtgg tggcgatgag gggggcgttg ccattgggaa gtggaagtgt tgtgggtgtct 780
gaaaggcgtg actgcata 798

<210> 713

<211> 797

<212> DNA

<213> *Drosophila melanogaster*

<400> 713

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 actggagaag cgctatgtgt tcacactgga ggattgcgat tcggtggctc ccatgtatga 780
 gtaccttate cggcaga 797

<210> 714

<211> 491

<212> DNA

<213> *Drosophila melanogaster*

<400> 714

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 cgccaacgat tttttgttga ctacggtcac actaaggaaa ttttaaagta ttcgaaaaat 180
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 gtggcttttg gcggcaatct taaagttttc tcacacagct tactcgctgg tattttccaa 420
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 cacgtccaaa g 491

<210> 715

<211> 1013

<212> DNA

<213> *Drosophila melanogaster*

<400> 715

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cagcacgcat aatctcttgg ccccgtttgc cgcctaata gtagtattag ttttatatat 180
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<210> 716

<211> 902

<212> DNA

<213> *Drosophila melanogaster*

<400> 716

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 gtggaaccaa cagaaactaa gcgaaagcga tttagattcc gccagactg agataagctt 480
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 atatatttcc ttaatagtaa actaaactac gtttttagaa tacatgatct ttgaaacaaa 600
 gtaattaatc tagataggtc caggttttca attttataac atggccttaa atttgattat 660
 gtttaatcta cgaaatccgt acgataagcg aataataaaa gcgaaaaaga aatgttctaa 720
 tcaaacattt agggaaaata aacaaaatcc aaaaaagtgt gaaactgggt gatttcaatt 780

agaggaagta cgactgtttt ttcgttttca tgttttatatt atttctttgt ttgtattttt 840
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aa 902

<210> 717

<211> 64

<212> DNA

<213> *Drosophila melanogaster*

<400> 717

gttttggtgcc tcgcgagtca catttgtttg ttcgccgcat tcgagcgtac gacgaagcga 60
attc 64

<210> 718

<211> 526

<212> DNA

<213> *Drosophila melanogaster*

<400> 718

cttggtttta tcacctctc tctctctcta tcgcgcgcgc gcgctctttg tggaaacagg 60
tataactgtt tggcgtgagg gagcacgaaa ctccagtga gacttctccg catcgccagc 120
gaaacaaacg atcaaaatga atactctgat aacgtgtgaa ggtgagcaac aaaataaagt 180
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ggaaaacaaa gcagacgcca ttggaatgcc cgtccgttct ttgatgttgc taagccggac 420
atggcaattg ttgcttttgt tttcgagagg ggggtgtgaa actcataaat atcagctatg 480
gcgaggggggt ggggggcagt ctttgctgac gtaccgactt ttaatt 526

<210> 719

<211> 143

<212> DNA

<213> *Drosophila melanogaster*

<400> 719

gatcagcact cagagtcagt tacttttttt cgctccatac gtgactcaca attcgcgtgt 60
ctttcaaaaa taaaagcaaa agaagcggtt ggattcggtt ctgatggctg gataaatgaa 120
aaaaaatcag tcagagccaa caa 143

<210> 720

<211> 110

<212> DNA

<213> *Drosophila melanogaster*

<400> 720

ttctggcgaa tgcaatgaac tcggcttgtt tatttaaaaa taaaatatac atttgcaaag 60
aaataaaaag atcgcagaac aaaaatcgaa tcaacaaaca aaaggaattc 110

<210> 721

<211> 1070

<212> DNA

<213> *Drosophila melanogaster*

<400> 721

ggaagtacaa atagccaaca attgaaatgg ctatcgacag actggctctc tgttgattgt 60
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tcggatcgta acgactaccg actaccgaca tcgacgacat cacgcatcga gggcatgac 180
ggtgtgcgcc tgctgttgcg gcattttctt caacagggtt cttagcgatc gcttatctgg 240
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cgggtctcat tttttaccga ccgctttcct aaaacttgct aacttgaaag agatcacccg 360
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tttctgaaat ttttaagcaaa gtccaatagt aagagactga aaatagtttt aactcggaaa
1020

atctgtcgtg gatttggttt tcttaatatc tgcacgttcc aataatataa
1070

<210> 722

<211> 765

<212> DNA

<213> *Drosophila melanogaster*

<400> 722

accagacca tctaactaat gagcaggcaa gcactcactt accaagccgt acacacacac 60
acacacacac acacatatat atgatgtgcg aggcggacag aagctgaaac tgatgcgac 120
cggacacggg tcttgtgttt cagttctctg tgtggcatgg ccaccgtggc cacgttggac 180
atcgtggcct aaaaggacac acacgaagcc cttttggccc tatgctaatt tgcacgccat 240
aaatgagacg aatgtgccga gtggtggcat gtgaagtgtg gttgcagttg ccgtcgtgca 300
cttagagaaa aaaatgttat cgatcaagtc catttgtaat ttaatttatg taaaacgtat 360
atataacaga ccaattctca aatccataat tacctctttc aaggatttta agaattaatt 420
tttaaactga aattactcta taaatctaaa ctatttttcc ctgtgcattt gagtagtggt 480
tgctgttgca gttgcaattg ttgcaagtgg ataactgctg cggcccgtca tggatcgagt 540
ggaaagaagt gggaagtgga tgaagtggat ttgggagtgg ggggcgtggc taggagagga 600
aacgccggct gaaagaacaa atctgcaacc tggggtggcc ccgcccagag tttctgtgat 660
gatggggccg actgccagag acatgtgttg ctggttccta tatggctccg tagttgggat 720
ggctaatgcc gccgacaacg acaacgcccc atttggatca cacac 765

<210> 723

<211> 568

<212> DNA

<213> *Drosophila melanogaster*

<400> 723

agctactctc tattcgtatc tcacaaatac acgctgaaat ggttctcgta aagagaacgt 60
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tgccgatgat tttgatttcg ttacttttagc cagcgtccgc gtcagttcgc tctatgtgat 180
tcagtgttaa ttttcataat attatgtaat agcatgtgcc gccgcctggg tgcgattcta 240
ttctatgcc taccttaacg gcaattatat agtaatttac ttgcggcgat ttaatggatt 300

tagtttggct ttctaaggct tccagggggc actttgcgaa agttcattga actcgacagt 360
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 cgctttttgg gcctgggtgat gtgggaaatg catttcgagt gcgtgatatc tgtggcgtct 480
 ccagtgggta agtaatagat actgtagttc ttcttctctt tcttctctggc ccacccagta 540
 atcccaagac cgcgaagaag agagggtt 568

<210> 724

<211> 580

<212> DNA

<213> *Drosophila melanogaster*

<400> 724

gaaccgtgca tatgaataat tgccccgtct gctggctgtc atatagatcg ctgcgacctg 60
 atagccaaag aataaagcca gaacgacgaa agcaacaact tatatctatt ttaaattacg 120
 ttcaattaaa tgcgcttcac ctacaaagtc tgcgacagtg acgtcaatat cgaaaataat 180
 tgataacctt cgatcacgat cgggaagaga ttgtaacaga cttgctttga tggctcgcac 240
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 attcgttcaa tgaaacgacc gatccatata gatataataa gagggggcctt caaatctttc 360
 gggtttgatt ggtgaagcac ttgcactata tatctacttt tttttcttca cactgttatt 420
 gttctctgtc attgccgttt tttatcgctc cggegccttc taccctcttt tatacataat 480
 tcaatgataa aatgtcaaaa atcaataaca ataaataaat gataaacgag agtatcactc 540
 ccgtctttgt attccaccaa aaataaatat cattccgttg 580

<210> 725

<211> 403

<212> DNA

<213> *Drosophila melanogaster*

<400> 725

ggcacaacaa accggttaact ctgaagaaat ttcgtgcgtg ttaaacagaa tctaacgaaa 60
 gagagagacc actgggctcc tgtttgctc tccgccttaa aacgtgtttt tcacaactca 120
 caaaaagttg taaggaatgt ctcataaaaa agttaaatata ttacacact cgaagctgaa 180
 gcgcacaata gagcacaaaa tattcagaat cgcaaaatat tccatgattt tttttgcctt 240
 tgttccagag ccataattac aagaccgcga aggacagcaa taaaccaaac aaaaatattt 300
 attgaaaata aattcattct acattcaact tcaacgactt tgactcgaca cttaattggt 360

aataagagca aattatcggt aaaaacttat gtccattgtg ttt

403

<210> 726

<211> 465

<212> DNA

<213> *Drosophila melanogaster*

<400> 726

gacagttcgt gtcgcccgat ttgttttagga tgttgtatct gacaactgag tatttgcact 60
ttatctaatt tgacaaatag actttaactg ccaaactagt tcgccgcttg aacaaactgt 120
agctcagcaa gaggacaaa tgatttctcg caaattcgaa gcacttaatt tgcaatttaa 180
gcgtatccat gcataattgc agtcaaagtt tattcaccgt aaaaaaagag ggaacgcca 240
gcttagttaa aatgcacgaa agaagtaatt aattcatatg ataaatcaaa tagagcacgg 300
aagcagtga tgcgtcgggt acagaacttc gattgccctt gcaaagtga ttggatgtta 360
attgggcatt aaagtacaaa acttgaacat ccaaattgagt tgggcatatc aatatatcgc 420
atattctggt acaatgccct acattttgcg caccttaatc gaatt 465

<210> 727

<211> 52

<212> DNA

<213> *Drosophila melanogaster*

<400> 727

cgcggcagtg tctcattgat cgctgaaacg atgatggttaa ttcctggaat tc 52

<210> 728

<211> 490

<212> DNA

<213> *Drosophila melanogaster*

<400> 728

tatacgccat gcatattcac agacaaatgt acaagtactt ggactagact gcatatattg 60
tatatacata ttcaatcgca catggacaag cgaaccttgc agatacaaaa gggttcgatt 120
tgtcaaatac ccaatcttga gattggcggg gatacttata gttatagcga ccctatgcag 180
gaagtgcagt ggctcagatg taattatgta tgccgcttgg cttgagtaaa taatctcaac 240

agtgggctgga cgataaatgg aaaggggggtt ggttgcttag atgggtcttt ataaaatata 300
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 gattcattat taaaatgtaa ttttctcatt tgggtggtact aaaccttctt tatcgcatgt 420
 tcttagtgcc ttcccgctat atcaacctcc gtgggaaatg aagtagatac gtagatattt 480
 agaacatact 490

<210> 729

<211> 1153

<212> DNA

<213> *Drosophila melanogaster*

<400> 729

gtctaccact agctctttgt cttegccttc tagtctctct catcttggca gcccgttcta 60
 gtgcgcgtat ttttagtcgc aacacattgc ccaattcgcc agccgctatt tgtgtcgtcc 120
 atttgttcat tcatcgggct ctttttccga tttcagtggg tggcatttaa caataatccc 180
 tgcgttcgct gtccacgtcc acattacgat acgttttagtg cacggaaga aataagcgtg 240
 tggtttcata atattagcta ttgaaaaaag ttcttaaatt taagcctcac tcgattctga 300
 tgcattgaaat attattggat tgtaaattgag cgtcatgttt tgggtatacaa atctcaaagt 360
 aatttaaaaa ttctcatctt accgtacctt gaaccactac caatcatctc agtacaagca 420
 tttcagcgaa tttctcactg tgcactacaa tgccaggcgg tacaagcacc tgtatttatt 480
 tatgggtccgc tgccgtaatc gactgcagtc gccgcttccc tctctctttt gctaccaaca 540
 acttgggggta gggcacctga actagtttca aacggcgggc gtcggccttt tcagcttttt 600
 cgcatttgcc attttccgc ggttcgcaac atcagcgaca tttgtcacag tttcttaaag 660
 aacatttgaa tatccaaagt ttacttgccg aacttgactg cggcattgcg atgatgatgc 720
 tgcccgttgt ttgtcattca gtcatttaa ttcgatacca atcagtattt cgtgcattgt 780
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 catataaact aatccagtgt gacaaatctg gatatatata tcatataatt aattattttc 1140
 atgacaacca ggg 1153

<210> 730

<211> 1144

<212> DNA

<213> *Drosophila melanogaster*

<400> 730

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acattcgaat acaaagtcag caaacattga ccatttatca gaggcacgca ttgaacttga 120
aatttgccgc tgcttttgcc aatttcttgc gcgaaggga tggacatcgt gggagcttac 180
acaagagcga acgagagcga tagtaagcgc taagagcaag atggaacgag agtagtttta 240
attttgttat tgttggtgcc cgttatcacg ttgcaagagc gtgatgcttc actaagatat 300
tacacgctga gaaaactgga gcgcgttctt aaagttcaga tgaactgaat gatctgtaat 360
ttaaacaaaa ctaatagaac tgctatatc aaaattcgga atgtaaataa aagagttctt 420
ctgtctttaa acttcatttt gtaataataa taagttttta acgttgtaga taatcaagta 480
atattatgtc ataaatttgc aagtgaata aaaacggtaa tacttgatt ttcttcgacc 540
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aatgcattgc tagaaatgtt cctaacaatt aagcatgcca ccaattctgg caattatttt 660
ttaaagtaca gttcgtgtcg cccgatttgt ttaggatgtt gtatctgaca actgagtatt 720
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aactgtagct cagcaagagt gacaaatgat ttctcgcaaa ttcgaagcac ttaatttgca 840
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1080
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1140
taat
1144

<210> 731

<211> 858

<212> DNA

<213> *Drosophila melanogaster*

<400> 731

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 aagatatcat tcgaaaatat ttttagaaaa agaataatta tccaaaaaga atcacatttc 180
 aaagaacatt ttacgcattt gaattaattt attaagttct atctcgaatt atgatctaaa 240
 agtactttta attcgcttgc ttgccaatcc gaccatttca ttttgaagt actcctttgg 300
 cagaggcaag caattctcgt gcaactcgat ggcgtccttg tccatgtgcc acaccataaa 360
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 ttgacactgg cggcactcaa acaccgatc gtgggtatcc acgcgcagga actttcttat 480
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 ggggtgtgtt tcgacatcat cgcctcggag caaatatggt actgcaaata attccttggg 600
 aagtgttgca gacccgaaaa gtgtacaggt ttatttttag agttgccgga aatgtgttga 660
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 ttacttccat ttccaatgac ttctggttgc gttttacttc ggtactgcaa agggaagttt 780
 aggaaaattg ctcttaggcg aaaccaaact ctttgaccg gcaccttcat cttctgatga 840
 ccacgccttc catggaac 858

<210> 732

<211> 882

<212> DNA

<213> *Drosophila melanogaster*

<400> 732

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 caagtgccgt ttttctgtct tgctttcttt aatcgaatat atttcggtct cttcttttgc 120
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 gtagaatgat tttttacata cataggtcag cttaaaacaa ttgtgaaata ctacttaata 300
 gcgaatgaat gaataaagca aagctttggg ttcgggttatt attatttttt tttttgtttt 360
 ttctttatgt gttttgtgtg tgtttgatat atacatgtac atacatatgt atgtacatgc 420
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 aaagataaat atgattaata tgtataaata cagagaaagt aaggtaagta agttttaatt 540
 ttttacctaa ttaaaataat tggtttgaaa ataattgtac gcataattta gtgtgttgtg 600
 tacactaatg tacatgtaca actttatatt gcaatttcaa tctgaacatc cactatctaa 660
 tggtagactt tataccgcgt atttccctta aatgtattga ggcccccgga tttatcccta 720
 tttttatgcc agttaatacc gagccacag aaacctcaac ttgacacaga tgttctaggg 780

agtgatttaa ttaaaaaact ttgcaatta aatgcataaa ctgtaaaaaa caaagcggag 840
tgcaggccat taagcccca aaaaaggctt gatgaaggaa at 882

<210> 733

<211> 532

<212> DNA

<213> *Drosophila melanogaster*

<400> 733

ggcccgagca gctgacagtt gcgcttcagc attagaccaa agtagtttga ctttttagtt 60
tttagccgcg aagcgaatag tatatacgtg gctctgtgtg tgtgtgcggt gtgtgttgtg 120
gcagctgcac ttgcagcgag agacagaaat acatttcgta caaaattccg ccctgcattt 180
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cagtcgcccc gacggtccgt tttctgtttg ggcccatttg ccgttggcca gctttcagtg 480
gttcatttcc cattcgagtc ggcaacaacg agccggggaa gtcgcagagg cc 532

<210> 734

<211> 113

<212> DNA

<213> *Drosophila melanogaster*

<400> 734

ctgtggcaca agctaaagag agaggatgag agcgagcgcg atcgaagaga gagcgccagc 60
tgctcccatt ggagcagcta acgtttccaa ttggaccagc tcaaagggaa ttc 113

<210> 735

<211> 1145

<212> DNA

<213> *Drosophila melanogaster*

<400> 735

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tattgttggc ttgttggcag agactgcgaa aatctcttgg caacatgtag ccacaacttt 120
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 1020

cttaaacaga gaacggagaa atgagaggct ttgtggacac ttaaaagtat gcggctctct
 1080

tgaccgactt cagtcgctga cgtcgctgga aaatgcttgg tttgcggccc aaattattga
 1140

attgg
 1145

<210> 736

<211> 447

<212> DNA

<213> *Drosophila melanogaster*

<400> 736

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 caatggtaat gggatcagtt tcaatttcaa ctgtaactac aaattaatca taatttactg 120
 tataacaatg tattttttcc ttgttaatgt aattgtaaat ctacaagggc atttaaatat 180
 tacacaatta aaatctttgt tctggatatc acttcgaaaa actattgtat attacgaaac 240
 accggtacat acgctgtatg atctgagtca tttaacacaa caattttaag ggtagatcaa 300
 gaaaacgatg cttcaatttg aaaattttgt aatcgaagca atcaagttgt acatttttgt 360
 gactgaatta gtagttatat tgttatcaca ttctatttat attagctaaa atgttaaate 420

gataaatatt aagttttcgg ggaattc

447

<210> 737

<211> 551

<212> DNA

<213> *Drosophila melanogaster*

<400> 737

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ccgtttttcg gggttggtgg gtgggtggtg gctgggtttc actttccacc accgccgcca 180
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gtgggggaaa attgcggaag gggctacaaa aaaagtgtct aattcactag aattttccac 300
tgtaggccag aatttggtac attttccac tttacaacgg aacttttgat agcagttaca 360
tacttgatta gattaaatgt cttaaaaata tatgtaggag tttagacttt tgtaataaag 420
cttcatttcc atagaaaatg tttctatcaa gccgtatttt ctttaacta ataagaataa 480
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ccaaaattaa a 551

<210> 738

<211> 885

<212> DNA

<213> *Drosophila melanogaster*

<400> 738

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<210> 739

<211> 1083

<212> DNA

<213> *Drosophila melanogaster*

<400> 739

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 cctgtacgtt ttatttttgc agtactcgac ttattgtta ttattatttt tcgcgactct 180
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 tgccgctgcc tgccttgggg caattatttc caatttagca aaacaacaca agaggagcag 660
 catggaagct gaagctgaag ctggagcata ggcattccaa gctatagatt ggcctctgtc 720
 cgagatctgg gcttggcact gctcctattg tctttccatc ggttcattgc ccgatgcaca 780
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 attataatat tataataata aattccgcat aatatatatg ctttaagtat tttctctcta 1020
 catacaataa ataccacatc aatttctgaa aaacacctcg atgcattaat tttgaaattc 1080

cgg
 1083

<210> 740

<211> 1796

<212> DNA

<213> *Drosophila melanogaster*

<400> 740

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tagtcttagg tatgaagccc atagtggcag agagaagcat atgatcatat ccccgtagg 180
aataagaata ttattgttat ctgctctta cttataagct agcgtaaga gataagaatg 240
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gcgagacgcg gcattgggtg gcgtgtgctt aaagggaaaa gtcgaataaa ggcattgtga 360
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atcttatagt aaatgttcgg cataatgtat gtatgtaacc ggtataagga agcctttccg 480
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attatagagg tctacgccgc gcaagaatgt tttgaacttt acatacccag actaacgact 660
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1200
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1380
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1560

gagggtattat agtttttgcca tatacatttc cccagtgtga catagttggg aatgtaggta
1620

aaaatccata taaatataat ccaatttggt tgacaggagt gtacggcaaa cagttcacca
1680

atcgaccaat cagtaatgaa tggcaatgac cccacttctt aggtagtact ctcattaatc
1740

gaaatatgac tgttcgtttc tgccataaat atcccctagg ctggcttggtg gcatgg
1796

<210> 741

<211> 819

<212> DNA

<213> *Drosophila melanogaster*

<400> 741

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aaaccattt ttggggcagt tgcagttgaa gtaagaagaa ttacttgctg cagggcactt 180
aatcacatca gcggagcagg agaaggattc agagagagtc actgcgaagc cctcacttga 240
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acgtgtttta agtttcgccc gccagcttag ccaagtcagg cggagtcgga tcgcactcgg 480
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cggcgcagta attgtatatt gctgcaaata cgcaaatcaa ttgaatattg tctcagcatg 660
cacatgtcta ctatctactt gtgtatztat accgtataca acttaaatgg aaattttggg 720
ggaattaaaa tttaaatgaa acccaattgg cttggtaact gttgataaat aaattagata 780
ggaaaacggg taaacaatat taatcgaata aaaagcctt 819

<210> 742

<211> 1003

<212> DNA

<213> *Drosophila melanogaster*

<400> 742

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 gaccaaagg ctggtcagca tggataagag cgcacgcaaa attataagat gatgtaaacc 180
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 gaataaatta ttttttata taaaggggga actaaatcgg agttgtatag tcttcacacc 420
 gaacatcaat ttcattgtca tacggacgag attttagtaa taaaattatt atttttatac 480
 attttaaatt gaaattatag atataataaa tcatacaatt tttaggtaaa acatttgtat 540
 aaaatttcag atgcgtagta ttaaaaaaaaa ctgaaaaatc ataatccttt ccttaacttg 600
 ctgtagctct ttgggtgtac taactttttc taaatgcacc cgatccaacc caatgagaag 660
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 taaattttgc atttgaaagt tgaactttgc ccacgtgcaa atcgatgata aaggctttgc 840
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 cagttttctt tccaaagacc atcaattttc attcccaaag cctgggaaat tgcttagaag 960
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 1003

<210> 743

<211> 384

<212> DNA

<213> *Drosophila melanogaster*

<400> 743

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 ggaatatcgg tagtggcaac gccgttacga acggagaacg gagaaggata tgtgaagggt 180
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 atgcaggaca aggagcggaa gaagttggaa ggagcggagg accttcaagg atcatcaagt 300
 cttaaaactc ccacaaaatc ttctgtagg gggagccggc ctaacataag ccgcggttgc 360
 agggcaaagc ggagagaacc gtga 384

<210> 744

<211> 1040

<212> DNA

<213> *Drosophila melanogaster*

<400> 744

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atacatttcc cagctatgaa tttcatttga tttttactaa atcacaattg tcaaattgca 120
atgagatcgg ttttgctctt tttcgtctaa tatactatga agtgtctcat ggtaattcgt 180
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gacttcagtt aggcattctaa aaattgttaa accattgggc aaagaaccag tgagacttgg
1020
aaatgataat tctattgcag
1040

<210> 745

<211> 519

<212> DNA

<213> *Drosophila melanogaster*

<400> 745

ctgtgtccgt ttctatttac gtttcttttt tcaacggcta ccctcgtgtg cgcgcgcttt 60
ttgctttttc ctgtccactt tccaactccc ccttcccccg cctgctgagg aagccagcag 120
catgtgtgcg tgtgtgtata cgtgtgtagc tactcgccga agaagaagag aagaggagat 180
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tatgcgatac gttgcgctct agattcggtt ccatttttta gcggcgactt tactaataga 420
 tatacgtacg tacacatcga tgtctaactc aactcctccg atcgacagct attatgtggg 480
 gggttcattt ggggtctggt tgggtgaatt ccgcggaat 519

<210> 746

<211> 597

<212> DNA

<213> *Drosophila melanogaster*

<400> 746

gtgcgggtct ttggagaatg tctgtgtgta tctctttggg tgtggaacgt atctgtggat 60
 taaagaaaag ggctatgac cggtttaatg tctggaactt ctgctgagga tcaaaggaga 120
 tgtgccacat caaacaagg gaggaatttc atcatgaatt gaaaatgaat ggggagaaat 180
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 tgacaaacat gagaccccg agcgaaagt ccacagagat cactccatta tgcgactact 540
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<210> 747

<211> 99

<212> DNA

<213> *Drosophila melanogaster*

<400> 747

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 atactacaac tgaaagtggg ggggtttttg gtggaattc 99

<210> 748

<211> 580

<212> DNA

<213> *Drosophila melanogaster*

<400> 748

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cgttcgcagt tggcgttggc ggcttcttct ttaactctcg cgcattattt cgcaaagctc 540
aagcctgctg cttcttcttc tgcaccccc ccccccctctg 580

<210> 749

<211> 1036

<212> DNA

<213> *Drosophila melanogaster*

<400> 749

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atatattgta tttatttctg gtcgccgtgc ttttccttac gagccgaggg acatgcacat 180
gcacacatgc tggcttttaa ttgaaatgaa cttaaattag cgcgagggtta ggcaaattga 240
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1020

agtgggccgc gcttgg
1036

<210> 750

<211> 1091

<212> DNA

<213> *Drosophila melanogaster*

<400> 750

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ccgtctccct cactctcacc cggcttcgcc cagtaacaac aactaaagca caacaacacc 120
cggcacttaa acagcgaatt ttcaagggga tgggggtatc tacaggagga ggaggagcag 180
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1020

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1080

caactatttc a
1091

<210> 751

<211> 495

<212> DNA

<213> *Drosophila melanogaster*

<400> 751

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tgtaggttgt gcctctccag ggaaaattct agaaaatgca tttccttttc gaatgagtct 180
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atTTTTtaga aacaatatat ttaagtttgc aaactaaca tattatttat ttaaagggaac 360
atacattaat aaaggggtat atggacaatt tctttagtca ttttgcttaa attttcaacc 420
acataactgg gctaattttt tccacacatt tccattttac acctatttca aaccaacact 480
tgcccaaat taccg 495

<210> 752

<211> 466

<212> DNA

<213> *Drosophila melanogaster*

<400> 752

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cagctgtttg gcgtcgcccg cgatttcggt cagctgactg ccgccgcacg cagcgcggcc 120
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gatatcgagc gatcccgct aagaccataa atgtgactac gaaagtgagc taggtcagtc 420
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<210> 753

<211> 556

<212> DNA

<213> *Drosophila melanogaster*

<400> 753

acggaaacca aaaaaatttg tgcaaactta gtgctggaac aaaaaacgat gactacgct 60
tttcatcgat gggggcgaat atatcgcttc accgatgttt gaatgactat agcaactatc 120

gattgctacg attttttttc gaacaaacaa ataattataa gggatttaat aaataaatta 180
 aagaaggttc aagaataata taaaacttat gatagtttaa cgaaattatg aaatataaat 240
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 gggccattcc cccataggat ttcaggggag gcctccagca gaggaaccgg tgcacttggc 480
 tgcgaacact ttggagagtc agcccgatga ccatgggcga taccatctcg gagctgctgg 540
 cgcaaccgc accacc 556

<210> 754

<211> 925

<212> DNA

<213> *Drosophila melanogaster*

<400> 754

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 tatgtgagtt agcagctgct aacaactgtt gtattgggcg caaatttcaa aatatgctat 180
 tgtactgtag ggcacttccc aaaaatgaaa caaattgccg ccttgttttt taaaccacat 240
 tcaatgtaaa tatgtatttg ctgtttatgg tatagacttg acgtctgctt gaatataacg 300
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 gcttacacag gcgtaattag taataattaa cttaattgcg tagcgtattc attagtgggg 540
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 attttgcgtc gttcccgctg gctctctcct ttaaagtaat tatggccagt tgtatcggat 840
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 cctactggag ccgaatggcc atggc 925

<210> 755

<211> 1125

<212> DNA

<213> *Drosophila melanogaster*

<400> 755

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ttaaaattcg aatgtataat aataattaca gtgttgccca actaataagt ccagtaccct 180
cattgttcat aaaaagcatg accattgaaa atgtatttaa aatttgtatt ttaagcttat 240
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gagtacgtat gccttaaaat gtcatatcta accggtaaat tgtaacgggt tccagttcta 360
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tcatgctggg agtggataat cccgctcata ggaagctcct gctcgaggga gtccggttct 600
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atttcctaga aacacctgtt ccatattcgc taacatctcc acaaagacg ctcacaactc 780
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1020
aaaaaaatgg ggtgagcaga ttaccaggaa ctcatactcc tgtgggtttg aattaatgaa
1080
aataacttaa tgtaattaaa ggatcacaac gcgtcacaaa tcttt
1125

<210> 756

<211> 1475

<212> DNA

<213> *Drosophila melanogaster*

<400> 756

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cataatgtat gtatgtaacc ggtataagga agcctttccg actccatgaa gcatataaat 180
taatgagcag gtctagacga tctggccttg tcagactgtc catttaaagg tcgagatctt 240
tgggtactatg aacgctagaa agttcagatt atgtctgcag attatagagg tctacgccgc 300

gcaagaatgt tttgaacttt acatacccag actaacgact accagccgcc caaatctgtc 360
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 aacaggatat caacagggat attaatcggg catgaaacag tgacaggccc agtctgtcag 480
 gataataaac caggatacgg actttccgcc tcagcctact atggccacat atgccaacac 540
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 gaataatgca tgcgtgggtg gtgcctgtgc tttcacttcc ccaattttctg ccaccccacg 720
 tgaacacgct tttatgcaca aattacctgt cacttgtgct tacgtgggtg tagttgttag 780
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 1140
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 1200
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 1260
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 1320
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 1380
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 1440
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 1475

<210> 757

<211> 848

<212> DNA

<213> *Drosophila melanogaster*

<400> 757

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 agagcgcgag aggaagaaga agcagggcgc acatgtgcac tatagtaatt cctctctcac 120
 tttgtttatg ttttgttttt gtaacgggtt atttcaattg ttgtagctta agctattttt 180

ttctaattgt ctatgaggaa gtgtgtgcaa gctctttgta gttgttttgt acttaggttt 240
 ttttttttca atttttctat tttgtgcgaa ggtgtttcca tttgtaatta caattacatg 300
 cctctgcctt cgagtgtgtt tgtatgtgtg ccccgtttgt ttgatgtaat catgggttac 360
 aaaagcgttt tgctattgct attgctgttt caatttgtgc gataaggctg ttttgcctta 420
 tgattttgcg taattacatt tgataatggt tcaatgtgaa aacctttgcg gtaccaggca 480
 tatgagggca atttaagttg actctgtagt tactgtagta atgtatctat attcataatc 540
 aagtgcgaagt tctttgcatt tgctagcaca gtgaacaata tataccctct attatgcata 600
 ttgcaattcg aattcaagaa aaacaagaac gagggagggt cgagaagttt aaatagttat 660
 ccacatatct tgaagttata aaagccatgg aaatgcatag cttaaacata ggaactgtag 720
 atacatcgaa aatcataatt gtttcagttt gctgaagaag actgccccaa gaatatgcta 780
 gaatttgagc gtataatata gacagcctct agacaattta attaaactta cacatgagag 840
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<210> 758

<211> 527

<212> DNA

<213> *Drosophila melanogaster*

<400> 758

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 gtccacgtcg ctcatttgct ccgtgcccgc tcgacagctc caattcgaaa acgacgtaaa 120
 cgccagccgt tcgccaagcg cgcgtaattc aaagttatca actcgaaaca ctgtttcccg 180
 gaaaaagtgc acaccgttaa atgtgaaata ttcaatcaag tcaactggag aatataaaaa 240
 aatattaaaa aaaattaaag tgaactgcat tatacacaga ttgatcagtt taagtagtgc 300
 cagccatggt cgtccaagtt ctgtgatgcc gcttttgggt cgctcctacg cctgggtcgt 360
 cccgctttcc ttcgggacac ctgctggcca cccttctgat ccgcccacgc cgcccagtga 420
 ctgactgaaa ggggatcgta ccgccctgaa caaaaactca aacgcgttac cttttttttt 480
 cgtttccatc tatttgggtat taaccgttgt gaaatgggaa cggccac 527

<210> 759

<211> 646

<212> DNA

<213> *Drosophila melanogaster*

<400> 759

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 ccccaaatg ggccaagctt tgtggacccc tcgtctcac tcctcctgcc tcgtctcactc 180
 ccttgaccgg gtccttaccg cttcacaccg ctttagagtg ggtaacaagg tcagcaaata 240
 gagtgacccc cacaggagca tatctgctat gtatatacat atatatgtat atttgttgctc 300
 aatatgctcc acaattggag ctaacattac acctcttcca attgggagtt ggccactggt 360
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 atatacacac atagtatttt gtttttcttt ttttaagttc tgtgctattt tttgttggt 480
 ttttgcatte caacattttg taaaaattac gattggcact cctctgtatt ataacgaacg 540
 agaaaatgat ttgcatcaga gaacaacgtt ttgggaagta cagaaacgta atttggttcc 600
 ataaataata aagttaaaat ttaatccata accgatgtca gtttaa 646

<210> 760

<211> 93

<212> DNA

<213> *Drosophila melanogaster*

<400> 760

gggcgtggat tgaaatttgg caacgatcgc gtgagcagga gtaagtgaga gagggcataa 60
 gtgagaaaga gatactggat ggtgggcgaa ttc 93

<210> 761

<211> 1064

<212> DNA

<213> *Drosophila melanogaster*

<400> 761

atccagctc atccttttcc ttcttgctt ttttgcctt tctacaaatc gagaatttca 60
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 ttcttaatgc gtgcatgac gtagtctgac atcgtcacaa aataggtaaa ttgttgatat 180
 agttttgggt tacaacacaa taaacaaaca tgcgatacaa catcgcagat gagctggtct 240
 atcggttatc gatattctac caataaatac tgtaagcgta catttttaaaa agtacggact 300
 caaaccattc attaatgtg taaaaaaatt aaaatcaaat gatttttgat ctgtgagaga 360
 taagacatat ttcattcttc atcacatata tatatttatt ctcgtaattc attatatatt 420
 tgcttacaaa aaggaaatac aatcacggct gctggatttg ttaaactaaa caaaagactt 480

aaactaaaca tttgacttag atacatactt ttataaatga ttattataaa ttataaataa 540
 atatgtgtaa ataatacggt tcaaatagct taaataggaa acatcttatt ttcataact 600
 ttggaaaaag cggtggcatg gtcacatata agcttgtaaa tatgaataaa tacaacaaac 660
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 ccttcgacag agacattttg ccattggccc tgaaatggag agggattttt ttttttaatt 780
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 1020

atctccttac gcacagccaa acgttgctgg ttgtccagcg ccca
 1064

<210> 762

<211> 1345

<212> DNA

<213> *Drosophila melanogaster*

<400> 762

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 aatagttgta gaaaagcgcc ggcaagcgga actccacact ctttctcact ctctctttcc 120
 acccacaccc ctagtccacc ggaaaaagaa aattcgtttg cggcggggggt gtatttttca 180
 ccaaaaagag agtgtgtgca aaacgctaga gagagagaga gagagagaaa gaactgacgt 240
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 cgagaagaag cagaacaaac acacacaaaa attcgacagc tggagcagaa atcaagcttg 360
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 tgccaatttt ggtgatcacc attttagcat attttttctc atttaataag tttgcaaaaa 480
 aacctaggta cagtgaatg gttataatta ataaaggat ttacattgat cctttttttt 540
 acataacatt tattaagaaa gtaacaaaaa atacatcaa actttataaa atgcactctt 600
 aacaacacaa aaccatatat acatacatat gtacatatgt atggcccact ttactgatca 660
 ttactgtgac atataagtag tttttaacaa gtggttttct tttgcttttt ggcaccgtga 720
 gaaaaaaatt cagaactgcg gctgtctggc atccactgtc ttctattagc ccggtccga 780
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1080

ggtaaaaatg agtgtcgagt tgaaggaatc cccttggtcg ccttaaactt ttggctaacc
1140

cactttttat aataatgaaa aatttaacat tgttttgaac tcacgaagtt ttagacaaaa
1200

acctgtttat agatgggatg ttcgttcata ctggaattgc ccataactca ccgcaaatga
1260

atctttgact ttttgagaat gcttctactg attgattgac aattacttaa ttgataaatt
1320

ggaaaagaat acaggggagg aattc
1345

<210> 763

<211> 597

<212> DNA

<213> *Drosophila melanogaster*

<400> 763

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tcagcaaatt ctattttatt cataaatgtc ccaccaacca atgttcttca agacaatagc 540
ctacagcact agtattccgt cagcatgtct gccacaatg ttggcgcagc agaattc 597

<210> 764

<211> 577

<212> DNA

<213> *Drosophila melanogaster*

<400> 764

atcgtgccca actcccggcc atcggttatg gcgtgtcctc gaaaacgggg aaaaaagtta 60
caactagcag taaacgtgaa aaaggaccag caaggacgag aaaatctcgg cgaggcgaaa 120

gcgctgtggtt ttcattgtcg tcgtcggtcg cctttggctc atcaataaaa atttccttga 180
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caaagaagtt ctacttcate ggcaggggaat gaggggggaa aatttaatta agcctcttcg 480
cgattgttta taaattcatg ttaatgatat ttggacagcc ccctttttcg gatgccgaaa 540
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<210> 765

<211> 940

<212> DNA

<213> *Drosophila melanogaster*

<400> 765

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tggtcgaacg gtcacactgg ccgagagata acggaaaatg tttcaaagggt aagtaaagat 120
tataaacgta ttaagcttaa tactataatt agcttactat tccaagtatg tataattatt 180
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aagtttgga actaaatagt tgtccgagta atcctcgcct gctggcctcc gtctacaatg 780
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atccccgatcc ggagcagctg aagtcagagt acctgccgtg ggagcaggtt gaggtcctgg 900
ataccgaagc actgggcgaa cgtgtgaagc catcgaattc 940

<210> 766

<211> 1131

<212> DNA

<213> *Drosophila melanogaster*

<400> 766

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cctaattcttc atgaaatcgt aaacatcggc gaaatgacaa atactttcta tatacctcga 120
actagtacct aaatatgtat acctgaagtg cgtaattgaa accgaaatag gcgctgaagt 180
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1020
tttaattctca tcaccagagc caccatatat gtatggtaat ctggggacgc aatatataga
1080
cagaatcgta gtttcaaagt catcctgact tcagcgacct aatgggatta c
1131

<210> 767

<211> 687

<212> DNA

<213> *Drosophila melanogaster*

<400> 767

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aatttcatac tcgtggagac ggtgagtgc attgccgcca ccgctctctc cattacccat 120
ttcgacagcc gtctctcgt ctccactta tgctttttgt ttgtcatgtt ggctttggcc 180
tgtttttgc tttggttgtt gttgtacagt gttgctttt caatttactt ggcacacata 240

caccgcgcga caaagtaacg agcaccagca agggcccaat gcaatttggtt tatttgcaaa 300
 tacaatttcg atttggcgcc agataacggg atccaagggc tcccggttacg gatgtcagtg 360
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 cctgttgagg ttaaattgga agcgcggcct aaccttaatg ggtttacaag tttgccgcaa 480
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 aattggaata taaacttgaa aagatgtggc tcgggaaagt tccacttatt agatggagca 600
 cttttaaaaa accgattaga ataccgggtt aagcaaaaaa ggtagcttat tgcattggaaa 660
 aattaaaatt aaaagttaat ttgggaa 687

<210> 768

<211> 510

<212> DNA

<213> *Drosophila melanogaster*

<400> 768

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 ctaccgccgc tgcttctgct gctgccgctg ccgctgccgc cgttgacgtc gcagccgagt 120
 ttgataaagc tggtatcagg cggcgagttg cgctaaggtc gcgatgtcgc ctttatggaa 180
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 tctgaatcga cattccaaat gacagatacc gcgtgcagag agagaaaata ttggcaccag 420
 acaatatttg ctttattcag ccaaacgttt tcacttaaac caacttggtt gaaattagct 480
 ttgattattt gcattgagtg attactgac 510

<210> 769

<211> 1144

<212> DNA

<213> *Drosophila melanogaster*

<400> 769

ggccaggcaa agcgacgcgg acgcggacgg cggcagcgt gcgacgcaaa tgacagtgac 60
 agtgcccaga ggcacgctgg gtatatcggt tgggaggtat tcgcaccctt tttcctcgct 120
 tatggtttag atggttttta gtttttatat ttcgttagag ggctaattggc actcgttttc 180
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atcgtttaaat tagtttttca aattattttaa tacatataat aaatagaatg tttttaaatc 300
 aaccgattgc taatgataat tttacacccc ttttagcgct cctcttggtta aatatatttt 360
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 gttcgctgtg tgtttgtaag actgtctgta tgtttggtcg ctgtgtgccg ctttgagggt 540
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 acat
 1144

<210> 770

<211> 113

<212> DNA

<213> *Drosophila melanogaster*

<400> 770

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<210> 771

<211> 1166

<212> DNA

<213> *Drosophila melanogaster*

<400> 771

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<210> 772

<211> 582

<212> DNA

<213> *Drosophila melanogaster*

<400> 772

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 agagcgagtt aatggcacaa ttgttgcatc tgaacagagc ggggcagctg catgattgac 180
 aatcatgccg caccgcttgc acccgttgac tttgctgttg tttgtcgctc agcgctctct 240
 tcgctgtag ttaacagcga tgtaggagt ggaaacacgt ccgactgtag cgtaaattca 300
 aacgtatctg gcgggttggg tttccgatga aatatcttcc atccgcacag tgtatttttg 360
 actgcgaagc gcgtacgacg tgtgtctgtg ttgcgttgcg ttcgaataaa aaagagaaga 420

aaagcgaaaa agtggtgccc tcggtgaagt ttattattat tatgattatt attattggcc 480
 gttaccacgc gttttggcat caatcaacaa ataaacacac aagaaacatt tggaaatcgc 540
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<210> 773

<211> 727

<212> DNA

<213> *Drosophila melanogaster*

<400> 773

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 aggcgataat atgccacaaa caagaaacga aaactgacta aacgtgcaaa ctgaatacgg 180
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 gatccggtga ccagcgaaat acgctggaca atagcagatg gtaattacgc gggcactccg 660
 ctgtcttcac actcactgca cccctatttt ccggccacaa gtgtgggact cgaacatatg 720
 atggcaa 727

<210> 774

<211> 1010

<212> DNA

<213> *Drosophila melanogaster*

<400> 774

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 cttgagccgt gcttaacggg ttttttttcg gggctaagaa cactggttgt gcacacagaa 180
 aatgttgaaa atcgtattcg tagtcgcggt tctgtcgcta gtgaagtgtg cacaatocca 240
 aattgcttgt gagttgattg aacaaatgtg acgaaaagag taataagtca aatataatat 300

gaaaaataaaa ataattatag ttcttaaatt aggattcctg ggaactacct ttttaactttt 360
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 ctacaaatat ttcaagattc tatcaaaact tgtataatca taaaacgtgc ataaggaaaa 600
 gtttactaga ttatgagaaa tataaataaa tgcgttctgc ttatattaac taattatttt 660
 caacactcct tatcatgaac tcacgcaaatt tgaaattcct ctgactccca tgacagttag 720
 caaccagcca tgctcgggtc gaaatccaaa aatcgtggga ggtagtgagg cggagcgcga 780
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 catgaaacca gctcaaatca aggagttggg gggttgcata gcatcagga gtacctcacg 960
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 1010

<210> 775

<211> 1426

<212> DNA

<213> *Drosophila melanogaster*

<400> 775

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 tccataatat aaccactcac atttccgcct ctatgtctgc atatgcgatt tgccacgctt 180
 gtacgtacat gcgattgtat tcgagtattg aagtattcaa gtattcgaat actgaagtat 240
 tcaagcattc gagttgttcg agtatctgcy tattcgagt gaaaaacatc ggagaaagaa 300
 gtgaattatt atcagggcgt attgttacct ttttttttta tccattatt actcgagctc 360
 ttgaaaaaga aaaaaaaaaa agatttttact tctatgccac agcgattgtt aggattgcaa 420
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 ccaactttat tgtgaatcta gccagccaac cgagcgcac aatctgcgtt gtattacatc 540
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 gcgtaaatgt atatatatat atacatatgt acgtatctac tccctcgact tgaacgacct 660
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1020

acacttaaag ttgcaaaaat atatatgctg cagttttgag ataacttttt tttctttgtc
1080

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1140

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1200

ctgcaaaatg tagcgggttt catttctttt tttcgggtggg ttggtgaacg gggggcagag
1260

ggcagggcgg aagagagcaa ttcgtggcgc tatcattaaa caaataataa atgcttactt
1320

tggcataata tttattttgc gcgcctcgtt gtctgcgccg tcagaaattg taagccgttt
1380

tttgagtgat aacaatgggg caaaaagcaa atggcaaatt gaattc
1426

<210> 776

<211> 403

<212> DNA

<213> *Drosophila melanogaster*

<400> 776

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ggctgggctc ttatcttctg tagagaatgc aaagatgttc gtggaagcgg aaccaatgcc 180
agggccacgt cagccgcagc tataggcaaa tcgcaagaag ccggcgataa ggcggcattc 240
aatatgtata atacgacaat cccgattgtg aacgttgtca agccgggcat tatgtcatct 300
tcaactgctg gtgcccccca gttctcattc aaattcgagt gcgtggatgc gtacctaatt 360
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<210> 777

<211> 1111

<212> DNA

<213> *Drosophila melanogaster*

<400> 777

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atgacttttg gcagtggatg gcgtaagata a 1111

<210> 778

<211> 499

<212> DNA

<213> *Drosophila melanogaster*

<400> 778

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 taataataag cagcataaga acaacaaata ccagtatcct cagacgaaga tgaaccaagg 180
 gagaaaagag agaacttaca aaagcacttg aaaaaaaagt aaacctgaaa accaccacaa 240
 taaaattatt agacaacatg tgctgcgatc cttatacaat actttcaaga aagtatttgg 300
 tattttgatt taagcataac agaaggaaat gcttatgtta tgttacttgt ttatactata 360
 aatccagtgc aaacaattcg gttctctcag tgggtaaaag tgaaatgtat aggggtgctgg 420
 catcatcatc tgctccccc tttgcaaagg gaatatctga gcacacctga gtgggctgga 480
 caagcggatg acggaattc 499

<210> 779

<211> 371

<212> DNA

<213> *Drosophila melanogaster*

<400> 779

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tgacgatgat gatgcagaag agaattgatga tgatgatgac gacgacgaca acgatggaga 120
ggagacgagg ctgcttgaat agatgctcaa tcgtttgggt tgaatgaaga aaagcatgtg 180
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tgtgtggcag agattggagc atgaatagga atgccaagaa ggagacgatg gaggaggagg 300
aggaggagca gtagcaccag cgtgagtgcc acttgcggtg gcataatgtt cttgttgatg 360
tttgactaat g 371

<210> 780

<211> 1013

<212> DNA

<213> *Drosophila melanogaster*

<400> 780

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ggcattaacg gttatcttta tggtttccgt tatgtcttgc gttcagttcg ttgctgataa 120
ctctcctgca cagttacagt gcactatcga tatggaggac ccataaatac gagcattact 180
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1013

<210> 781

<211> 1063

<212> DNA

<213> *Drosophila melanogaster*

<400> 781

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tttgctccga ttggtcgaga aaaagcgaga aaaacgtcat gccgttctct tcgccgcaaa 120
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1020
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1063

<210> 782

<211> 118

<212> DNA

<213> *Drosophila melanogaster*

<400> 782

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cagttctctc gttctcccg cgcacacat tcatgcaatg ggcattctgca gcgaattc 118

<210> 783

<211> 176

<212> DNA

<213> *Drosophila melanogaster*

<400> 783

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tgtaagtggc ccatatattt tctcatgaaa aacaaaaaat ccataaaagc ggataaaaaat 120
gttcgccgcg cacattactt ttgttggttt ttggtggttg tgttcgtgtg gaattc 176

<210> 784

<211> 537

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(537))

<223> Area matching *Drosophila* Genomic sequence

AC006073.

<400> 784

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attcgattaa atgcgacttt attaattgaa actataattt atcagagggc gcacattttt 120
atcgcaactta ccaccaatg aatcaaaaac tcggggctgt ctctttctac cgaaaacttt 180
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accgacgcgc tgcattgcaac atgttcgcc tcgaacgtca aacgacgagc atcgaacgtc 480
gaacttcgaa catcgaacgt ggagccgacg aagagtgcgt cggattttac ttaccgc 537

<210> 785

<211> 720

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(720)

<223> Area matching *Drosophila* Genomic sequence

AC004299. Matches in area of ORF with sequence
similarity to Human C-TAK1 gene.

<400> 785

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agaaaaagtt gcgactttcg agcacaagta cttggcacca cacactcagg gaagagtgcc 660
acgacaaaaa aatttagaga aaaaacccga aaaccgaatc acacaaacgg aggactatgg 720

<210> 786

<211> 599

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(599)

<223> Area matching Drosophila Genomic sequence
AC004115.

<400> 786

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tccagcctga gactgcacga tgggtgtcctg agggacgttg agcagcaaca acggcgcaaa 120
cacgagaata cctacacgct gcagcagcaa atagacatga ccaagcaact gaaagccagg 180
gaggcgtcta gcaactcctc tgacacgccc gtacctccat cgacgcatcg cgcacagagt 240
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tctttacgct ggttgatcg ttttcaagtt ggtgaagcct tttgcgcatg ggaatataat 540
taaacaacgt ggtaagaatc aatcttacca agcgaaataa gactgcaggc taacaaggg 599

<210> 787

<211> 581

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(581)

<223> Area matching Drosophila Genomic sequence
AC004716.

<400> 787

ggcgaaggta aacgcgaagg cttccgaggc acgtaaaaaa aaagttcaaa cccgactagg 60
acaacaacgc gaacaggaca ctacacgca ggcaatcagc cgcacacgca cacagtcacg 120
agtcggaaaa gcttgtaagg accacaattc gccgcactcc gaatgtgtgt taaagcttcg 180
tgaaatcctg gggaaataat atcccgcгаа tctccttgca gcgcaatgtg aaagggaatg 240
ggcattcata aatttataaa tttaaaaaaa aatcataata aaattagaaa aaatattttt 300
atttataccc aactgcccta aaagtataat ttttgtatat ctttaatttt aaatatttat 360
atttggttta gataatattt tcaaaaaatt aagagactta ttaccaattt tcatactatt 420
tggctcttgca tattctttcc ctgctttaag tagaaagcag tctgcactgc tttttagttt 480

aagtagaatg atatatTTTT tcatagacca taagcaaaaa atcttttagc tgctaaatga 540
atctacgtgt ggtaatgctc ctcttctcag ttcaaaccaa a 581

<210> 788

<211> 628

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(628)

<223> Area matching *Drosophila* Genomic sequence

AC005889.

<400> 788

caccaacgat tggctagttg ggagggggcg gtggatgtct aacattgcaa cgtgaccatc 60
gcgcattgcc tttgcacttg taacatgttg ttggagtcgc gtttttttcg ttagcccggt 120
ttttgttggc tttgttgtcg ctgtaaactt gttcgcggtg catgccaatg aggcgcattc 180
gacgtcaggc ggatttggtg acacagaaac tggattagag gcaacaacca atcaacccaa 240
tgagtgaaaa aaaaaacaac ttggaacca aaactagaca ctaagccatg aaaattgtgg 300
gaaactaagt atttacttta tgattcaata attatacctc ttaaataaac tggttttggc 360
aacgtaaaaa aatttggttt cacacaaatt gtaatttgtg tacggtactt ttgaagcaaa 420
gcaaaaattg ttcttttaggt atatcttttt tctatttact aataaaataa ataaataact 480
ttaaaaaaaaa atttgtgtgc taaaacccaa atatttactt attattatgg gtatgtaaat 540
ttggtcagca cctgcccact gtgcgcacgt catcggttgc atgccttgtg gttggtggtg 600
cttctgcttt ggggggtttct tgggtttt 628

<210> 789

<211> 536

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(536)

<223> Area matching Drosophila Genomic sequence L4908.

Matches in area of 401AA predicted protein.

Sequence similarity to mammalian glia maturation factor.

<400> 789

```
ccccacagat acggtgagag aacgacaaga gagagagagg gagcgagagc agctgtgcga 60
tgccggcaga ccaatgttgt tgttattgtt gttgtttggc ttggccatct tttagttgtt 120
attattgctt tttagtagtg acctccgaca acaaaccgaa atcgaaacaa gttttaagca 180
acaacaacaa cagaaaaaaaa aagaactgca ttaaagcaga gatttatggt tctttaatca 240
aagtctgaag aatgcaaagg cattcctttg ccatgagtat tgcatttgta aaaaaggaaa 300
ctgaaaaaat ttgggattta tgtttttctt tttttgtcta acaaattttg tgctattata 360
atggaaatgt taatgatatt tgtggctctt ggggaaaatg ttttatatca attcatttca 420
cctgggtatc tacttgccgt agaaatcaaa tgcaataaaa aattacagtc aagatttagc 480
caattgttgc gtattttgag ccatttgtgc ttttagacac cggcttggtt gaattc 536
```

<210> 790

<211> 86

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> Complement((1)..(86))

<223> Area matching Drosophila Genomic sequence. Matches
in area of ORF with sequence similarity to a mouse
G protein.

<400> 790

```
ctatagtcgc tctagctccg ttctccgaag agagagagtg aacgaagaga ggcgaggaag 60
agagttccag gaaatcgcaa gaattc 86
```

<210> 791

<211> 573

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(537))

<223> Area matching *Drosophila* Genomic sequence

AC004306.

<400> 791

```
ggcgcaactt gttttcgatg ttgttggtgt cgttgctgct ggcttacgtt tttttttatg 60
cgccgctcgg gttggtaatg atcttcgtgc atgtgggttg gcgtcggttg tgtttttggt 120
gctggtgatg tcggtggatg tagagaagga tgaggaggtg actgcgactg ttgcgttcatt 180
tagcggggca gaggcctttt tgggtttggt gtatggtata tggccagaag gagggcgtgc 240
gatacatggt ccaggtagac acatgacgaa gccacagtcg aactcccata acccgtcatt 300
ttactaattg aatacatttg tagtgaaaac gaacccttcg attcggtttt aaaatcattt 360
tttagagatt taattttgat ttttcagtta aactttgcac ataactgata agtgtagcgt 420
tcatactttc ggagtttcac tgtatttata aacaaattca cccacatggc agcctcgatt 480
gggtggcggc atatcccgcc gatttcggcg tgggctgatt ttagccgcat tcgatttcca 540
tttcgggttc aagacttgcc cttcaacttt ggt 573
```

<210> 792

<211> 648

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(648)

<223> Area matching *Drosophila* genomic sequence AC006472

(71606-72257). NPS1077 lies in an intron of a
gene at 62506-79351bp coding for a 1876AA protein
similar to hypothetical genes from yeast and
human.

<400> 792

ctccttacct atgtaacgtt tcgccaacgt gtgcgagcga gagggcgcggt gtgtaatttg 60
 ttgtggagca gctgcgacgg cggggccaaa gctgttgtct cgctcccccg ttcggaagtga 120
 ggccttgatt cgggactccg agctccggat caaatatttc aacagttttg gatccgtagg 180
 gagggagggg gatattctagc ctcctagaaa agttttgccca ttcaaattag tatcataaca 240
 aatacttggc ttagaatggc accatttgcc caacaatccc ctaaaaagta atcgtttgtg 300
 ggacaaacta tgctacagat cccgttttct tgacagtaaa tggcatattc ctcaaaaatt 360
 aaaaaaatg ataaaaaaaa aaatgataac aaaacagagt catatacttc agtattttga 420
 aattctcaac aatctatatc tgccatttaa aaagcctgat aagttttcaa gttattcgaa 480
 ctcagtagga ttaccaaatt ttcactgata ttcaatgttg gaatggaagt actaggataa 540
 cccacggaat ttatagtaag aaaaggtcta ggaatttggt ggattcatgg agaaattatc 600
 ggatagaaaa tccttactac ttaacgatag cccaattgag atatagct 648

<210> 793

<211> 463

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(463))

<223> Area matching *Drosophila* Genomic sequence

AC006092.

<400> 793

gtctgaggta ttaaatagtg aaaaaaatg tctgccgcgc cgaaaattga caaagcgacg 60
 ccgccatgtc gcaacctata gccatctccc tctcgcagcg tgctcccagc accaccagtg 120
 ttcattctatg tgtgtagtgc atatttcgag cgttaaaatc tgttgaaaat ttaaaaccat 180
 tcaaacagtg gaaaatattg tgcacacatt atagggtttt cacatttccc ttgcggaaat 240
 cggaaaagca agcgtatgtg tgccgaatgg aaaaaaccaa gacgcagggt tgcatttttc 300
 ttgatttcga ggggtgcatt ctgtgtgata agcgtttttt tattctgtct ttaaaatgat 360
 tgtagacttt tgtcccgta tgtttcgata atggatatta cgcagcggca aaattattat 420
 ttaatgtctg ttattgagtc aatgaacttt ctgcggtttg gcc 463

<210> 794

<211> 519

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(519)

<223> Area matching *Drosophila* Genomic sequence

AC006073.

<400> 794

```
ggttcgagtt tgaaatgagg tctcaggagc ttcgtgttgc atcgaacctg ctcgatggca 60
tctattggtg agaggggCGT tctgtgttcg caataaccgg aaacggaaat catatttggT 120
caagttctaa tgccatcaac gattgcaatt aaatggccaa atgtcaattg tttcaagctg 180
actaagtgcg agaaggacaa aaaagtgttg tgcgaaaaga gacaggcgcc aaaagcctga 240
acctgccatt aaccgttaat gcacggatcg taaatcgaat tgaaaggaag ggtgtgtcat 300
gccggactta taaataaaat taacaaccag ccgggggaaag aggttaaggc ggaaatattt 360
gcgccactgc gactttcttg ctgctcgat tgggtccggt gttttttgtt gcttgtaatt 420
aatgggcaaa caattacaaa aaaaaataa agggagtcgg ggcaagaaga atgaggcccc 480
cagtgaatt taccagtatt aaagggcgag aagcaagtt 519
```

<210> 795

<211> 704

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(704))

<223> Area matching *Drosophila* Genomic sequence

AC007176.

<400> 795

```
atacacccta ttacgttta ctaagagagc gaccaacgCG agacgagtcc caaaatgagc 60
gctctttttg ccgaactgtt gaatgccggc tgcaaaagca acaatacaac tgcaacatc 120
accacccccca ttgcgcttat gtttttagcaa cccctaaaac aatatggcgg cgagtaacct 180
```

acaacaaaat aaataaaaag aggaaacttc cccccagaaa gagcaacaat tttccacgcc 240
 aaaatacact ttttttgcgc gcgctacagg ttgctgaga gaacgaaaga gagcgtggag 300
 agagcagcgg agagcgagtg tcaagagaaa agcgcaacaa aagcaggaag cgataaacga 360
 taaatacaca cagcaaaaac gtagcagact ttgcgaaaag aaatttcatt ccgtgtagat 420
 aaaagataca ttaaaatagg agagtatatc ttaatgcaa ttttttccca tactctaatac 480
 aaaaatcaaa atattctcta tgccaaataa tatcgacttt tatttatatt acaaaacagg 540
 ttcttttcag tgtactctgt gcgcatgttt ttttccaatt tgggcaacga ccgcatccaa 600
 agcattacca ccaaacgttc tcttgggcac cagccttttt cctctgcttt gctattcttt 660
 tacttagcat ttctctggtc tatgttgccg caaactttca gagg 704

<210> 796

<211> 307

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(307))

<223> Area matching *Drosophila* Genomic sequence

AC004423. Matches in area of 702AA predicted

protein. Sequence similarity to *Xenopus* DNA repair

protein XPGC

<400> 796

agttggctca gcaagaagtt ttttgcattt ttaggggttg taagtgggaa atgaaatgga 60
 gaaggtgttg tgtgtgctcg tatgcagcta aaaaatggcg gcaaacacac acaccaaacc 120
 cgaccacac agacaacaaa ggctaaaaga gcagctgttc cgacggcttt ctctagaccc 180
 ggtgaatcaa cagcctccca catccgaacc atccacatgc ccgccccacc atccaattcc 240
 acttccactt ttaacagaag cacacgcacc accggcacgt ggtgcgccat atgcaaatta 300
 agaattc 307

<210> 797

<211> 412

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(412))

<223> Area matching Drosophila Genomic sequence. Matches
in area of ORF with sequence similarity to Septin.

<400> 797

```
gtcgaaagtt aactgcggtt ttcgataacg atacgtgttt gctatcgcca ttgatgggtcc 60
cgttcatggt atcgagccat atttgtccat tttatagcca aacgtttgat tcatttttat 120
ataatgacat agtttataat catatataat ttcaatgtag tttttaatag gtttgctatt 180
tctgtaatat atattcggcg aacttagata taacaataga acagttttta agttttaaga 240
tcataaatct ttaaaacacg cgagattaag acaacgcgat atacgtttac gtaaaggatt 300
tttttatgga ggtggagaac tttaagttgg cattactgtt caaaatcgcg accgacttaa 360
catttgccga gttattgceg atatatgacc acaaatgttg gaaaaagtca tc 412
```

<210> 798

<211> 478

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(478)

<223> Area matching Drosophila Genomic sequence
AC004313. Matches in area of ORF with sequence
similarity to potassium channel genes.

<400> 798

```
acagaagccg tcaactcagg cgaagtgttc gtagcggaac ggaatggaaa cggaacatgc 60
acacgaatgc cagccgaagc aggagtacga agcatgccat cctgtcgtgt gtcagcgaaa 120
gagaggcaga gagaaccaca actcgtcttc aatgggaatg ggtctctccc tctctccctc 180
tctctctctc tctccgcaca acgcctcctg tggctgtctc ctcttccatt tcctacgagc 240
gacaggatgt gcagctgccg actgcgactg catttggtt cgcgcccccg actccctgtt 300
actggggatt ttgggatgca ttcccgtaca aagcatacgc atctgggcaa ttcgattccc 360
```

ggattgagca acaatccacg cggataacag gactacagga taataggaag tgggtgaaaa 420
atatacactt tatgatttat gatccttaag cgggaattta ccacattaaa catatattt 478

<210> 799

<211> 489

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> Complement((1)..(489))

<223> Area matching Drosophila Genomic sequence

AC004641. Matches area of 402AA predicted protein
. Sequence similarity to Xenopus FLAP
endonuclease.

<400> 799

atcgtgacgg tttgctcgcg ctctccgctg cgccgccttt tccgttgcac atgtgtgcgg 60
gcgttattgt gcatgtttcc ggtggccgaa aaaaaatagn nntatagaaa acagaaacca 120
agaataataa cagccatacg ataaacagtg tgccaatgtg tgtgtctgtg tgtgtgtgca 180
tctcgcgtaa caacataatt gcatttatcg gatggcgcaa gcttcaattt aattataaat 240
aacatgttca actttttata ctattttccc tgcgtcaaag tgggcgttgc aactgcccc 300
ggaaaatcac gcgccccggt tcaaagttaa agtttgctgg gtaacgcaca cacacacaca 360
cacaatcact cacacgcggc acacgcacat ttcaataaac taatggagcc tggctttggg 420
tttggtntaa ttccaacca cttgagcaca cagcacacac agagaggaaa aatcaatact 480
cgttatggg 489

<210> 800

<211> 558

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> Complement((1)..(558))

<223> Area matching Drosophila genomic sequence

AC004306(57408-57954). No good predicted exons in
this area.

<400> 800

```
gcaagcacga tgaagaagga aagcgagagc gaccgaaccg cacaccacga gaaattccaa 60
cagactgaga tggaaacaac aaacgatgac gccggcaatg ccgacgcaca aagcagcgca 120
cagtggggcg atgtgcggtg gattcggtat ccattctaaa tagtaatacg ataggcatga 180
acaatatttt caacaactct tttgcgaaca ctgtaagcag aatgacatgc atttttgcag 240
aattgtaatt ataattaatt ccggcactaa aattaaatga tttttgttta gtttttaaac 300
acgatttact tgattcgtaa atattatcaa gtattaatta attacttaag cgaatagtta 360
aaactggtaa attagcccca aacaatattt taatggtttc aagcccacta tggccaagtg 420
gccacacctta caaacgaaat ggatccgcac aaaagaagaa attgcaacaa acaggcggca 480
aggcagccac cgctcatttc aagtcgcttt ggtgggtgctt ctgctggctc tctccgtttt 540
tagtaattgg ggtgtggc
```

558

<210> 801

<211> 623

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(623)

<223> Area matching Drosophila Genomic sequence

AC001646. Matches in area of 724AA predicted
protein. Sequence similarity to Mouse serine
C-palmitoyltransferase.

<400> 801

```
ggccagttac tcggccagct gttatactga aaactgcgcg ccttcggtat ttttaaggtag 60
ttatcgtatt ttcacatata atttaaaagg ccacattttg tggaacaacg cttccggttg 120
tgttctctgc ttttagtact gccagctcct agcgaatacc tccaccatgc aagcagttca 180
agccgcagtg ctgttttagta tactttctga gcgccagatg tcgcaaaaga gaagtcggtt 240
tttgtattaa ttagattttc aaagaaattt atttaacta aaatggtttc tatttttagtc 300
```


acataggggt tcaacttaaa ttatttgaaa gcaattatta tgaaaaatat ataaattaat 360
 atgtgatacg aagggttttta gtgcgagata agctaaaaaa aatgatgttt tatattccat 420
 tacatattag aaactacaag ttttcagact taagacgtca agcattttcc ccttgagcat 480
 taaaatctgg ccaaaactta cgcaaagaaa aattccgctc gccggcaata ataaattaga 540
 ttaaaatgca caaagaaaag gagggaaaaca gaatttcagg ccacaggatt tcagataaaa 600
 gtgccgtaag cggcaatgta gta 623

<210> 802

<211> 544

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(544)

<223> Area matching *Drosophila* Genomic sequence. Matches
 in area of ORF with sequence similarity to U5
 snRNP genes. *Drosophila* ESTs AA803646, AI518976
 and AI108114 come from this gene.

<400> 802

ctcttgtgtg accgacacaa tgtggtcgca gcagtgtcct atgaaaatac acacacccta 60
 agttaatacc aaaaatatac taaacattta tttgtccag cacccaaacc attaacatca 120
 gtttttcaac agaactatgt taagcgcagg tgttaactta tatttatttt ataagtggac 180
 tttgttgtcc tgaaacttaa tcatcaccag aatcattatc atgctctcta gctttatttc 240
 tcgtttaact tatgaaaacc acaaatatca aagaccaaca taacatagct ttacaccgga 300
 aaagtatagt agatagtata gccaggagt cagctctagc tgtgttggtt atcgttatcg 360
 cggctagcag cttgttttgt tttgcttaca cgacaaataa ataaatataa aagaagtatg 420
 agtaatttaa aatcggacct ggatgaatac ttgctactgc agagtgatca gaagaaccaa 480
 tttcaacgtc aagttgccac agctggaagt tccattttct cagcttcgac ccagaacaaa 540
 tagt 544

<210> 803

<211> 201

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(201)

<223> Area matching Drosophila Genomic sequence

AC004154. In intron of predicted gene with
sequence similarity to mammalian geranylgeranyl
transferase genes.

<400> 803

gaatcaacta aaaacattta tttaccacct gctcatttat atgctgcagc cctatcagct 60
gttcgctgcg gcgcccacta tcagcgcata cggccacact gcgggggcg cagggatgcc 120
aaaaattgat gtggataaca tagaaatatt taaaattgtg aaattattcg attttgataa 180
gtatacttct taacggaatt c 201

<210> 804

<211> 524

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(524)

<223> Area matching Drosophila Genomic sequence

AC004766. Matches in area of 1442 AA predicted
protein. Sequence similarity to C. elegans
ZK1128.2 gene.

<400> 804

gtctggactg aaacggtccg ggaaacgagc cgaaagtagg tctgagtggg aaattaatcg 60
aggcacattg agtgaagtgc acaaagcttc gccagctttc aggagctttc ccaacaattt 120
ccccctatct tcccaaggcc aaaataaatt aaatttttaa atgttaaata cctgtttgtg 180
ttgtgaatgt gttgctgttt ttggtaaagt attaaatgcc aatagttacc tgaaagtaca 240
ataaattaaa ttcaaatcag tggaggtcaa cagtataacg aaacacactc aaagaaatca 300

caaataacga ttaactcact aataaagga ctttatggat agacatataa actttttcaa 360
gctttgttag ttatggtaag ttatggaaag gagcaaaagc tttataaaa gcttttcgat 420
tagaaaaagt gttgccagct taaagtattt ataagaaatt tgaaaaagga tttggtagaa 480
atcttttagag tgaaacatgc caattacggc taatacatgg tagt 524

<210> 805

<211> 621

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(621)

<223> Area matching *Drosophila* Genomic sequence

AC004361.

<400> 805

cacagcagac tgcgtcacgg atcggatctg tgtggatctt cagttcggtt tagttttcaa 60
taccaaacc aattccagcg gcattgaaag tgcgtgtggt ttgttggtgc cccatgggct 120
ttttgtttaa ggtcttgga aatgaaagt ttctcttcat cgatgctgca ggacattatg 180
tttgattaac gaaacgcagg tcgagttttg gactgttgta aataaatttt acaaccttta 240
atgctgccac ccagacaacg taaaaacgag aagcaattga aatgtctgaa ttatgtttgc 300
tgaattattg aattatatag gtggtcggat actacatgct acatgcatgt aactgaatgc 360
aagtacttaa ttacgtcagg agaaatttat tttcatttcg aaaaacgcaa taaatgttaa 420
gcagaaactt caaggggatt taaggagcat tgcataaaca accaaaaatc ccttttagatt 480
tcataaaatt tacaatatct ggtatgattt cgaagactga aatattgatt aaaagaattt 540
gtacgatttt tcaatcgaac aatgggtcaag cccgatgcc aactcatttt ggcccggcag 600
taccacacca ttataacaca t 621

<210> 806

<211> 569

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(569))

<223> Area matching Drosophila Genomic sequence

AC007185.

<400> 806

```
ctcaatgcga attgttttca agcgccggag agaatctata tagaggggct tctccgactc 60
gcttcgaata cgtttttctgc agcgcgcgcg ttgcgcatcg aaaatcagaa aagctggcaa 120
gcgtttaaaa acaaattcgg caggtacaat tgttacatgt tttccctca gttgactatt 180
tcgtcgcagg tttttggcca gcggaaacca tcgtaataac cgttattttg ttatattcgc 240
gtaaatcggt gtttgttcaa ccacagaata cttgttggtta cgcatttcga aaatggaaat 300
gcaaaaattt ccaagcagtg aaaatcaaaa cgaataaaat atattggctt ctttcgtgtt 360
tagccgcgta cgtgtgtgtt tctgtgttag tgagtgcagc aagaaataaa accaaaaagc 420
aacaataaaa taaatagaaa acaaaagcaa aatcaaatec aaattcaaag gcaaatactt 480
gcaaagtaag ttgataatat caggagtggg ggggtgctagc atatgttgca ttattttgcc 540
cagcatttac atggttttca caatttctt                                     569
```

<210> 807

<211> 462

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(462)

<223> Area matching Drosophila Genomic sequence L49408.

Matches in area of 401AA predicted protein.

Sequence similarity to mammalian glia maturation
factor.

<400> 807

```
cggcagcacc aatgttggtg ttattgttgt tgtttggctt ggccatcttt tagttgttat 60
tattgctttt tagtagtgac ctccgacaac aaaccgaaat cgaacnnnca acaacaacag 120
aaaaaaaaag aactgcatta aagcagagat ttatggtttt ttaatcaaag tctgaagaat 180
gcaaaggcat tcctttgccca tgagtattgc atttgtaaaa aagtaaactg aaaaaatttg 240
```

ggatttatgt ttttcttttt ttgtctaaca aattttgtgc tattataatg gaaatgtaa 300
 tgatatttgt ggttcttggg gaaaatgttt tatattaatt catttcacct gggatatctac 360
 ttgcgtagaa atcaaatgca ataaaaaatt acagtcaaga tttaccaatt gttgcgtatt 420
 ttgagccatt tgtgctttta gacaaccggc ttggttgaat tc 462

<210> 808

<211> 233

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(233))

<223> Area matching *Drosophila* Genomic sequence

AC005750. Matches in area of 1813AA predicted

protein. Sequence similarity to Rat CPG2 protein.

<400> 808

ctctgagctt tactacgatt actatacagc tcttctctcg cgactttttg gactggacaa 60
 ggcgtagcac attgaacggc agtggggttt ggttttagtat cgaaccggct ttctacgaca 120
 gcggattgga agcgcgagc gacaaagtcg ccgggtaata atgtgatata gccggctatg 180
 ttcagcaggc aaaactgaaa taaaagtaat aaacaccgaa agcccccga ttc 233

<210> 809

<211> 525

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(525)

<223> Area matching *Drosophila* Genomic sequence

AC005269.

<400> 809

```

ccccagccgc gtgcacagcg cacaccaacc gacacactca cagacacacc ccaaagccgt 60
gtctgagtag ctgacgtagt tgttgacccg gaagtctgtg aacnnngaaa tacttttaaaa 120
ctggctcgaa acctggcaga cgcacctcaa gctgaaatct aagacctggc cgcatatatt 180
tgcattaact ttggaagtct gactttaagc agacacggat ttcattaata aacgaaaggc 240
atagtgcgaa agcaggagag tatgggagct caacagttga cggggagcat tgccaggccc 300
aagaaactgg gagataacaa agatgagtca cgaaaagcag gcatttcaaa atcctcttaa 360
tcaccaccag tgaatgcatg taactcaatt aaagtcgtca attgattaca tttatttttg 420
gttgaaaacc cttctaggac acgggtaaat tctacctggc aatgcttcgc gtttcgcctg 480
taacaggttt caaagcaaaa aggggcttcg acacagagca cacac 525

```

<210> 810

<211> 531

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(531)

<223> Area matching *Drosophila* Genomic sequence

AC005554. Matches in area of ORF with sequence
similarity to Rat fatty acid synthase gene.

<400> 810

```

gtcggggatc atcatgtctc gatttttctc ttcagttgtg gagcgagagc ttacgcaatg 60
gagcggagtg atgagcacat tatccgaggc aattttttan nngccgaaat gccgccgggc 120
cgttagaaat gaatatgaaa ccatctactt taaatatgat tgtaatgtaa aaacttgcac 180
caacactaaa aggatctatg gactccccga gcgtatggcc aaaatgaagg actccgatct 240
ggagaagtgc gacgacaagt tcttttagcgt ccaccagaag caggcggagc tgatggaccc 300
ctgcatgcgg atgctgctgg agctgaccca cgaggcgatc atcgatgcgg gcatcaatcc 360
cgtacagctg cgcggcagtc ggacggggccg tctacatagg cctgtccttt gtggagacgg 420
acaccgagat cccaacatg gagccgaacc agtatcaacg gctactggct gacgggctgt 480
gcgcgtgcca tgttcgccaa tcgcatctct acacgttcga ctttcagggg c 531

```

<210> 811

<211> 443

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(443))

<223> Area matching *Drosophila* Genomic sequence

AC004758.

<400> 811

```
ggctcgcccg aagagagccg agtgaaaccg agcgcgccacc cgaatgccga aaatcaagta 60
tacgtcgcta cgatcggttc tcaccgcctt tcagtgtctt nnncaataac aaaaataata 120
gcactgctaa acggaaaaca gaaacgttcc tcttctaacy gtctcactga gttttgtaaa 180
ttggtcattg gctgtgcgaa aaggagagac agagagagaa ccagagaact gtcgcagcga 240
ttgcgattac ggttacgcgg cgcagtgaaa aagtgaaaaa gtttaggcgg aaaacacttg 300
cctctggctg atttgcgtgt ttggacgcgc gactccctca gaacttgaaa aataaaggaa 360
aaatcgga ttaagcaaaa aagtgatcac acatcaagaa gccaaacttg attacgattt 420
gcggtcgaga aggacttata aac 443
```

<210> 812

<211> 498

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(498))

<223> Area matching *Drosophila* Genomic sequence

AC005894. Matches in area of ORF with sequence

similarity to metalloprotease genes.

<400> 812

```
gtccagcctt tcgaagggag tgcgtgggtg ggtgtgtgtc ttttttatta aatgtttgcc 60
gtggtggggc tggccatcac tcgagccgct agctggcaca tcctttttat taaaattcgc 120
agtctataaa ttgctaagga gcccatgtgg gatggggcggg cgtgggattc caatggccat 180
```

gggactgcga tgagcggagg aaatggggta tgactggcgt acatgtttca aaagacgtgt 240
 gtgtacccaa gacttttatg agacagcaac aggaaatgca tggaaatggt ctgggctggg 300
 ccgcccgcg agaaagggga acgtgtgttt ctccaaatgg agcaggtcaa aaaacgaatg 360
 tgggaagtcc gaagaatgat tcagaaactg aaaatatacg aataattatt acaaaatctg 420
 ccttgcataa aattacttat aactttgcac tagttgcatt aaaaaatgaa agatagtcga 480
 ccgaagtttt taagcctc 498

<210> 813

<211> 320

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(320)

<223> Area matching *Drosophila* Genomic sequence

AC004564. Matches in area of ORF with sequence
 similarity to Immunophilin genes.

<400> 813

ttgtaaatga agcgaaaagt caaagaagaa gcagaaacca gcataaaaaa tgtttgtgcg 60
 ctggcggcctt gtaaaagtat gtgtgagtgc gtgcgtgtgt gtgtaggcag cagacaactt 120
 tgaagaagaa gagacagaat acaaaaacgt acggagttcg aaaactccgc cagagaagtt 180
 tgtctacact gtgcaacaaa ttaggtggga atgggatgtt atcttatcag gttgggtgta 240
 ttggttataa ttggcggcca aattgggtta ccaaaaaatg tgtttaacaa tcaggttaca 300
 tctgaaaatt ataataaatt 320

<210> 814

<211> 429

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(429)

<223> Area matching Drosophila Genomic sequence

AC005716. Matches in area of ORF with sequence
similarity to follistatin genes.

<400> 814

```
ctccagactg tctgtttggc agtgcgagtg tattggtgta cctcctctgg tgtgtgagtg 60
tgtgtgtgtg tggaccctga gtttggcaat gcagttgccg aggnnntgcc ttgttgttgc 120
tgcggcgctc cttgcatttt ttcgcgctgc tgctcctgta ctcttgctgc cccctttgt 180
tatttgtgct gtgccccaaa gacatttcag cgagcctcga ggaatccaaa gcatttggat 240
acgaaaactt tgggtacagt aaaggctgct gggttcccg caaacagtgg aatgttatgc 300
cttagccgga tcattcgca tcggtgctga aatctgcggc tcattatcta agtatggcca 360
gggtgaatta acactttcac cgcactgaca gaaaaacatt ggccttttta aggggaacca 420
aataataat
```

429

<210> 815

<211> 71

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> Complement((1)..(71))

<223> Area matching Drosophila Genomic sequence

AC007180. Matches in area of 217AA predicted
protein.

<400> 815

```
ttccaacggc tcgagacagt ccgagcggca cttgcaacat gttgcaagtt cgtgtgtgac 60
ttcgggaatt c
```

71

<210> 816

<211> 75

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(75)

<223> Area matching Drosophila genomic sequence

AC004758(92123-92197). In intron of gene at
87648-113518 coding for 945AA protein similar to
Human retinoblastoma binding protein 2.

<400> 816

aaactataca cacacacaca tacgcacgca ccgccagtca gtcaggcagg cacacattgc 60
ccacccactt ttact 75

<210> 817

<211> 116

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> Complement((1)..(116))

<223> Area matching Drosophila Genomic sequence

AC001661. Matches in intron of Drosophila wing
blister gene.

<400> 817

atctgggtctg aagtgcagcg cttgcgatca gttcgtgttt gacggtcggt tgcgtaggaa 60
gcaagacacg cgacgggtct cgagtgtctg gctttgcctg tgcgatggct gaattc 116

<210> 818

<211> 512

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> Complement((1)..(512))

<223> Area matching Drosophila Genomic sequence

AC004758. Matches in area of ORF with sequence
similarity to Human Retinoblastoma binding
protein.

<400> 818

cacagtttct tatcggcgga ggtcgacgaa tcggatctcg tcttatcgcc gaccccccg 60
ttattgtttc gtttctgtat tagattcaaa atcagttcgg tgataggcgt tactcagtct 120
agccggcgcc gcgtttaaca ctatgccggt tcaggacag gacttgaaac atccatagga 180
tccatcgagc atatacgcaa ggttttctaa gtacgctttt ttaattaatt ttatgaaatg 240
tggttcaatg cagtgcgaga tgggtttttc aagacttcgg taagctaaaa aaggaaagt 300
tggcattcta aaagagtggc ctagaattat attctaagtt attaataataa ggtaagtga 360
ctcttttatt gtttttagaa tactgggtgtg tgaaattaaa ccttggtttt aagaatttga 420
atttgataaa tatattttaa ataactagta gacataagta tttagttaac ggtaatgcct 480
atgaaatggt gctgctcact caacaaccac ag 512

<210> 819

<211> 54

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(54)

<223> Area matching Drosophila Genomic sequence

AC004334. Matches in area of 433AA predicted
protein.

<400> 819

gtctgatgca gctgatctga tttattacca gtttactgga tcactcgtga attc 54

<210> 820

<211> 557

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> Complement((1)..(557))

<223> Area matching Drosophila Genomic sequence

AC005149. Matches in area of 424AA predicted
protein.

<400> 820

```
cacgaaccca agaaacaggg cccgaatgga aaaagagaga atcgagagaa tcgcgggctg 60
agaaatgcgt agaaagagac aagcgacgag tagcgagcag tggcactaaa accagcttag 120
tgcactgtgg aaaaagtttt aacaattctt aaatatctga agagtaaggc tctaattttc 180
tgtaaataac aacagtataa agctatgtgt ttaaataatac tagataaata atggatgcat 240
ttacatatct atctgaattg gctagttact tatattcggg ttgaaaatag tacaaaattt 300
ctttcagtgaggagaggaa ttaaaccgaa ctcaacccaa acccaaccgg ccgccagtcg 360
cacgctgcta aatggacgga tgggcccgtg gacggactta tatggagact ggcactggcg 420
gaagcgtggg aacgtgcatt cgtacgacga gttattggca gttagagcgc tacctgttta 480
ccgacccgac taccgacta ccaccgactg cttttttttt ttggcccatc gaaaaggtag 540
ggtacaattg gcccggg                                     557
```

<210> 821

<211> 202

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(202)

<223> Area matching Drosophila Genomic sequence

AC005333.

<400> 821

```
tggcaggcct ttgcatttcc acttgtgcgt cacgtgctcc tggctgttgt tgttgcattg 60
aacttgaact agtggcaaag ttgttgctgt cgttgtgggt gctattgcac ttttgctgtt 120
```

cttccgacat tggcgccctat tttgccggct gtttttggct ggcattcggc gcgttttctc 180
accgcgcacg cgctctgaat tc 202

<210> 822

<211> 534

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(534))

<223> Area matching *Drosophila* Genomic sequence

AC005334. Matches in area of 309AA predicted
protein.

<400> 822

ctttgtgcgc tgaagcagca acaacagctg gctatctcgc tctagcaacc acgtcagacg 60
gcaaacgtca attataagca aacaaagcga cgttgcctca tttcacgaaa gccgcagcga 120
ggcagagcga gagcaagcga aatggcgctt cgcggaacg ttgccaaact tcagcgtcga 180
ctgcgtgttg ttctttagt ttccatgctt ctttagtgca tggaatttta acatgctgta 240
ccaccaaccc tctttacggg ggatggggga ttataataac gcgctgctga cgtcgctgct 300
cgcattttcc accttctcgc attcgtattg ttgcaaagga aatggggcct atacaagaag 360
tttatctttg aatatacata catacatatg tatatttaag tacatgccgt attccgtgct 420
taaattgagg cacaggagga gaacatatct tgggggccat tgaaattcaa taaattaaat 480
gctctagtga ataaataaaa gcgtatttta agtgggaaat aagcaatgcc atta 534

<210> 823

<211> 438

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(438)

<223> Area matching *Drosophila* Genomic sequence

AC006421.

<400> 823

cttgtccttc tcagaacaac agttataagc tcagtctgcg ccggcagcgc tgtcgacgtc 60
gactgcagca gcagcgccgc tcatttgtgc gcttaatgac gtcattatTT ttattttaaC 120
agtgccaaagc aaattgcata tataccgttg ctgctcctgc gcagtcggcg ctctgccggc 180
gtcgctgcac cgccagtggg gcttgggcta ggggggtggg gagagagcga cagagagaga 240
gccagagcga gagagaacga gaggcagtga gtgagagaga ccccggtcgc tttctcgctc 300
gcacccgctg agctgggcct gcggettcgg gttcctcgcc ttcgttctgg ttgcttcgtg 360
tttgccgatg tgatgctgct gatgttgctg ctgctccttt tgctgtgcta cttatgctga 420
tgattgcgat gctggggg 438

<210> 824

<211> 524

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(524))

<223> Area matching *Drosophila* Genomic sequence

AC005443.

<400> 824

ggcacggcat cctttggcgc gagagaatgc gacatccgga gagccggaga gcacgaccat 60
tgagggctct gttcgggaga gctgacgcct ctgtgtctaa ctaaaccgaa gaggtcaag 120
gcgtcgcatg atacttcac agtcattca atttcaagac tagaaggta aatagatctt 180
tatttatatt atgattcaat taaattatta attttatatt tcaaatttt aaaaaaagc 240
cttatggta tgccttaaa atatattatt tttaatttaa gttataagat agaaaatctt 300
atatggagtt cttaaattatt attcataaaa cgtaagtggg aacatgtgaa ttagttaaac 360
aataagtggg actctctgtt aaataaatac attttgcct gaattggatt acaaaatcac 420
tcgttcttca aaacacctca aaatcaattg aggtctccat ccttttcggt atgccgctg 480
aatcgatttt cggcaattcg cgccaaatac ccgaccgac aatg 524

<210> 825

<211> 492

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(492)

<223> Area matching *Drosophila* Genomic sequence. Matches
in area of ORF with sequence similarity uridine
phosphorylase.

<400> 825

```
gtgcagttcg cgtaccagca cacacaacac acacacacat gcatgcgtac atacgcgcgc 60
gctaagtga tacatacata cgtatgtatg gacgtacagc gtgctgcgag gtacagtcgc 120
cgctaattggt gaaaactggc tgtgcgaaaa agcaggcaga gagcaagagg aagagagagc 180
ggccccgggg tgggggtggca acttcaactt tgccggctgc acttggcaac aagtctgcaa 240
gcgactgcga ctccaattga gggtaagggt cagcgctcgc gcatcagctg ctgcgcatgt 300
gtgacgacca cgacggcggc cgtgacgcga cggtggcttc gcgaaagctg cgctccgagt 360
ttctggagcc cgcattgcga tgggcaagaa cagagaaccg gttgcaagcc cggtttggtc 420
actttttgcg cttctcatat ttaagtgcgg tgcgatcgcg ggtcgtccaa tatcgccgat 480
ttagttaggc ta 492
```

<210> 826

<211> 535

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(535)

<223> Area matching *Drosophila* Genomic sequence
AC005889.

<400> 826

```
gtccagtcta caaacagaaa gaatttcaac gcgacgcgtc gacaataaag taaacaaact 60
```

gaaattgttt tccttcgtca tattttcctt tctcttgtct cgtctgcgac ttgttgaaac 120
 tatttcaagc gcagaaatca acttaagccc cagctaccca gctcatcaat aacaacatcg 180
 caacatctct ggcgctcaat taacatgggt ttgtgaaaat ttattgaatc ccttctttaa 240
 tgaagtgcc a tgtcccgaag gctgttgctt cccttcacgc caaacgtgct catcgattgg 300
 aaacgggtcta tggccgttta gtttgggtgc tgataaacct agattcagaa tcttttagata 360
 tatatcttta gatttatact ttcttgtgta attgaatttt cttaaattctt attctactgc 420
 ccaagtaatg aaaattccca acaaataacg aaggcaagga tatcatcgct ttcttggttt 480
 aatcaatcaa acggcaaacg gactggaaag aagtgatatc agaaatctgt aagtt 535

<210> 827

<211> 47

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(47))

<223> Area matching *Drosophila* Genomic sequence

AC005130. Matches in area of 826AA predicted
 protein. Sequence similarity to Helix-loop-helix
 genes. *Drosophila* ESTs AA949050 and AA817663 come
 from this gene

<400> 827

gcttagccat attacttggt tgtatttgca aaagttgtaa tagattc

47

<210> 828

<211> 551

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(551)

<223> Area matching *Drosophila* Genomic sequence

AC005554. Matches in area of ORF with sequence
similarity to Rat fatty acid synthase.

<400> 828

```
atacgcccgt tcaattgctg taaaaggata gttctcacca tcgcattgcg agttttattca 60
ccggttagatc aaccgatctg gagagactat gaaaataata cttcaatgaa cttgagaaat 120
cacgccacct tatctcacta aacaaatggg acacgcgtcg agctcgtgtg tctgtgtgtg 180
tgtgtgtgtg tatgtacaca cacatggcgg tggggacttt tggggctgcg tcttgactat 240
acgccgctct ctttggcacc cacctccgat ttggatgccg actacaatag caaaacataa 300
acatagaagt ctggccaagc caacggccat ttgatagata agcttgctgc tgagtcgccc 360
gatttttacc ggcaatttgt agtggctaca cgcggaaaaa taggggtatt atatgaaaat 420
ggttcctgta aatatggttc catatttata tgatcaataa catttgaatt tcaaagaact 480
ctacggctac acgattcgaa ttcgtttgtc tgagtggact ggttatttgc tctgtgtgtg 540
accgtcatgt c 551
```

<210> 829

<211> 499

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(100)

<223> Area matching *Drosophila Drongo* gene.

<220>

<221> intron

<222> (101)..(146)

<223> Intron in *Drosophila Drongo* gene.

<220>

<221> misc_feature

<222> (146)..(499)

<223> Area matching *Drosophila Drongo* gene.

<400> 829

gtcgcgctat tttgtttcga gtgcgctgtg ctgtttgggt tcgttccgtt tcgtttcgtt 60
gttcgttttc cattcgtctt cgaatccgca ctgcaaaca acaagaagag ggggaagcag 120
caaaagtggc gagtgcattc gcagcgtcga aatttcaatt gaaatctgaa atctgtgtgg 180
caattgcagc ggcaactcgg gttaaatagat tgaattgaag cgaaattctg cgagtcgaag 240
aagtgaaaag taaacaataa cacgggcaat cggaaaagtg gttttcgata aatcgaccg 300
cacacacaca cctgtcagtg tgagtgtcaa agtgagtggt tggagtggtc gtcgaaggag 360
aggaaagggtc aagccaaaat ttgcgtaaag aaaaggaaag gaaagcttag aagaggggaa 420
aggggaatta cgtcagttcg cattccgata aaaattttga ttccttaaac cgatcctgat 480
agccagcatt acgatggca 499

<210> 830

<211> 580

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1) .. (580)

<223> Area matching *Drosophila* Genomic sequence

AC005554. Matches in area of ORF with sequence
similarity to Rat fatty acid synthase.

<400> 830

gcttaaaccg actccgccag ctccgctcat tatatagttt cccttctttt gttgaatcat 60
tcgatttcgc acatcgtacg agtttctcgg cgaataagaa agcagcttgc cgttcgcgtt 120
ggctcagtggt gagtgtgtgc ggcttatggt aacgcgaatg gtgttgcaact gttaacgcga 180
ctgccacaag ttgctgttaa ctgtcaaccc agtcgctggc ttcaaagcag caagccgccc 240
ataacaaata atgctgtgtg ccggtatatg cgcagtcaaa gctccgactg cgcgccatca 300
cctgatttgc aatttctaca ccaactttcc accagctgaa cattcaaaca aaaaacctaa 360
tcgcccggca tcccgcgcca gagagcgaaa gctctgcgct tcggggtggt aaagagcttt 420
tgcttaacag cgaaggggtg gcagacaagt tgcagatgcg gcagaatgat cacaatttta 480
aaatatttaa tacacgaaat gagttatact aaccagactt tcgcatcctc ttctccaatt 540
gcagccccta cactaaacct gtgcaagccg tggaccaccg 580

<210> 831

<211> 256

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(256))

<223> Area matching *Drosophila* Genomic sequence

AC004722. matches area of 834AA predicted
protein. Sequence similarity to bromodomain
containing proteins

<400> 831

gatgagatgc caccgagcgc gcgattggtg gaggtcacca tgttttgcgt cggcttctgc 60
agggcggtcg acttcctgag actcgcttg ttggcggcac tgaatagggt gcgcgtcgag 120
ttgaggctct gcagcgaggt gtccagcttg ttgcgaatcc tgtccagatc ggcacgcat 180
cgctggatat ccacgctat ggtgtgtcga tcgctttgca gcttcttggt ctgctgcaac 240
atggtctcca gcaatt 256

<210> 832

<211> 406

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(406)

<223> Area matching *Drosophila* Genomic sequence

AC003054. Matches in area of 822AA predicted
protein.

<400> 832

atctggattg aggtcttgcc acagttagcc gagcaaagcg cagctatacc aattctccat 60
ggcgcgtctcg gccacagtgg gtcaattctc catgctccac tctgggcaat caatttctcg 120

atattgttgt gcagtgcacg tagattgagt cactcctcct cgcattcggc attcccattt 180
gtatatatat aactcatat tcgtaattat tgtaatgagc catttctcta gttactttcc 240
tcgttggtcg catgggctgg gtttttaatt aattttccat tgaccagcc tgacagctga 300
gcctcagctt tttcctcttt tatttctgag ctgagctcag aggctctgcc agcccaagag 360
catttcatat taattctcat ttttcgggc tccaattcgg ggcttc 406

<210> 833

<211> 460

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1) .. (460)

<223> Area matching *Drosophila* Genomic sequence

AC004280.

<400> 833

gcccattcgg agcgcattgt gattgatgag cggagagagc gagcgagagc gcggtacatt 60
agcattaacg gcgcatgtgg cgcgaaaatg cggatggaat caccttgtgg ttgttgttgt 120
tgccgcgtgc accaccctta aagaacttgt tttgcactga cagaaatttt gagccgcccg 180
tggttggaat aatgcaattg caacagtgac cgtggataat tgggaactcg aactgcgggc 240
cggggtgcgc aggtaaaagg cgcaggtgca ccggagcgca gatacaggta aaaagtgaag 300
cggttatcct gaggaagaaa caagtaatca tgcttggccg tggatcgtct atttgaagtg 360
taaatatgta ttgtaatgca atatggtatg tattgaagtg tggttggtatg aaggaaagca 420
ggccggaata ctgattactg ctaccgtatg taggcagatt 460

<210> 834

<211> 99

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1) .. (99)

<223> Area matching Drosophila Genomic sequence
AC004722. Matches in area of 289AA predicted
protein.

<400> 834

ctttgaatga aaacaccgaa tagcatataa aatgcatttg ctccttagta aaaaagttaa 60
gaaggtttgc cgctgttttc gtattcgaat tacgaattc 99

<210> 835

<211> 178

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> Complement((1)..(178))

<223> Area matching Drosophila Genomic sequence
AC001661. matches in area of ORF with sequence
similarity to Mouse Surfeit gene.

<400> 835

gtccttactt gcaattcatt ttcgaaagaa tcaagttggt tgcttttatt gaaagtctgc 60
agtctgaaat taattgaagt gaagaatata aaggccttgc ttactcttga ccaatctcag 120
gtaagtataa accattatag acggactaag aaaaggcaaa gaatctgtag gtgaattc 178

<210> 836

<211> 602

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> Complement((1)..(602))

<223> Area matching Drosophila Genomic sequence
AC005269.

<400> 836

gcctagccaa aagctaggca aacaggccaa gcccacccc ataaaacccat gtcacatttc 60
tggtctggtt tttatctggc caagaaagaa acaaacacac actgtgcac attagagcgc 120
aacgtgccga gcccataaaa agatttcgac gtcttcgac gagtcataat acacccctcg 180
cattgcctt ccccatgaaa tcacccacct gaggcacgac ataataatat tgggtggtgtg 240
gctgcatttt ccttgcacgc ttttaggcgc aattttttaa tggttctaga atatgcgccg 300
aaaacgcaac agttgctcat gttttcatcc ttaaaaatta agtagtgaaa tttgaaaagt 360
ccatattaaa aacagttttt aaaattttta gacatttttt gtttctgtca ggagcacatc 420
aatttaaaga cttttatggt ggtcatcaat acagtattca cttttaacat ttacattacg 480
tctataattt aaagcacagc tggcagcaca gttaatgagt aatattctgg caccacaaac 540
ggcttaaaaa agttcaaac cgcaaaacaa ggtccttggc tttcaaggac atgacctggg 600
tg 602

<210> 837

<211> 562

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(562)

<223> Area matching *Drosophila* Genomic sequence

AC004362.

<400> 837

cgacggacct ttcgaaaact tgacgaacac gaagcagagg ttcaaagcaa aatggagtaa 60
acgagtgaag aacaaaataa tgaattatgt caaaagtggc gcaaatatct ttggtacacg 120
aagaaaaaga ttggtagtgg catttagccc ttaccacaaa tctacgtaca tacatatgta 180
tgtatgttta catatgtaga attattaata gtattttaat tattgtaaaa tcgtggttat 240
atattttttt gtgagtagtt actctatgta cgtgctccca accaatgagt gagcgagata 300
gactgctaag tggagaatgg gagttcattg atatttctcg ggcgttttgc tttcgcttcc 360
ccttcgtctc caccttgctt cgcgccatct tcgttcttct ctcttctcct ctgcttccat 420
ttacctgcca cattcatttt gtggtggttc ttcgcaattt tgctttcttc ttaatttttg 480
cattcttttg gacgtttttt agtttgcggg tcgcttttgc gccgttaact ttggaccgac 540

tgcggggtgt ctggtgtgga tg

562

<210> 838

<211> 521

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(521)

<223> Area matching *Drosophila* Genomic sequence

AC004370. Matches area of 1277AA predicted
protein. Sequence similarity to human nuclear
transport receptor.

<400> 838

gggccgtcta ttttaagcact gcctctcgag gagagagtaa ctttctttta acgctctcgc 60
tgctctcttt ttcgctctcc ccgaaatcgt tacgacgctc actcgctctc tctctccac 120
gccattggcc catacaatac actcaaaaaa tcgccgcggc atttgtacag ccgcagtcga 180
taagacaaca acaacagccc agagcagagc gatcgttgga tttttggtat attattttgc 240
ggtgattttc tgataatata gtatctatat agtaaggctt tagggaggtg ccatatatca 300
ggcggcgcta cggcaggcaa aaggatttac tcgtaggccc cacttgatgt atggaataat 360
cccgttttcc tttttggttt gctaaccacc ggatatgtgc ttcccgtcgg acgggttcgt 420
acaagacttg actttgcccg gtccgttcga tggcttagaa attgccgctt gcttcttctt 480
gcgccaaaat cgggtgcata cattttcgct atacttgata c 521

<210> 839

<211> 619

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(619)

<223> Area matching *Drosophila* Genomic sequence L49408.

<400> 839

gttgtgggtg tgcgcgagcg tgtgagctat agctctcatt ctataaaccg tatctctagt 60
gcaaattgtgt gtgtgtaatt cgagtaaagc cggtagaagt cgcagctggt tttgcctatt 120
tttacgctca cacatat tttt gcaacaaaga aaaacaacaa ttctctagcg gcgattttat 180
ggctcgtgca attcgtctca ggttcggtta tgatcaaaaa tatttggatg ctaatttttag 240
caggctgccg ttactaataa atacgaaatc gtgtttaata gttcatcata gcgatcctta 300
aaatatattc aggaaataaa cggaaacaac aagtgaatat atgcataaat agttgttgat 360
ttcatagctt agcataatgt ttttcaaatt tcattttatgt caagtatttg aactgaaatt 420
tttttcggtg caccogaaca cacgatttct gctatcttct actttggcgt ggccatagag 480
ctcagccaaa aatttgcaca aaaattaatg tcagctgact tgctttgggt cacttctcat 540
tttcgtggcg cttcacacac acctggcatc atctgcaggt gaagagtcga aagataagcc 600
agaacgctac gttaatggt 619

<210> 840

<211> 535

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(535))

<223> Area matching *Drosophila* Genomic sequence

AC005447. Matches in area of 802AA predicted
protein.

<400> 840

ttccgtgcga ttgccgagcg gtaagcggcg agcgtctaaa cgctcactca ctcacacact 60
caagttcata ttttgtatgg tacagtgggc ctggttgcca gatttcgtcg aggggcgcag 120
tttggttttg caatttacca atttacaggc gttttgccgc ccaaactgcc caaactgccg 180
aactaagctg ggagcgtgac caaatcaatc gactgttcag acacagcatc ttgagtggtc 240
ttgtaagtaa gacatttacg ccaattttcc aatcaccaaa cctgttggtg agcaacagcc 300
gccaaagggtg cgtatgatta atgcctatcg ctgtctgtca tctgagctga ggctgggaca 360
atgggcagcg cagcactcga aaaagtacct ggcaggcgct gtatcataat gctctcgtg 420
tcacggcac ttcaatagct aaaaaaacct tatcaaagct ttaaggcctt atcaccgaca 480

aactgactct ttggcgcttc ttatcaacca ccattggccg cgatttcagt gagtt

535

<210> 841

<211> 342

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(342)

<223> Area matching Drosophila Genomic sequence

AC004120.

<400> 841

ccaccaacca agccacctac ccgccatctc gacgatgaac tgtcgcgctg tttgctgcca 60
tttctgtccg ggcttggtat tgtttaactg gcaatgatta atggcaatga ggcagggcag 120
agcagagcaa aagcggagca agaaggtggg caccgagttt tgaactacac aaaacggaac 180
atcatcacat cgctggcatt tctttttgcc agtgaccag aaacatttct tcgccagctg 240
ccattcaaca cttgaggggtg attagaattt gcgccatcac tgaagcgggg gccgataaaa 300
gcggagcatt ttattgattt gtctgactca ttggatgtgc cg 342

<210> 842

<211> 512

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(512)

<223> Area matching Drosophila Genomic sequence

AC005454. Matches in area of ORF with sequence
similarity to mitochondrial translocase.

<400> 842

gtacacggtc gacaacaaca aatgcagtat agcgaacgaa tgtgacgatt ctattatgat 60

cgtttatggt cggttataag gcgtggaaaa gtgtcatcca ttcccagaca tctagacagc 120
 caaacttaag atcatatggc tgcgttctag acattctgaa gaaagccaaa aacaaaagca 180
 tgtattcagc aaaagtcgac aagacatgag taactccaat cgaaatattt gggctataaa 240
 cccaaaaact ggggtgtattc acttgtgtac tattacctca tgtcttttta ttctttttca 300
 gatactctac gcgttaatac accttctgta cacattgctt aagttggaaa atgtatgttt 360
 atggagccta atataataat tccattgttg ttgttaaata acgattacat atttaattat 420
 gtgcagcaag ataaataaat tattcatcac accattgtca ccgtcacaat atcttaaggt 480
 tttggttaatt catataaatg gtaataccat ca 512

<210> 843

<211> 515

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(515))

<223> Area matching *Drosophila* Genomic sequence

AC005130.

<400> 843

ggctgcggga aaccaggaag agatatgatg gtggcggggg cgtaggggaa tggaaaagca 60
 gtgtagaagc aaacgtcgag cgacgtcacg caaaagttgt ttgcgttggc gaatagagcg 120
 caaaagtagg caacgttata tgttcattgc ggtgactgtg tgtgcggtaa agtgggtcgg 180
 tgggtggaat gtttacacac atgacctgc catgggagta tgcgtgggtg tgagtatgtg 240
 aggcattgct atgagttctg tatgttggtt ttcttgaaca aactttaatt gtttttgatt 300
 ttcctaagga ttcaagtgc gcgagtttta ttacttggtt gtttactcat ctgaaggatg 360
 atgcatagag gtgcggggac agtttgcctt ttagaagcct tttcaaacgc ccagttggta 420
 aaaaaatgag aaagcggaaa ggggcataac agaaatgggt ctctcttggc taattagatg 480
 agcgttggtg tgcttcctg aaaaaagggg aattc 515

<210> 844

<211> 499

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(499)

<223> Area matching Drosophila Genomic sequence

AC005439.

<400> 844

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gcttggcggc aaaagaatga agcacgacgg ccgcagagag aacaaggcag cgaagagaga 60
gcccgcgctc tcttaggcgc tctctttcgg ccacaaggca ctcggctggt gcattgaccc 120
cacagctcgc tgaccactt acgaagctgc tttttgccac tgcgaatgcg agttgcgaat 180
tgcgaactgc cgacgctgcg agctcgtgcc tccgtcgacg ccgctgccgt catcgttgtc 240
ggtgtttctg tttcgacgaa cgagcaactt gtgcaatagt cgcagcagca acagcaacaa 300
gagcagcaac aacaacggct gcagcggcaa cagcaagcaa ttcgcagtcg cagcagaggc 360
gactgcgctg ccacatgggc aactcaaaat tggactgtgc ttcactcttt gctagcacag 420
tggttgaaag taaggcgttt aataatgata aataatatat atgcattatt gaatgaaatg 480
gaagaataga ctgcagggg                                     499
```

<210> 845

<211> 565

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(565)

<223> Area matching Drosophila Genomic sequence

AC005127.

<400> 845

```
ggtaccacgt ttgtgttggt gtgaccgacg gggggatgcg agaaaatacc accaattaat 60
acaaataggg ttaaaatacc aattagcgtg tacacaatcc acaattagcg tggacacgca 120
ccgaaactat ctttttagcca gtacaacctc caaagttatg acgattggta acgccgtttt 180
cgacttcgaa tatttgtagt tgccaacctt cttgaagatt gtatgcgtgc gtgaatttaa 240
atTTTTTTTaa atcgtgataa tgcgtcgagc aacaatctaa gctaaaatta gatggcaccg 300
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gcgttttattg atgcgaaaca tatgcaatgc caacaatctt aatatgattc tatgcttttag 360
ctcttttgaaac ctttaaagtgt tggccaagca cccaaagtgt tgaactatag catgtgtttt 420
atTTaaaatc tatttTgtgat agagcttaaa acctaaacag tggggTgtgg gattaaggta 480
tctacaactg cgtgattgga agagaccag ttgctttgtg acggtcacaa cccgatgctg 540
tgtcaagctt tacgctttat gataa 565

<210> 846

<211> 586

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(568)

<223> Area matching *Drosophila* Genomic sequence

AC005889. Matches in area of predicted gene coding
for 1365AA protein. ESTs AI106939 and AI296430
come from this gene.

<400> 846

ctttgcaccg atgacgtatc ggctatttgc aatttcacat agttgcgatt gcgtttcggt 60
ctatattgtt ctaaattgtt gtcgctgccc ccactcacac atacgccctc acaaaacagg 120
tgcagaatgt gataacacac acacacacac acactctccc gccgagcaag ccggtaaaca 180
aaactggaaa gagagagtgc cagagagcaa agcttccttt ttttggcaaa gagegcgaag 240
aagcttcgtg ttgccattgg tggtcgacgc cgggtgggtg ttggtgggtg tgctggttag 300
cgttttttta cacaattgca ttcaaaaaat gtgtgcttag tatttcggca actttgtgac 360
tgagcgaacg ttctgtgttc tctgcttttc attatttcgg agatttttcg agagtaactt 420
gcgattttctg gcccgattg agtcacacat ttagagccta gaccgtgata agacccgaaa 480
aaaatattaa acataaaacg caagtaagag gagccacgag aaaccaaaca aaagtgaaag 540
ccattgacat ttgtcctgcc aagtttgaag tgatgacctt gaattc 586

<210> 847

<211> 503

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(503))

<223> Area matching Drosophila Genomic sequence

AC005558. Matches in area of 1277AA predicted protein. Sequence similarity to human nuclear transport receptor.

<400> 847

```
tctcagactg aaactcgaaa taaaaatgta cagtttaacg ggagcggttct ctgctctct 60
ctctctctct ctctctccca ggagaaagat agatacaaat agagagcgct gctaactctc 120
tccctcgtaa tttgtataca caccgttttg tctgtttgcg tatgtgctta catttatctt 180
tcactttttt tctgctctgc cttatgcgta tttatttttag tacataaaac aagacggcta 240
aacaggggtgt cgcaaaagtt agttggggtt cttcgggatt caattgaata atgatcatta 300
tcccatgatc atgaattagt tgagatacgt ttggcacgga taattcttaa gtggtacagt 360
aacgaattgt atagatttca agaaatagtt ttgaaaataa ttcgttgctt tccatatctt 420
tcgattccaa ccaccagatt actttgtcct ataaaatgta tcttcaccct tagaaacaca 480
acctaaacct ttactaatca gaa 503
```

<210> 848

<211> 620

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(620)

<223> Area matching Drosophila Genomic sequence

AC004351. Matches in area of ORF with sequence similarity to LUN/Forkhead genes.

<400> 848

```
tgtctcttgc cgaccctacg tgggctggaa gaactcgggtg cgccacaatc tcagcctgaa 60
cgagtgtctc aagaagctgc caaagggcat gggcgtgggc aagccgggca agggcaacta 120
```

ctggaccatt gacgagaact cggctcatct cttcgaggac gagggcagcc tgaggcgccg 180
 gccgcgtggc tategctcca agatcaaggt gaagccgtat gccggccatg ccaatggata 240
 ctacgccagc ggctatggcg atgcgggaat ggtaagctcc atcgatttca taacaactta 300
 agatcatata atatctatag tactttctctc tttgccacc aggacaatgg caactattac 360
 gcctcgctg cctttgctag ctacgattac agtgcagctg gagccacttg gcgtctcgcc 420
 ggctgggtgg tcaaggattc gcccgatccc tggaacgccc atgccggcca cagtggctcg 480
 tcgtccggtg gggccgtggg catggggccg tgggtcccct ggcccagtat acgaacatat 540
 ctggctggca gccggaggca atggtgaatg gctcggctac acgccccgc tggcccactt 600
 cgcactggga atgggcccac 620

<210> 849

<211> 519

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(519))

<223> Area matching *Drosophila* Genomic sequence

AC004766. Matches in area of ORF with sequence
similarity to Lipase 3 genes.

<400> 849

gcgtggatgt acctgctcga gtaaataaca tcgatgaaaa catcgataat atcggtttgg 60
 gtattgtcgt gacacacgca cagtggtgca ccacacatcg gttcggttaa atataaacia 120
 atataaatca aatTTTTtga tttaaaaaaa agtggttaacg taaactggtc aatTTTtatat 180
 tctgctaata agaacaagaa taaaatTTTT ttacaattaa ggaatatcat aacaagaatt 240
 gatttaacgt ataaataaat gccatgaata tattttccca cctaaatata cattacagat 300
 atTTTTtact atgatcagta tgttgcggac tatcgactac cacaaaaaac gctggaaagt 360
 ctatcgatga ttttacaaga tgcttcatcc ctggaaagtt ggcgcgcaat tcaaactaag 420
 agtgcaaaat atttctcaac agtcacaatc agcaaataaa ataaaaatat ctagtcgctt 480
 atattttatt atattacact taatataatc cattgattt 519

<210> 850

<211> 80

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> Complement((1)..(80))

<223> Area matching Drosophila Genomic sequence

AC006247. Matches in area of ORF with sequence
similarity to mammalian Valyl tRNA genes

<400> 850

gactggagtc gcagaaaaac atatgaaaac gtgtgcagtt tgggaccagg gttgccaaca 60
gatattatta ttttgaattc 80

<210> 851

<211> 370

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> Complement((1)..(370))

<223> Area matching Drosophila Genomic sequence

AC005129. Matches in area of 1208AA predicted
protein.

<400> 851

ggtaaagtgt tgagctgtcg ctgcggctct cggcaattta tactcgcagc tcggtacttc 60
ggctccgaac atccacttcg gcttcggcac gggcttcggc ttcgtccgct ctccaaattc 120
ttattttttt ttttattatt actgtgagtc gagtgaagct cgctcttttg tgctctttgc 180
cacgatgact tgtgcacttg ccagtgtctc cattgtgaat gggcaacgag gggctgggtgc 240
aaacgaaccg ccaccaccca ctgcacagtg ggacggatac ttaaatacatt agattcaata 300
ttaaacagta gattaaaatt aatagttttc ccactttatg tattatagaa taagttttcc 360
ttttgaattc 370

<210> 852

<211> 748

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(748))

<223> Area matching *Drosophila* Genomic sequence

AC005894.

<400> 852

tgtgagtcga ggtgagccaa atacgaacca tccggaccga gccgagccaa aacgagcccg 60
actatgccag ccgaactcat taaaaagccg agcggcattt aaggatgcgc ctgcgcagca 120
atctcttata ctgcgcgaa agctctgcga aaaagctccg agatcgagcc gagcttggtg 180
acacttttcg ttgaaatacg gcggcacact tggcacggag ctcaagtact gccaagtggg 240
cagtgtgagt ggtgctccca gggaaggaca agccttctgg agaattggaat ggaaagcctc 300
agccggaaat ggagccctcc agtcagacca ccaagatcat ctccggcatgg aaatggaaat 360
ggatgtagag gtgaagggtg tagtggaatt ggtgatggag atggagatgg cagaggaagt 420
gagccactct agacacgaat cgtgaatcag cggcgcattc aacgtcaaca cgtaatcccc 480
gcaaggactg actcgttctc gtcgtcctcc tcattctcgc cgaggtggag gcatcataat 540
aatgcccccg attaaagaac aaaaagccag gctgaagtgc tgcaagtcatt ttgtgtgctc 600
attgtgcaaa cagatcccg gtccttggtc ctggttctcg cgccggaaac gctttaagac 660
cccgccagcc gagggcttag tgcgggcaca taatgtctgc taatatttga aaatgcgtcg 720
cattaattga catgaaagag tcacgaaa 748

<210> 853

<211> 535

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(535))

<223> Area matching *Drosophila* Genomic sequence

AC005447. Matches in area of 239AA predicted
protein. Sequence similarity to C.elegans gene
AF002196.

<400> 853

gtgagagcca ttaaccaaga gaacagtaat agagcgcatt ctctctttcc atgatcctct 60
ttagcttcat cactctcaca tacataaaca caactttgca tatgtgtaac ttctgtattt 120
ttaacagttt caaactaaat gcatatgcca taaaccatta ggtttgaaca gaaagcatta 180
aaagtataa tcccataata aatgtctact tttggcagtt ttccaggaca aaccacccac 240
tccgccatcc gccgaccagg aggcagccca gctcttggaa agttccggag cggagcaagt 300
cagcttcatg cagtcgctga agaacctgat gaccaaccgg aacttcatct tctgtctct 360
ctcgtagggc atcaatgtgg gcgtctttta cgccatttcc acgctcctca atccggtacg 420
aacatacttc gcatacttcc actcgattaa tgagcggctg ctaatggggt cttattgctg 480
ggatctgttt ccaggtgggc tgaagtatta tcccggcacg aagtggacgc cggac 535

<210> 854

<211> 581

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> Complement((1)..(581))

<223> Area matching Drosophila Genomic sequence

AC005643. Matches in area of 242AA protein.

<400> 854

gcaccagcca gatgggaaac tgtgcggcag tgggtcgaag agccaatgct ctcgaaaaat 60
ctatttagtt agctattaat tatccacttg atttctaaat ataaacaatg gtgttcatta 120
aagcagggaa gttttaatgg ggtagtagg tcagtcaagt atttattatt tagttttggt 180
ttttattaac tagctatgcc ttcataaata aaccaattgc aatagtttag ttattatata 240
gattttttga tatttaatat atgtttctga ggtagggat ccaaacgact atgcttagcc 300
atctgcaaat ccccttcacc ccatatgagg tcagtttgct gtccggcaca gctgggttatt 360
tatttttagg catcgcaatt ggatttacia attaaatgtt tctgccccac gatttgtagc 420
cgcacttggt ccaactgcct atagtattcc atatgcatgt gaatgggggt tgtctatagg 480

ccctcggggg cctctaagct tgctagcggg ggtggttccg ctataattct gggcacgtct 540
tatgactgcc aggggtggtg aatagaccat ttcattacat c 581

<210> 855

<211> 342

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(342)

<223> Area matching *Drosophila* Genomic sequence

AC005554. Matches in area of ORF with sequence
similarity to Rat fatty acid synthase.

<400> 855

ggtcagaatg ttcggatcgt agtgattcat cgtggaaatc atgcgagtac cacgcgagta 60
aaactggaaa cacgacggaa cttctccgat cgtttataag ccaattactt tgtgagaaat 120
gcctcgcgat agtatacatt tggaaaatta tcttgattga gacaatgttc tgattagtga 180
agttcgaccg tactgaatgc gttcattatt cttaaacaat caatgcgcga ttgctacgtg 240
tattgatagg attagggat atgtacatta agttctacag gataattcat cagcataatc 300
cgtacgaaac tacttccttt ccactagggg cgctttccgc aa 342

<210> 856

<211> 77

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(77))

<223> Area matching *Drosophila* Genomic sequence

AC004532. matches in area of 1145AA predicted
protein. Sequence similarity to *C. elegans* gene
AF067608.

<400> 856

agctggccca gtggctttta ttttcgaccc gctcgcagac atcagttgca gttcggaagc 60
ggaatcggat gatgcgg 77

<210> 857

<211> 496

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(496))

<223> Area matching *Drosophila* Genomic sequence

AC007186. Matches in area of ORF with sequence
similarity to Human YL gene.

<400> 857

gtctggctta gtacattacg tactctggtc acattgcttt agtgaaaaga aaaacgaagg 60
tataaacttg tagaactgcc gtctaaaagt gaataattta ttgcaatcgg tgctaaaaag 120
aatgatatga gcttattaca ctgcagctaa ctaatgtaaa actcttcacg tagaagtggc 180
cgaactgtta gccgttaatg aagttagagt tctttaggag gacgctgcca acgcgacgtc 240
gctgcgggaa agagatggaa agcgttagcc ggcgttcgtc cgaaatttct ccgctattca 300
actggctttt gaagcctgga gtgagcataa attaatggtc cgcaccttaa ttatcgcggt 360
gtcgcaatta ttgtgctgtt gcagtagtgc aaagtgcggt tcgtgcatat gtgtgccgtg 420
tcaagtatta acgggttggtg tattccgccg ttctgcactg gtaattggtg gcagctatag 480
ctgcactttt ccataa 496

<210> 858

<211> 582

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(582)

<223> Area matching Drosophila Genomic sequence

AC007176.

<400> 858

```
gcctgtttta tttacgccga aagcttaaac acaagaggcg aaaacaaaac cgaaaccaa 60
atctaaaaaac gtgtttcaaa tgttcctatc tgtgttgtgt ctctgggtcc agtatttggg 120
gtttggcgta caagcatgtg gatatggata cgaacagAAC ggaaagacga aacataacat 180
atcgaatgct atttactcca tgtgtcttgt ttcacgctcg atttgcgtcg ccagcagagc 240
taaaaaataa aaactacgc ttactgatta aaaaagctgt cgccgggctt tatattttgc 300
gtcgaactga ttgtgtgcag tgattactcg gaagcgggaa ttagaaagga ccccggccag 360
atattttattt gattaaaaaa tgcaaaagca tgctgctagc aacagaaaag agaattgtt 420
taaattaatc ataaaatagc actagttttt gactagttt acactttata ctttacccta 480
aacaccagct cgggcaacct ttttgaaaac tcgagaattt actggttata aaatagggtc 540
actggaccct aaacaaacag gaaggggtga acaattataa tt 582
```

<210> 859

<211> 483

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(483)

<223> Area matching Drosophila Genomic sequence

AC004423. Matches in area of 604AA predicted
protein. Sequence similarity to C. elegans gene
AL0214481.

<400> 859

```
gttccaacca ggcagcagta acaaaactgg atgatgccgg tgagcagaat gtagccgagg 60
tagatgtcca ccagcttcag tcttgggcgt attctgcacg tagtcgttgt agaacttgga 120
aatgacgctc gacagctcca ccattttgct attttatgtg atatttgtcc ggatatttaa 180
ggataaaggc gctttttaac aaattaatcg cagacacgct acaaattggg agagaactca 240
aaagtaggac cgttcgtcta gtttgaaaat aatactgata gctttatcga tgaaggcgca 300
```

```

agtacagtgg gcaactcaata ccttgaagtt taataaagaa taggtttata tattaataaaa 360
tttttgtggt ttagttaaaa ctaaaacata acaaattctta tagattaatg accgctatcg 420
attttttttt aatgttgcac atgtttgaga ggtaatggta taatttaatt tatataaaaa 480
gaa 483

```

<210> 860

<211> 560

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(560)

<223> Area matching *Drosophila* Genomic sequence

AC005811.

<400> 860

```

gtctgccccca tcttttgtgt gccggcagcg catgtgtacg ttttaactttg tgtatgtgtg 60
tctctagcgg gtgtgtgtgg agctgacttc ggtgctgcgt cttcttcttc gtggtttgct 120
tcgccgccgc tgtcgtcgtc atgggtgttg ttggtttgtg caaggcgtt tgcgtacaaa 180
attcaacatt atttgaaggt cgtcctttgc ttattctgcg cgtcgtttt tactcgttcg 240
ctctctcttc ccagcggggc ttttttttga atgtccctct ctgctcgtgt ctcgattttg 300
tctttgtgca gtgcgtgggt ttttgtcttc gctaaacaca tcgaatggtc ctagtgtgtc 360
ttaaagggga aagaatttat ttttaagtctt ttgatttatt agaattgggt cctggaacac 420
acttcaccgg ttattaagct accaaacatt cattggctcc aaaatgggtgc tttccaaaca 480
aagaagggtg attcccaggg aaacataaaa ggtataaaaa aataaaagac cccaaataat 540
ttcttaaata cccatgctga 560

```

<210> 861

<211> 596

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(596)

<223> Area matching Drosophila Genomic sequence

AC005653. Matches in area of 528AA predicted
protein. Sequence similarity to C. elegans gene
U40420.

<400> 861

gttgagacaa actgataagg ataagcaaag atcactctct tgatgctctc tttgcacaat 60
tctcaatcgt tatgatatcc tttcgatatg ccattgctta tgctgtgacc ttgaacttgg 120
ctggacgaga cgggacagtg acaatcaaca gttccatctt ctgcatttta aaatgcattt 180
aagcagctct tgcagcacat ttcgcctgcc acaaagtgcg ggcagcatcg caattttgtc 240
gcgcttgggt ttcgtgtcca cacatataca tatgtatatg catgtatgta tgtacacaaa 300
tacataccta gcactatagt gcaactagcc ctctggttct tctttctatg tggttgctgt 360
tgctgctttt ttcttgtggg cggttaacgc tcaagcgggt cgaacgccc tggtgcgcc 420
cttcctgcc ctcccacct cgccagctct ctggtttttc gcatgatgag cttgcctggc 480
tgctgcttg gtcttgggt tctttacacg tcttcaacg acgttcgctg gtgggggcc 540
cgctttgctg gtgctggtgt cctggtgctg ctggtgctgt gctgggtgtg gtgggt 596

<210> 862

<211> 539

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(539)

<223> Area matching Drosophila Genomic sequence

AC004516. Matches in area of 17300AA predicted
protein. Sequence similarity to C.elegans UNC89
gene

<400> 862

atcatgcccc tcattttgtt ttaacaaaaa tttgagtaca agaagtagaa aattcgatgg 60
tgtgctaaaa ataacattgg gccacagctg ctatcgatta tcgatatatt cttactcttg 120
caagaatctg acaaaattag ccaagacact aatcaccact gcttggcaag cagtttaatg 180

ggcgccaatt tcgaaatgca atatttttta ctcaagtcaaa gtgctaaagc atattatctt 240
 tttttttcaa cagatatact caacaaaagc cgcattggata aagtgcacac gagacatggg 300
 taagtccaag cttattatca agatatgttg tcattaacaa gctttaacaa tttatttagca 360
 acatcgagac ccttccccga ttcgttcgca acttgcgaaa tctgcgctgt tgcgatgggg 420
 atgcgatatc gctggaatgt cacgttgagg cccgatccgg agcccgttca tcatctggga 480
 aaaggatggg catgttgtgc ccagcgatcg ggactacgtg atgtccttcg atgggacca 539

<210> 863

<211> 505

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(505))

<223> Area matching *Drosophila* Genomic sequence

AC005285. Matches in area of gene with sequence
 similarity to guanine nucleotide exchange genes.

<400> 863

agctgaaaac taaaagtccg acgcgtctta cagtgtgacc acaccgctca gtgataaccag 60
 gttttctata ctatctatga ctatcgctga attgcggtat ttaaataccg attgggttgg 120
 atagattgtt cactaagttc ctttttaata cgctagtggc gccactgctg tttcaaaaaa 180
 taccgctga tctgggaatc gggtatttct gctttatgtt ttttaaaaca tttatttata 240
 gatggcgctt tgggtatttt tattattttc atacattacc gttatcaatt tataaattgc 300
 aaacttttta aaacaaagtc aagtttgccc cagaaaatcg aaatgctgtg tttttaagga 360
 tttttcttta tttataatct aatggcaatt tcttccattt caaaaagcgt acaattctga 420
 gtttcatctt tagaggtctt ttataactgg gcaatgtgct caacgatttc tttottgctc 480
 tacttttggc ttattatatt ttgag 505

<210> 864

<211> 504

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(504))

<223> Area matching Drosophila Genomic sequence

AC007137.

<400> 864

```
cgcggtatcgc tcggctggcg gccctcatt taccgttoga aactcgtcta ggccagagca 60
tctttgcatg tgttcgtgat tctgtgtgag cacgttgcgt ggatcgctct acattaagaa 120
agaagtgtat tagcttcgat ttattgcacg gttgcctagg cccctgcttc tgcctcggtc 180
gctgcctctg ctggcgtcgc tgatgcagtt ggcgtcgtcg tcgacgctgt ggattgtgag 240
tctcgcgtgg aagtgggaat catcactggg ggatcgggga tcggtctttt atcgttgtgt 300
attcattcag agcaccata cactcgccga agacgtcgtc tattttgcgt ttttcccttc 360
tgttatgttt ctgagctgag ctgctgctct tttcttagct tttcgttatt aggaaatcga 420
aaactgaagc tgcgactgcg actgggggtct atcatcagtc ccgtgagacg gtctcaaact 480
attggtcgtg gtggcgcttt ttgc 504
```

<210> 865

<211> 191

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> Complement((1)..(191))

<223> Area matching Drosophila Genomic sequence

AC005643.

<400> 865

```
gtgcgagcgc ctttttgaga aaaaccaagc gaaaaaagtt aaatcgatag cgaaccgcgc 60
cactgaagcg ggattatcta acacggctta cagtccgttt cgcccagaat cgcgacttta 120
ctttccactc ttgcacttg tctcgatttt tccagctacc tttgcgctcg ctaaaaaaaaa 180
ctctcgaatt c 191
```

<210> 866

<211> 468

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(468)

<223> Area matching Drosophila Genomic sequence

AC004642. Matches in area of gene with sequence
similarity to mouse lysophosphatidic acid
acyltransferase gene.

<400> 866

```
caggagacgg aacggcttct tggtccactg ccaatcgttt tgaaagggtt gaatgaacgt 60
gcactgaaaa caaaaggcac atttacattc agattatatt gttattgggt atgtgttttt 120
gacagacctt tgcctgcact tattacttaa atcaacaagg cacatttaca atcagtttat 180
attgttattg ggtgtgtttt tgacagacct ttgcctgtac ttattttcac taaacaaaat 240
gttataaacc aataaataat aattgtagt ctaataattt atagtctgat attatggaac 300
acaagtgtgt gggctataca cacaccataa tttaatatct actttgggtt gtgccttatt 360
aattacaaaa tatagaataa atcttttagct atagctaaag ggaaatcgac aaaagtcgta 420
tcggtttgcg gaatacccct gggcattccg caagtgcagc cacgaaac 468
```

<210> 867

<211> 578

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> Complement((1)..(578))

<223> Area matching Drosophila Genomic sequence

AC005749. Matches in area of 1481AA predicted
protein. Sequence similarity to Human KIAA0596
gene.

<400> 867

```
ctctgggggtg gaccttggtg gtaagctcat gtttgaaacc atgtaagggt tcaagtttac 60
tgtatacccg tgcccagtcg cccaaaaaat atgtcgtaa tttaacgttt agctttaagg 120
aaagttcacc cttagctgga cttttggggg ggtggctgcc caactgattg tgtcccacat 180
gttggccgat tacgtcacct gctgcgcggt catttcttcg taggctgtaa taaacaccga 240
ttgccaaaggc aattttaaac gatccgtaat tgactcacac accggggttt ccgaacttta 300
tttttgttca gtaaagtgtg aattatgctt tattacatgg ctttcaatat ttcttaggtg 360
taacaataca caattcctgc agttagtcgt tttagtcgct tatagatgag gatattattt 420
ggttctgaat gaagtccatc ccatacatat atatattata taggttggga gtcttggtat 480
cctggggcat atgacgttgc atatgtgcag gactctgaag gttagatttc ttgacccaaa 540
tctttgcgca acagaaaagt gaagccttag tcatgggc 578
```

<210> 868

<211> 598

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(598))

<223> Area matching *Drosophila* Genomic sequence

AC007185.

<400> 868

```
attttgctt tctgtctgtc tgggttggtg cgcctagaac tttccatcaa aatgctgcga 60
caaagcaaat gggccccaac attttgaaa acccgaataa caatatgctc ttttttttac 120
gaaattactt ttctatcggt atatggtatg tccacatgta tttaaacaca tagctgtcaa 180
aagtgtcgat ctaagacttc cgacattgcc tattgaaaat taaaatgtat gattttgtac 240
atatttttct ttttccattt tcgatttcca ttattttccg tcaaacgcct acaaagtgtca 300
aaaatcgaat gttgcctatt ggggcatccc gagaataaga gttcaacctg ggttggttat 360
tttttgttgc tcccgtgct gtttttaagt ttctcaact acgccgccca atccccctc 420
cactatcact ccgcgctat cgccatctct tttccgtgc ttggtgctat tgggtgtgca 480
gctgcttttg gtggttacgc attcggagca aaatgggtgcc tgcgtgtgtg tgtgtgtggt 540
gaaatgagtg cgctgtgtgc ctgtttgcat ggctggataa taatttggtg aggcaaat 598
```

<210> 869

<211> 634

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(634)

<223> Area matching *Drosophila* Genomic sequence

AC004340. Matches in area of predicted gene with
sequence similarity to human sec24 homologue.

<400> 869

```
tttcgagcta aacgaacttc cacgtcagtt ccctaattcg atcttttttg ctcttttttgc 60
cttgccacgt aagctatcgg taatcggcag tggaaaatcg aatgtcaatc gattgtgctc 120
tttcggctgc catcgccgaa tcgataatcg tgttgaactt aacagcgctg ctgttagcga 180
acagctgcga gttatgttat gtgtaagggtg gtgcaataga atgcagtgcg gtcattaaat 240
acgttggggtt aaaataaata agtgaataag atataatcaa agtacattta aaataaatat 300
gtatattttc acaattttat caaaatattc cttacattca ggggtttata ttaaatttaa 360
tttctggctg ggaggaaatg ttaccaaagg ctacagaaatt tcctocaacc tgccggccca 420
agccctgggt gtccaccgta aatgaagtcc ttccgaatt ggactaccgg gttgcatgat 480
cttggtaaat ccgcagtcct gtgtaacgct ctatttcgct actttgaccc gtggggcattc 540
aacttgccgc cacccttcgg ctgggttcga tgataaagct tcatgaaagg ttgggggatcc 600
cggaacttca ctctcagat aatccttaaa gaaa 634
```

<210> 870

<211> 415

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(415))

<223> Area matching *Drosophila* Genomic sequence AC5456.

Matches in area of gene with sequence similarity

to Human GMP synthase.

<400> 870

```
tttcggcttt aattcgcgaa aaaactgcag gaaatccaaa aggaaagtc ctggaagcgg 60
ccataataac gcagccgtga aaaccacagg gatttcacgc ccagctgtgt cgagcagccc 120
tggataactcg gaaaagaagc tgcagcagcc gaagaaattt tgagtgtgtg cgtgaggaag 180
gaaaacgggg gaccgcaaac aacggatcgc gaatttcgtc ttaagacaaa gtcttgcgct 240
gcttgtcacg gtattccacg gccttgccga cggacttccc ggttctggaa aaccgcagcc 300
aggctaaaac gagagaaggt gagagtcgca atatggcgaa aaagatcccc gatcccagcc 360
aaatcgccat gcggtgctgc tccgccaca attccgaacc ccgcccgttg aattc      415
```

<210> 871

<211> 198

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(198)

<223> Area matching *Drosophila* Genomic sequence

AC004375.

<400> 871

```
attccaggga tacagataca cacagacaca cacaatacac tggcacacag gggcacccga 60
ttccgcggtt tgttttgcgg ctaattgttt atacagcgca gattattctt cgcactggat 120
gtatttgttc atccggctat tttcgtttgc ttttgctccg cacgagcaaa tttgcagcgc 180
acacgcagcc gagaattc      198
```

<210> 872

<211> 316

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(316)

<223> Area matching Drosophila Genomic sequence

AC005472. Matches in area of gene matching Human
NAT1/death associated protein.

<400> 872

```
agtgaatca ataaaagtga ggagctcccc tagatgccat agtcgctcca tcgcggtaat 60
aattttcaag agcaagcagg gtcgaaattc gtcaatcaaa acgttaattt gcatgaatca 120
tttcgagaga aaaaaaaaca caaagaaagt ttacgcgtat gactgtgtgt ggtaggtaca 180
cctattttgcy ccacaaaatg gcgtcggcac cgtcggaaaa tctgaaatgc tgtgtttgga 240
ccgttgcccc ctgcctttgc ttggagttat ctacagtgcc ccctccccgg gggaaagaca 300
gccctctcat tgggaa                                     316
```

<210> 873

<211> 495

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> Complement((1)..(495))

<223> Area matching Drosophila Genomic sequence

AC004154. Matches in area of human rabt
geranylgeranyl transferase.

<400> 873

```
agtgaatcca atcgagcaca gctgattcat ttgcgcgatg gttggcaacg cggcagtggc 60
ttatcaaaca gctgatcgac gcaggggtgt agtgttaggg ggttactata accccatcca 120
aaaataaaaa ttaaacttac ttaaatttca aatagctagt ttattttatt caaaacacat 180
gcacactatt gcaccagcag gctggactgc ggatccggct cgtcgatgct tagggagact 240
atgtgctggc cgggaaccat gacgttgccc agcaggcgcg gtcctggcc ctccaccaag 300
tactcggcgc acatggacag cacgatgttg gcgtcgcggt ccgtgcagtt gaagaatccc 360
accagcacgc gtccgtccgt aatcacgac cgcagaactc gaccagccac ttctggagct 420
tctcgcgtcc cggcgtcaaa ctggcatcgt catctggtgc ggggccgtcg ttgtgatgcy 480
gaaggctccg ggggt                                     495
```

<210> 874

<211> 116

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(116))

<223> Area matching *Drosophila* Genomic sequence

AC004328. Matches in area of gene with sequence
similarity to Mouse BOP1.

<400> 874

agtggggcga agagtcccgga gctttattct ctttttcgga ctgcgcgaca tgtcttaccg 60
tccgttctct cgcgtctctc gctgtcagt ccctctctg tgtgtaccag gaattc 116

<210> 875

<211> 581

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(581))

<223> Area matching *Drosophila* Genomic sequence

AC005112. Matches in area of 407AA predicted
protein.

<400> 875

gtgcgtcttt ttctgcagcg agtttcgtgt tctggtttta tttctctga ttctgattgc 60
gattgtgaat ctggttctgt gtgaatttcg tttttattaa taaaatgcac aacttccgtt 120
attaattttg caacgacaac aattgctgcg tgtgtgtgtg tgtgagtgtt tgtgtgtttg 180
tttgcggtt tgtgacagcc gctgacaggc gaaaagcaaa agcaacaaag tgacaagcat 240
gagcgtgtgt cgcctaggag gaaaagcgga aaagcagacc gaaaaataat aacaacaaaa 300

```

agtgggcgac aaacgggcgg tgggcggaac tcgaacggta caacctgtcc gcttttttac 360
caccgccccca cttcccccggt tttcttcaac gatttctgtc ctgtgcacgc gactcgcgct 420
atctcgctct ttnngntgcgg ttttttttct tgotgntagc tgattcattc ataaaaatcg 480
ggttgtaaaa aaagaacagc ggnacagaaa aaacgcgctg atttatttat tatgccattg 540
ccgacgcgtc gcgctgagtc tgggtgntata gttccctaga c 581

```

<210> 876

<211> 506

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(506))

<223> Area matching *Drosophila* Genomic sequence

AC004367. Matches in area of 387AA predicted
protein.

<400> 876

```

ttcctcatat tctgggtatt tctcctaata cgaatataaa atctatctac tggcacacta 60
ggtgaggaaa ttatggacca caaaagatta cttcatatgt gcagtgagag tagtagaaac 120
catccgtcat taacaaaaag aacttaaatt taaaacgtta ttattttatg tatctgtata 180
catatatggc taaacttgat taagtcttga catggaaggc atttttggca gtgcgggagac 240
acagcacttg atcaaagtgt atagctccca atgtggcatc cacagttggg acagtagtgc 300
tggacactct tgcagtagtt gatgaagtag ggaaggcaga tgaagggcca gcagctggag 360
aatcaggtta gcaaagttag taagcccgtt ggtatcctga cgccccactc accagcagat 420
ataccaggtc agacgcacat gtgggtcttg ccggtggggg acgtggcaga ctggtggtga 480
cctcgccctg caggacggac acttac 506

```

<210> 877

<211> 411

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(411)

<223> Area matching Drosophila Genomic sequence

AC005472. Matches in area of gene with sequence
similarity to Human NAT1/ death associated
protein.

<400> 877

```
gtgtgtgctt tgcgcactat cgatggggga aaaagaagag tgcgttttca tgggttttct 60
caagatattt gctcttgaag ccccgaaaaa ctagtaaaat aaatactgtt tgcaatgtgg 120
gtgtgccact tggccagtta aacatgcaga cagcgacaaa cacttgtgca caagagccga 180
gccgaacgct cgaattgagg tcaaaatcat ccacaactgg gtctgtgcgg aagcaggggg 240
ggctcatttc tcaggtcggg gtcgacgcct caatgcagca gaggggtggg ttttcgcatt 300
gggggggtgt taagtttttg cttatccctt ccccgacga aagactacat tattgcaggc 360
ccaaagtctg tatgtatgga tgtggtggta ctgcacaat gacaaatcgc a 411
```

<210> 878

<211> 492

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(492)

<223> Area matching Drosophila genomic sequence AC007121

(41693-21184). intron of gene at
22511-56594bp(complement) coding for 365AA
protein.

<400> 878

```
atgtaaataa ttataataga aagaccgaac tatgtcagta gtgtgtatgc acaaagtgtg 60
ctcaaaataa agcgaaaaaa ttgtgaaata ttttcgtata aaaatactca caccgaccg 120
agtctgattc tattcttgat taaaaacaaa aagtgaaaag agagtggaac agagagagag 180
agagtgcaga caaatggaag aaacaaacaa aacgcagaga aaaaaattac caaatattcc 240
gagaatactt ggcattaagc aatcgccaaa agactgggcc gaggggaaga gatcgcttg 300
```


gaactaggga ctccaatgcc gaccaactaa cacactggcc agccctggtc tgcaaccatc 360
tctatctcgc ccgccgtcca attagtgcag cattcttaaa gcggccgagg caactttctt 420
ctactcccca aacgagtttc agccacgcac caacacacca acaccaatac cagcaacaac 480
atgacggatg gg 492

<210> 879

<211> 291

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(291)

<223> Area matching Drosophila Genomic sequence L49405.

Matches in area of 626AA predicted protein.

Sequence similarity to human NAT1/death associated
protein.

<400> 879

gccactgcaa taatggcccc aaacgacgat gccaatcgt gacgccagtg acttcggctt 60
tcggccgcct ttcgggtttt cgaaattcat ccgtttcaga gaaggaatga actctcggtg 120
ccggagagtt gttcactgga aagtctact actataagct atttactctt ctcttacgct 180
taagattata tggattatta acatctcatt atgcgttgaa ccaataagtg tgttatatct 240
tcattaaatt aaatattatg tttaaaatca aataattgcg tgatttaata c 291

<210> 880

<211> 454

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(454)

<223> Area matching Drosophila Genomic sequence

AC004658. Matches in area of 394AA predicted

protein.

<400> 880

```
gttcccggtta tctgatccag acatataggt ctaaagcgct ctccggggcgc tgcctagagc 60
gcgactcgcc ggatggaaac cccgtttaat cgcaatcaca agccacagaa agtaaaagca 120
agcgaaaagc ggcgtcgcac acacacacac acacaacagg gagtaacgcg cagaacgaaa 180
caacagaaaa tgtgtgtaat acaaaaatcc gttgacgcgt tcgcatttgg ttttagcaga 240
ggaattgtcg agcgttcgta cgtacttgca tacatatggt atgttatggt actacatgaa 300
tgttaccata tacacatggt atgttacata catacatagc ttaccaaagt acttgtagat 360
cgtttccttg gcagaaatac gcctgcactt cggccatata agcttcaatt aatatagggg 420
gttcaatccc cgtatcgga caatttcgaa gaat 454
```

<210> 881

<211> 376

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(376)

<223> Area matching drosophila genomic sequence AC007757

(38974-39348bp). This sequence also matches

Drosophila EST AA951801 which has sequence

similarity to transcription factors.

<400> 881

```
ggttagggta aaattaaagc cgaatattat caatcccatt ccaaagttca attttgtgtc 60
ggaaccatag taaattaatt gttccttgct attaacaacg aaaaatgcat atttagctat 120
tgcagttgag acggcagcta ttgcttcttc accacgctgg gaagttgaga atcgcagaca 180
aataaatctt cctcctcctt cgtccggtcc gaccatcaac ttcgatttca atttcataca 240
tttcgtttgc gtgggacaag cgagcgacag cagtctctgg agtttagcgga tttatattgt 300
ctcgatttgc tgctgctggt gatattgatg atgtgtttgc tgctgtctgt tgttctcgt 360
aggggtgatt gactga 376
```

<210> 882

<211> 597

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(597))

<223> Area matching *Drosophila* Genomic sequence

AC006091. Matches in area of 564AA predicted
protein. Sequence similarity to yeast YII3
hypothetical protein.

<400> 882

accagacaa tacgaatttg ttttgctgcc accgctgcat tatcagtaga caatgaattt 60
gggggttacgc tttctggcaa acaaagtaaa agcgtgttgt ggctcaaaaa agcagcatta 120
attagcacag acgaggtcaa tgaaatagca atgatggcgt caataaaata tatgtaaata 180
ttttaatata tttatttaaa ttggaataag taaatagcag cctgttttac tttccgaaac 240
tcaataacta actttaacca ttccattcct actttaatca ctgccactgt acactttaag 300
atttgtttga atacgtatgg tttttttttt tgcaaacctg tccgtttata catacatata 360
tactatatag cagaactgaa acaataaaca catttctaata gccacaaacg aatcgccaat 420
gccgatcgct tttgggattc gcataaaccg ctcacgaatc gcgtcaaaat cgcgcgtag 480
ctgggtggagc ttccaaaaat tcccccaaac caaaagccaa tttaaattcg aaaaagccat 540
gatttagcct gatgtcttgc aatttatgcc ttcgacattc gttagtcccc cattttg 597

<210> 883

<211> 498

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(498))

<223> Area matching *Drosophila* Genomic sequence

AC005720.

<400> 883

ctgcagacga agcgccgaag cagcgtcggt tgacgtttct ttttcacatt ctctcacttt 60
tgctaagact ctacgctgg cggtcgggg tgacaaaggc tcctttaact attccactat 120
gctcaagttt ctggtaagtt ttccggtttc ctgattcaca cctgaaaatt actacactcg 180
cctaagtata cggtagcat atcagatacg agatacaact tttctgtggt ttttgtggtt 240
gtgttgcttt tcgcggcgat gacgcgcccc tgcacagtgg tgaaatgtgt tgtctagggg 300
ttcaaaatca aaaccaatta tttgattaaa tattaatgat taatataaat gacaaaataa 360
aatacatctg aaaatacctt cccaatatct aacttcaca aataaaaaaa tagttattaa 420
aagttttaag caaaattcca aaatattctt gctcggataa aacaagagtt ggatggtaaa 480
cggtagaagt gcgccaaa 498

<210> 884

<211> 375

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(375)

<223> Area matching *Drosophila* Genomic sequence

AC005814. Matches in area of gene with sequence
similarity to Rat NAB1 transcriptional repressor.

<400> 884

tgaggaacct tttggaaccg gccgacgaca gcgaagccaa cgaagccacc cgaagtccac 60
ccgatccggg cgctttcgtc tatcagccgg ggcaaaaaaa aaagggttaa aatcagggat 120
aaaaacaaaa ccaaacaat tggtcggagg gttagggacg taggacattg gtttccagat 180
ttgagggtta ctttttatct gccgatgctc aagattctct tattagagaa caatcgggtc 240
ctctctctct tcgcaattga gcgactttga gtgagttttt gtgctccgcc tcttgagaag 300
cactcaaaga tttggaatgt cttgggtgcc ggagagactt tccaaatgat ccttttaatg 360
tttttttttg gtgaa 375

<210> 885

<211> 486

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(486)

<223> Area matching Drosophila Genomic sequence

AC004713. Matches in area of gene with sequence
similarity to CD36 genes.

<400> 885

```
tgccgtactt tctgtgectg tgccctctct ctgcccttcc gctctctcca ctcttccttc 60
cgctctcttt tcacaacaat aaacaacaac aaacacgcgg aatgcgggat gagagccact 120
ttttagttgt tgttagtcaa ttgtttgcct attgaggaaa agcgcgcaat caatatcaat 180
tcgccaggcg tgcttgaata atttctcttc ttatttatatt tttctttgtg aatagggggg 240
tgtgtggtta aacaacaaac accaaccggt agcgtcatca ccgcacaacg cacatttcac 300
gagtgaatc aaaatcaaat gcgaaatgag cacaggctga aagcagcgac gtccgcagcg 360
cagtggctgc gcaagtttcg ctttttgccc agtctccatt ctctcttctt tctggctctt 420
cgcttcttga ttctttggat ttttcttgcc gcgctctggt ttggtgccat ttttctgtgt 480
cttttc
```

486

<210> 886

<211> 544

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(544)

<223> Area matching Drosophila Genomic sequence

AC005813.

<400> 886

```
acaaaccttg gttaatcggt aacattgctt acattaagcg gtgtaagaga gcagcactta 60
gagaattgta cactctttat cttgctcaat tgaacttga agagagccgg caactttgtt 120
tgttgcgacg ccaaatttca atgtcgacgt cgcagtcggc agcgtaagct ttcgagcagc 180
```

gaaaacaaca aacggatgcg agtaaagcaa aagagacaca aaaatgcagt tgtgaatcta 240
 gtactaagat taaattatta cagacaaacg taactttatt tgcactagaa aatattacat 300
 attatattat tatcttgtgt atatatatat aatacttacc gaacaccaag tactttacag 360
 tattcaagta tttcctttta acgtaattaa tgaaatattc attatcttta atcttaattt 420
 aaatataact aaacttcac tc aaatagga aggcgccgat taaaatcgga atagagatgg 480
 caaataaacg aatgggtgtgc tt tactaaag gtgagttgcg cagttgctag tagtgtgacc 540
 agac 544

<210> 887

<211> 549

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(549)

<223> Area matching *Drosophila* Genomic sequence

AC006936.

<400> 887

cgtttagctct tccgctcagc gaacccatcg ctggcacgcc cctcaacctg cagccaatga 60
 gtgaaatctg cggcactcaa ttctattcaa catggccgcc aaacggaagt cactcgaaga 120
 gcgagagagc gcgttgtgtg gcaagtgtaa atgtgtgtgc gtggctttcc cctgctgtgt 180
 tggtcgtttt gcagactttt tgcaccttta tttgtcattt gtgtgtaatt tcggaaaatg 240
 ttggcacatt atgacgctcg acgccagttg ggccgggggc gcgcgcttaa gtgtcctcca 300
 gggtaacttac ttcgtttagca gaagtttctc gccctcatcg tccttcgtcc tttgcggggt 360
 ccttggtgct gtggtttggt gctgtgctgt ggctgttgcc gtgcggtgcc gcactgtgtc 420
 gtttgccgat gtgtctctta tttcataac tgtaaattgc ttagatatt aagtctgctg 480
 tactagctgt ggatttccaa acggcactgt atgtgtgcgt gtgacagcaa aaggacgaag 540
 gatgggtct 549

<210> 888

<211> 306

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(306))

<223> Area matching Drosophila Genomic sequence

AC005425.

<400> 888

```
agccagagag aacttgacag agctgcatcc ggcgcgaaca aatcgaaccg gttatgtcag 60
atagaaattt taaaaatttc ttgtaaataa ataaaaatcg aagtatctgt aaacatatac 120
attgaaatta cctgagctct agtaacaact ctttaaaaag tagagaacct tacaattgga 180
atatataacg aaatacacac attttgcgga aatgtatggc tttctttcag tttcagcttt 240
gtttgccctc ctttttttta atttcaccag gttctcaaaa caagtttacc atcgtgcaaa 300
gaattc                                           306
```

<210> 889

<211> 579

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> Complement((1)..(579))

<223> Area matching Drosophila Genomic sequence

AC005720. Matches in area of 394AA predicted
protein.

<400> 889

```
cccacgacca ttagccagcc gcatcgcccg cgtcccggcc aaggggttgc tgagacccag 60
agtcgggggtc tggacgctc tttcaggctg ccctggccca catgctttcg togttcagtc 120
ctctcttaat ggggggctct cgtaccctca ccctcacaca cagaggcca cttgggtgtg 180
aaagttctgc tgggctctgt ctgtgtcacg cttatgattt aataagcaaa tgtgctgcga 240
aattgctgaa attgtttggc tgtccgtcat cccacaatc cgaatctcgc cccacgccct 300
gaaatcactg tccgccgtat ttcgcattga aatgctttag ccaatgcgtc acggaagaag 360
aaaagtgggc ggtagtccgt gcttgccctt tgattctcgt acctttaaat gcctttgcat 420
```

ggagctagtt cttgcctaataaatcataat aaaaagttct aggtctgcaa aaatctaaaa 480
tctcattcgg accattggaa tatttaatta tgttattatt atattaatat tcatagattg 540
tttccaagtgcaggtgatag agatttagaa aacgaattc 579

<210> 890

<211> 191

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(191))

<223> Area matching *Drosophila* Genomic sequence

AC004266. Matches in area of 931AA predicted
protein. Sequence similarity to *C. elegans* Zinc
finger gene. *Drosophila* EST AI259457 comes from
this gene.

<400> 890

gctcaaagtg agagacaggg agagagagag agtacacggc gtatgtgaaa gattcacttt 60
tacacatcca aaaaagagat gtgagttatt ttaaattgtag tattaaatta atctgaattt 120
ttgccatatt aggcaattat ttgatatcat tttttgatca tgatcttttg taaatattct 180
ttttggaatt c 191

<210> 891

<211> 264

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(264))

<223> Area matching *Drosophila* Genomic sequence

AC006936.

<400> 891

ggaaagaccc cgacccacac tcgtgtggcg cccataaaaa cgtcatcggt gcacataaaa 60
cccgacagca aacaatgcag cttgccattt ggctgccgcc gtaatagttc ttttaattgct 120
cacaaaagtc gtcaaagttc gactcctcca cccatataca taaatgtata tttaccacaa 180
gcataacccg tacaaggtaa agtcggttgc tcgttgctcg tttgggccca ttaatcactt 240
ggagtgtagg gaggaggctg gggg 264

<210> 892

<211> 537

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (488)..(536)

<223> Area matching *Drosophila* EST AI062190. This EST
comes from the *Drosophila* ferrochelatase gene.

<400> 892

ggccgcgcct tttattgcgt ttttacgaag caattgtgcc tgcattcggt ggaaaaacta 60
caaaatatta tttgatcgga ggaaacgaaa cactcgcagc aagcgacgag agcgaaatgc 120
agcgtgcaag agcgagactg caccacagtc agctttttacc gttgcacgca gcggtgatga 180
caagggaaag aaataaggac gcatgcgcga aaaattttctg ttggtcgctt gaagaacagt 240
atatacaaaa tattggtttc ggtttcaata aagagaaatt aaatggtaaa tgtgtaacaa 300
aaggaaaaat ttttaaataat ttagattact gttgagtaat agttggcagc tattttacac 360
acatagatgg cgtgacggtt actttttaca gaactctgtt acgtttggaa aaatcagatc 420
tgtgagatca tacattttgg tatttaaaact attttagcaa ctggtaacac tattcgacac 480
cggtgccatc aattttgggt caatttaaaa ggaactatgg ttttgcatat acaaagt 537

<210> 893

<211> 1068

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((4)..(579))

<223> AF104256. Area showing translational sequence similarity to human CRSP150 transcriptional co-activator protein.

<400> 893

```
actgggcaca atgggaaccg ccgagggcgg catgcgcaaa catatctgca ccgccattt 60
caactggctg ccacccagct ccggcttcaa atccaaacgc atgatctgta cgaaatcctt 120
aagtacctgg gcgggcaggt tcaacagccg gcagatgctg tgcagggaaat tgggtcggta 180
tggtggagct gccactctgg tgtcaaagta ctgctctata accagcagat cgtcctggct 240
aagctggaac ggcgccggat gcttgctggg catgggcggc agctgagaga ctttgagggtg 300
cagcgtctgc atgtgcatct gattcagcac cacctggcac tgcagtccat cgaccttgaa 360
gagcaccact cctggttctg tactgttttag ggcggtaacg gtctcctcgc tctgaatgtt 420
tctgtgcaat tgccttctca tataaacgca gcctagaaaa cgctctagag gactcatgtc 480
cggcacattg atatccttgt tcggatacgg actgggacga cacagagtct ccaaagcttc 540
atgggtgagg agagtaggaa ctgctccagc ccagggccga ttgagagtgc ctcgagagcc 600
tcctctatcc gtgccaccgg ccactcctgc tccaccaccg gtgctcttgt gatcaggact 660
ctgtccgggt cgtggagatg ggcgccggcat gctgggggat ccggggccaa tgttattcgc 720
cggcgacatg gcggtgaagg gagagtcctg gtggctctgc atgtagagcg tgttggtgcc 780
aggactatgg accatgtggg gactgggctg aggatttagc ggagacgacg gcatcaagcc 840
gcttggcgac ggatgtggca tatgtggcgc tggcggtgac gtcaggttga agttgcccgt 900
gtccctgggg tccactgccg ccacctgccg ccgcacttgg atgccgactg gcgggtgtgt 960
gcggatttga actggaaggc ggagtgtggg gggcaggaaa acgcagccac tgctctcggc
1020
gattgcggtc ccgcatttca gtacccaaaa tggtaggat ccaccaca
1068
```

<210> 894

<211> 597

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (101)..(597)

<223> Area matching Drosophila EST AI388606. This EST
forms a 1294bp contig with ESTs AI258281 and
AI258326.

<400> 894

```
gctgtggctg tagtcaagcg agcgcacatg agtcagattc gtagcttttg ttttgttcag 60
tcgagtgcga gttcttggcg attcagatac tcgctgccat ccgaaccgaa ctgaagtcca 120
agtcgaatct aatgtgcgta cttacgtgta gaacagttca agaaaatgtg cagacattca 180
acggtcgcat ttgtgtggat gtgtgggtgt agtgaagagt gccagcatta atcgcatttt 240
tcccctgcac gagcaccacg actagaaaat actcgacacg tctgtctgtt tttctgcttt 300
attgcttcta cgctattctg cttttccggt tcggttttcc tccgcttggc ctagtgaaaa 360
acaacaaatt tgattatatt gtgtaagtta tgtctagcat tgaaaagatg aaaagtgtca 420
ttcctataaa tacaccacca cctcgggaaa ggcactcgca atagagaaac tggccaaaac 480
ccaacaacaa acataacaaa caaaggaacc gcttgaatat aaccaactt tcggagtaag 540
gggctgacta aaaaggtatt agtgcgcaac catcatgact aactcaccac ccaaaac 597
```

<210> 895

<211> 491

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (1)..(491)

<223> Area matching Drosophila genomic sequence L49408
(58018-58506). No good predicted exons in this
area.

<400> 895

```
gttgagcgcg acagtgggag agagaagagc gcgcaaaagt acagatgccg ccacacacac 60
attttttact accacacacg tttcattgaa aaaacatata cacaaaagct aaggccgtaa 120
accactgca aatttgcgaa aaaaaaacg aaatgaaatg aaaactaata ccaacacatg 180
gcttaaaatc tgctgcgcaa atttttgggc gatggctctg tgtgtttcgt tccgtatgcc 240
aaaacgtttc gcttggtttc gtttcatttc cacaccgctt tttttttttt ttttttgctt 300
tttcccatgc ggcatttatt ggcaacctgc gagcaaaaga gagggcgact aggggttgtg 360
```

tgcaagggga gatggagcgc tacggcttgt ttatgaaaaa cacatgattt tttgtgtcca 420
acagtttttg ggggcatggg cgaagagagg aagcacagga gtgcgaaaac tactattccc 480
catagtttac a 491

<210> 896

<211> 475

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> Complement((1)..(475))

<223> Area matching *Drosophila* genomic sequence AC005714

(161048-161518). In space before gene at

162294-163466bp coding for 390AA protein similar
to human death associated protein 3.

<400> 896

gtccatccaa ggaatacggg gtttcggcac ctatgccgac gatcttcaga gtataaagtt 60
ttcctcgccg gttaccctga ttctgggcca gaacggatgc ggaaagacga ccggtggtaga 120
gtgtctcaag tacgccttga ccggcgagtg tccgccgggc agtgatcggg gcaagagttt 180
cgtccatgac cctaagatct ttgggctaaa cgagggtgcta gcgcagatca agatgcagggt 240
gcgggacagg ccggtggtgcc caagtgtcca tctgccgcac catgaagggtg tccaagaagc 300
gcaacaaaat gtcctttgaa acaatggact ccaccatcaa cttcctgacc ggcgctggac 360
agtcgaagcg cgaaaagcag gactctctaa gcggccgctc cgtggatatt cgacgtggcc 420
atctcggact tcatgggggtg tctccaggct attatcaaca atggtcctgg ttttg 475

<210> 897

<211> 461

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc_feature

<222> (1)..(461)

<223> Area matching Drosophila genomic sequence AC004375

(31191-31647). No good predicted exons in this

area.

<400> 897

```
cggtcaacca tccacagtgc tgtcgactat cgattgtttg tgttcgacta agatatcgga 60
gtggaatgtg tttggtttaa gtgtgggcat aaatcgatca atcgatcaac ttctatttta 120
gtacatattc aaattcaaac tcttccgtta acgatctaaa cggaaattta tcttgcttgc 180
ttcttttaat aagtataatc ttgaatatat tggcttgaag ttttcataag aaacactttt 240
atttaaaaac attttggcta aatttcagcg cctaaattat catcgatttt cgccgccaca 300
cccaaaggc agttctccca atggccctca aacctaaact ggtgtttccg atgcaggcag 360
ctcctccagc ttcagctgac ttgcgcagaa tgaactggtg ccgtttaccg tgcgcacca 420
gaagaaaggt atccccagtg aagtcctttt gactcctctg g 461
```

<210> 898

<211> 507

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc_feature

<222> (12)..(419)

<223> AF000177. Area showing translational sequence similarity to human CaSm protein.

<400> 898

```
gcatggacga cttaaatecg ctggcgggca cggctcacct cctggaagag gttgacagtg 60
agtaaatecg aatgaaagga aggccagtgc ttaaaaaccg gcgcattgca gagaaactga 120
tggtactttt gagagacgga cggactctga ttggatacct gcggtcctgtg gaccagttcg 180
ccaacctggt gctgcaacgc accatcgagc ggatacatgt gggcaacgaa tacggcgaca 240
ttcctcgtgg agtcttcac c attcgcggcg agaatgtggt gctactgggc gaaatagtaa 300
gctttactcg atacattttc aacatgactg attaacaccc tttaaatatg cgtaaaaggg 360
accgtgaaaa ggagcagaaa ctgccactca aagagatatc cgtcgatgaa atcctggacc 420
cccaacgtag ggaacaggag cagcggcagg agaaacaccg cctagtatcc aagcactaaa 480
ggacgagcct ggcccgtaga tgccaac 507
```

<210> 899

<211> 544

<212> DNA

<213> *Drosophila melanogaster*

<400> 899

```
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tttttaatga cttttaattg acttcaggat gataagagag ttcataaagg caagcaaata 480
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<210> 900

<211> 528

<212> DNA

<213> *Drosophila melanogaster*

<400> 900

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gcgattattg cagcggataa agcagctgat agcgtgcca acttgcgcac ggggcgatct 480
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<210> 901

<211> 521

<212> DNA

<213> *Drosophila melanogaster*

<400> 901

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gcttcgatgt gcatctcact ccgttcgtat tgctccgcga gattaaaaaa aacctatagt 420
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<210> 902

<211> 378

<212> DNA

<213> *Drosophila melanogaster*

<400> 902

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tatggtatgg gaatatgt 378

PCT NO : G800 / 03444

Tracey Carter.